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BIOLOGY AND GENETIC IMPROVEMENT

EDITOR
J. V. PATIL

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J.V. Patil

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Preface

Sorghum and millets – pearl millet, finger millet, foxtail millet, kodo millet, proso millet, barnyard millet, little millet, teff millet, etc. – are the main sources of food and fodder for millions of people living in the semi-arid and arid regions of the world. They are the primary sources of dietary fibre, energy, protein, vitamins and minerals for the poor people inhabiting these regions. The growing environments of these crops are characterized by low and erratic rainfall, poor soil fertility, poor agronomic practices, disease and insect pressure and abiotic stress factors such as heat, drought and soil salinity. These crops are grown under marginal conditions unsuitable for various other high-input commercial crops.

The research and development in sorghum and pearl millet is much more advanced as compared to other millets. With the cytoplasmic–nuclear male sterility (CMS) system in place, successful development and spread of hybrids have occurred in both these crops. Small millets in India are a group of six crops such as finger millet, foxtail millet, kodo millet, proso millet, barnyard millet and little millet. After years of neglect, small millets are finding a place in agricultural research agendas in many institutions in India. Doctors and nutritionists are increasingly recommending them as important in health management. Germplasm availability has vastly improved with the launch of the All India Coordinated Small Millets Improvement Project. More than 15,000 accessions of various small millets are now conserved. However, the rate of genetic advancement being made now, barring in finger millet, is slow in all small millets. Demand-driven crop improvement is the current thrust area. Also, millets, being climate-smart crops, have a significant role to play in the current climate change scenario to provide food, feed, fodder and nutritional security to the dryland poor. Teff is a very important millet grown in Ethiopia, accounting for 30% of acreage. Crop improvement has been very slow, and most of the area is under landraces.

It is felt that a review of research in sorghum and millets would help identify the focus areas of research for the reorientation of millets – from a forgotten crop to a smart and nutritious crop. *Millets and Sorghum* is designed to fulfil this requirement. The book has 14 chapters. The first chapter gives an overview of all the crops. The next nine chapters on individual crops – sorghum, pearl millet, finger millet, foxtail millet, proso millet, little millet, barnyard millet, kodo millet and teff millet – deals with the origins, available genetic resources, genetics, reproduction biology, production constraints, improvement techniques and achievements in each of these crops. Diseases – especially grain mould in sorghum, downy mildew in pearl millet and blast in other millets – play an important role in reducing yield in millets. The research that has been undertaken in enhancing resistance is discussed in a separate chapter on diseases. Except sorghum,

insect pests are not a major problem in millets, though incidences of few of them are reported on a small scale. Several pests – such as shoot fly, stem borer, aphids, shoot bug, midge, head bugs, etc. – cause yield losses in sorghum. The chapter on insect pests covers the research that has taken place in deploying insect resistance. Sorghum and millets are renowned for their nutritional benefits. Their nutritional profile and marketing aspects are discussed in a separate chapter. Biotechnology has emerged as a new tool for increasing the precision of plant breeding. Chapter 13 deals with the progress of biotechnology in sorghum and pearl millet, and its initiation in small millets. The success of plant breeding will not make any difference to the average yields of the region unless it is backed by an efficient seed production program. The private seed industry in sorghum and pearl millet is a success story in India mainly due to the availability of hybrid technology. However, there are still several issues to be addressed in these two crops and new strategies to be developed for sustainable seed systems in small millets. These are discussed in Chapter 14 on seed systems.

I am extremely grateful to all the authors and take this opportunity to sincerely thank them for their active cooperation and contribution in this book. I also extend my gratitude to several others who played important roles in the completion of this assignment and for their encouragement – noteworthy among these are T. Mohapatra (DG, ICAR), S. K. Datta (former DDG, Crop Science, ICAR) and J. S. Sandhu (DDG, Crop Science, ICAR). I also gratefully acknowledge the help received from Harshal Gawali in photography, and the secretarial assistance received from N. Kanak Durga, Sanath Kumar and Raghendra Rao. I hope the book will create better awareness of the research and development needs and explore the potential of sorghum and millets for the future. I also hope that *Millets and Sorghum* will prove to be a valuable reference book for students, teachers and researchers interested in the research and development of these smart crops.

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Introduction

Millets – The Miracle Grains

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Sorghum and millets are among the important sources of staple diet in the semi-arid tropic regions of Asia and Africa. Millets comprise of an important group of cereal crops known for their nutritional values. They are gaining importance in a world that is increasingly becoming populous and facing large climatic uncertainties. About 500 million people in more than 30 countries rely on sorghum as staple diet, and more than 90 million people in Africa and Asia depend on millets as staple diet. Sorghum and millets are very hardy and climate-smart crops suitable for environments prone to drought and extreme heat. These crops are adapted to a range of temperatures, moisture-regimes and input conditions supplying food and feed to millions of dryland farmers, particularly in the developing world. These are the major crops successfully cultivated in dry regions where fine cereals such as rice and wheat cannot be grown. The most important characteristic of sorghum and millets is their ability to tolerate and survive under conditions of continuous or intermittent drought periods that result from low or uncertain rainfall. Millets are perhaps the only cereal crop that can grow in arid lands, requiring only 350–400 mm annual rain.

The millet group includes the great millet sorghum (*Sorghum bicolor* (L.) Moench) and pearl millet (*Pennisetum glaucum*); and the small millets including finger millet (*Eleusine coracana*), Italian or foxtail millet (*Setaria italica*), common or proso millet (*Panicum miliaceum*), kodo millet (*Paspalum scrobiculatum*), little millet (*Panicum miliare*), barnyard millet (*Echinochloa frumentacea*), fonio (*Digitaria exilis*) and teff (*Eragrostis tef*). Of these, fonio and teff are confined to Africa. Other crops are important both in Asia and Africa. Millets are one of the oldest foods known to man and possibly the first cereal grain to be used as food. Millets are also unique due to their short growing season. They can develop from planted seeds to mature, ready to harvest plants in as little as 65 days.

Millets have always been the crops that can be banked upon during situations where there is a risk of famine. They offer a low but more reliable harvest relative to other crops in low-rainfall areas. Small millets are considered as coarse grains and are used as food in situations where other food grains generally cannot be raised, or purchased at economic prices. Therefore, small millets have largely remained as the food of the poor and the less privileged section of the population. The outer tough seed coat and the characteristic flavour of these millets are the main reasons for their reduced popularity among rice- and wheat eaters (Malleshi, 1989). Except finger millet, all the small millet seeds have a slight resemblance with paddy (rough rice) in their morphological features

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and have an outer husk, bran and starchy endosperm whereas the finger millet seed coat is tightly bound with soft endosperm.

Sorghum and millets have good potential as livestock feed also in the dry zones. With modest water requirements, they have the potential to yield good grain for the farming community and substantial quantities of palatable fodder for cattle. They can make good use of any irrigation water available after the main crops have been harvested, and hence may be fitted in to more productive crop patterns. Almost all the grain produced is used as food in India and in other developing countries, whereas in the United States and other developed countries these are used mainly as feed for calves and birds. Sorghum and millets constitute a major source of energy and protein for millions of people in Asia and Africa. Millets, being nutritionally superior to rice and wheat, provide cheap proteins, minerals and vitamins to the poorest of the poor where the need for such ingredients is the maximum. Practically devoid of any grain storage pests, these small millets have indefinite storage life. The untapped grain yield coupled with nutritional superiority makes small millets the potential future food crop, particularly in the more difficult rainfed areas.

Similar to maize, sorghum and millets also offer opportunities for industrial utilisation. They form an important raw material for potable alcohol and starch production in industrialised countries. The food, fodder, feed and industrial uses of these crops make them important in the agrarian economy of the developing regions of Africa and Asia having low rainfall and limited irrigation resources. Though these cereals have been important staples in the semi-arid tropics for many centuries, there appears to be no reliable historical record of their origin or pattern of dispersion. Since they have been cultivated for so long in so many countries, mainly by smallholder cultivators, they are known by many common and vernacular names (Table 1). In some records, no distinction is made between sorghum and millets; production statistics quoted, even by international authorities, often group the cereals together.

Origin and History of Sorghum and Millets

Sorghum, *Sorghum bicolor* (L.) Moench, which is also known as great millet, belongs to the tribe Andropogonae of the grass family Poaceae. Sorghum is mainly an annual crop, although some have perennial nature in the tropics and can be harvested many times. The greatest variation in the genus Sorghum is observed in the region of the northeast quadrant of Africa comprising Ethiopia, Sudan and East Africa (Doggett, 1988). It appears that sorghum moved into Eastern Africa from Ethiopia around 200 AD or earlier, and was probably taken to India during the first millennium BC. Grain sorghum appears to have arrived in America as 'guinea corn' from West Africa with the slave traders about the middle of the nineteenth century.

Pearl millet, *Pennisetum glaucum*, has many names viz., spiked millet, bajra and bulrush millet (Purseglove, 1972). Pearl millet includes a number of cultivated races. It originated in the tropical Western Africa, where the greatest number of both wild and cultivated forms are found. About 2000 years ago the crop was carried to eastern and central Africa and to India, where due to its excellent tolerance to drought it became established in the drier environments.

Finger millet, *Eleusine coracana* L., is an important staple food in parts of eastern and central Africa and India. It is an old tropical cereal widely grown in eastern Africa and south Asia. It first occurs in the archaeological records of early African agriculture

Table 1 Place of origin and common names of sorghum and millets.

Crop	Scientific name	Common names	Place of origin	Chromosome no.
Sorghum	*Sorghum bicolor*	Great millet, guinea corn, kafir corn, aura, mtama, jowar, cholam, kaoliang, milo, milo-maize	Northeast Africa (Ethiopia–Sudan border)	2n=20 (2x)
Pearl millet	*Pennisetum glaucum*	Cumbu, spiked millet, bajra, bulrush millet, candle millet, dark millet	West Africa	2n=14 (2x)
Finger millet	*Eleusine coracana*	African millet, koracan, ragi, wimbi, bulo, telebun	East Africa, India	2n=36 (4x)
Foxtail millet	*Setaria italica*	Italian millet, German millet, Hungarian millet, Siberian millet	Eastern Asia	2n=18 (2x)
Proso millet	*Panicum miliaceum*	common millet, hog millet, broomcorn millet, Russian millet, brown corn	Central and eastern Asia	2n=36 (4x)
Barnyard millet	*Echinochloa frumentacea* *Echinochloa utilis*	Indian barnyard millet, sawa millet, Japanese barnyard millet	India Japan	2n=54 (6x)
Kodo millet	*Paspalum scrobiculatum*	Kodo millet	India	2n=40 (4x)
Little millet	*Panicum sumatrense*	Little millet	Southeast Asia	2n=36 (4x)
Teff	*Eragrostis tef*	Teff, lovegrass, annual bunch grass, warm season annual bunch grass	Ethiopia	2n=40 (4x)
Fonio	*Digitaria exilis*	Fonio, hungry rice, white fonio (En.), fonio blanc, petit mil	West Africa	2n=54

Source: Sorghum and millets in human nutrition, FAO 1995.

dating back to around 3000 years, and was introduced to India at least 3000 years ago. It can be stored for long periods without insect damage (Purseglove, 1972) and thus important during famine. In India and Africa, two groups are recognised: African highland types with grains enclosed within the florets; and Afro-Asiatic types with mature grains exposed outside the florets. Uganda is the centre of origin of this crop.

Foxtail millet, *Setaria italica* L., is also known as Italian millet. Its origin is considered to be in eastern Asia, where it has been cultivated since ancient times. The main cultivation areas are China, Japan and India (Purseglove, 1972). Foxtail millet was also found in the early agricultural sites in Switzerland and Austria dating back to around 3000 years.

Kodo millet, *Paspalum scrobiculatum* L., is another indigenous cultivated cereal especially of India. The species is widely distributed in damp habitats across the tropics and subtropics of the world. The species could have been domesticated anywhere across its natural range extending from Europe to Japan. It has been grown in China for at least 5000 years (Ho, 1975).

Common millet, *Panicum miliaceum* L., also known as proso millet, hog millet, broomcorn millet, Russian millet and brown corn, is of ancient cultivation, and is believed to have been domesticated in central and eastern Asia. The progenitor of broomcorn millet

is native to Manchuria. The species was introduced into Europe as a cereal at least 3000 years ago. Spikelets and florets of broomcorn millet were found together with remains of foxtail millet in the early farming sites of the European Neolithic.

Little millet, *Panicum sumatrense* Roth, is grown throughout India to a limited extent up to altitudes of 2100 m. The seeds of little millet are smaller than those of common millet. Barnyard, Japanese barnyard or sawa millet (*Echinochloa frumentacea* (L.) Link) is the fastest growing of all millets and produces a crop in six weeks. It is mainly grown in India, Japan and China.

Millets – the Climate-Smart Crops

Most of the small millets, particularly little-, proso- and foxtail millets mature early and, therefore, provide one first harvest for human consumption. These are traditionally the indispensable components of the dryland farming system.

The climate change reports from across the globe have raised the threat of climate change to a whole new level, warning of sweeping consequences to life and livelihood, particularly to the world's food supply. Most climate scenarios depict a world warmer by 2 degrees or more by 2100, predicting sharp declines in crop yield for major grains such as wheat and maize. The anticipated climate change makes the drylands a tougher environment to develop and survive in. It has been predicted that there will be a 10% increase in the world's dryland areas with the climate change, with more variability and occurrences of short periods of extreme stresses (drought and heat) during the crop growing seasons. Some estimates suggest that with global warming, 40% of the land now used to grow maize in sub-Saharan Africa will no longer be able to support that crop by the 2030s (The World Bank, 2013). This will have hugely disruptive implications for livelihoods and lives in the semi-arid regions. In the light of changing climate, millets are considered as future crops for farming in the arid and semi-arid tropical regions.

Millets have a wide adaptation. They can withstand a certain degree of soil acidity and alkalinity, stress due to moisture and temperature, and variations in soils from heavy to sandy infertile soils. These crops are grown from sea level to an altitude of 3000 metres and with consequent variation in photoperiod from short to long days. The most attractive feature of sorghum and several of the millets is their capacity to survive and yield grain during continuous or intermittent drought stress. Sorghum can remain dormant during the periods of stress and renew growth when conditions are favourable. Sorghum is more tolerant of flooding than maize but does not grow at its best under prolonged wet conditions. Grain sorghum grows successfully on many soil types but best on medium textured, light textured or sandy soils, and less satisfactorily on clay or heavy textures soils. It tolerates medium to high pH conditions in the soil (Ross and Webster, 1970). Sorghums tolerant to low temperatures and high altitudes are gradually finding a place in Mexico, Brazil and other Latin American countries, in addition to their natural habitat in Ethiopia.

Millet Area and Production Statistics

Detailed area and production data of individual millets are either scanty or currently unavailable. Several kinds of millets are grown in the world, but Food and Agricultural Organization (FAO) data on area, yield and production of all millets are placed together

under the general heading of millet. Pearl millet, finger millet and proso millet account for a large proportion of the world production. Sorghum is the world's fifth most important cereal, in terms of both production and area cultivated. All other small millets together are considered the seventh most important cereal grains. All these crops are primarily grown in agro-ecologies subjected to low rainfall and drought. Some cultivars of finger millet are adapted to high altitude conditions in Asia, largely in the foothills of the Himalayas, and in Africa (Purseglove, 1972).

Trends in Area, Production and Productivity of Sorghum and Millets

Sorghum is one of the main staple foods for the world's poorest and most food-insecure people across the semi-arid tropics. Globally sorghum is cultivated on 42 million hectares (ha) to produce 62.3 million tonnes, with productivity hovering around 1.5 tonnes per hectare (FAO stat, 2014). Table 2 provides data on area, yield and production of sorghum in various regions of the world, which shows that Africa followed by Asia and America are the largest producers of sorghum, while 95% of world's millet area lie in

Table 2 Area, yield and production of sorghum and millet by region, 2013.

	Sorghum			Millet		
Region	**Area (m ha)**	**Production (m tonnes)**	**Productivity (kg/ha)**	**Area (m ha)**	**Production (m tonnes)**	**Productivity (kg/ha)**
Africa	26.52	25.64	967.08	21.12	15.00	710.23
Eastern Africa	4.75	6.47	1362.8	1.52	1.62	1064.28
Central Africa	1.89	1.99	1056.31	1.15	0.79	686.80
Northern Africa	7.28	5.28	724.9	2.79	1.10	394.80
Southern Africa	0.14	0.19	1319.3	0.25	0.034	134.51
Western Africa	12.46	11.71	940.37	15.41	11.46	743.57
Americas	6.84	23.58	3450.21	0.27	0.43	1622.1
Northern America	2.64	9.88	3739.42	0.26	0.42	1619.52
Central America	1.89	6.64	3520.19	0.0009	0.0008	947.78
South America	2.18	6.95	3191.6	0.0061	0.011	1828.76
Asia	7.88	9.58	1215.09	11.2	13.76	1228.19
Central Asia	0.0009	0.0075	8613.8	0.053	0.061	1137.3
Eastern Asia	0.61	2.94	4801.0	0.79	1.83	2324.0
Southern Asia	6.38	5.40	846.53	10.01	11.57	1155.77
South-eastern Asia	0.26	0.27	105436	0.21	0.19	883.3
Western Asia	0.64	0.96	1516.76	0.14	0.11	788.29
Europe	0.39	1.25	3185.2	0.49	0.63	1282.1
Oceania	0.60	2.23	3748.8	0.035	0.04	1142.86
World	42.2	62.30	1475.24	33.1	29.86	901.73

Source: FAO database 2014.

Table 3 Leading producers of sorghum and millets, 2013.

	Sorghum				Millets		
Country	Area (m ha)	Production (m tonnes)	Productivity (kg/ha)	Country	Area (m ha)	Production (m tonnes)	Productivity (kg/ha)
USA	2.64	9.88	3739.4	India	9.2	10.91	1185.9
Nigeria	5.50	6.70	1218.2	Nigeria	4.0	5.00	1250.0
Mexico	1.69	6.31	3735.0	Niger	7.10	2.99	421.83
India	6.18	5.28	854.37	China	0.72	1.75	2439.3
Ethiopia	1.85	4.34	2348.5	Mali	1.44	1.15	801.9
Argentina	0.89	3.64	4085.2	Burkina Faso	1.33	1.08	812.7
China	0.59	2.89	4954.2	Cameron	0.07	0.97	1385.7
Australia	0.60	2.23	3747.4	Ethiopia	0.43	0.81	1869.8
Burkina Faso	1.81	1.88	1040.9	Senegal	0.71	0.57	801.1
Niger	3.1	1.29	415.16	USA	0.26	0.42	1619.5
Total	24.85	44.44			25.26	25.58	
World	42.2	62.3	1475.24	World	33.1	29.86	901.73

Africa and Asia. The region-wise distribution of area for millets is 15.4 million ha in Western Africa and 10 million ha in South Asia. Finger millet is the principal small millet species grown in South Asia followed by kodo millet, foxtail millet, little millet, proso millet and barnyard millet in that order. Foxtail millet and proso millet are important in China. In Africa, finger millet, teff and fonio have local importance. Some small millets are grown in the United States and Europe on a very limited scale.

The five largest producers of sorghum in the world (Table 3) are the United States (16%), Nigeria (11%), Mexico (10%), India (8.5%) and Ethiopia (7%). Together these five countries account for 52.5% of the total world production. India (36.5%) is the largest producer of millets, followed by Nigeria (16.7%), Niger (10%), China (5.9%) and Mali (4.4%). All these countries together contribute to 73.5% of world millet production.

Because of the higher yield per unit area, North and Central America produce the highest quantity of sorghum (16% of total production). In Asia, sorghum is extensively cultivated in India, China, Yemen, Pakistan and Thailand. Production in Europe is limited to a few areas in France, Italy, Spain and the southeastern countries. In Oceania, Australia is the only producer of significance.

World sorghum production expanded from 40 million tonnes at the beginning of the 1960s to 62 million tonnes during 2012–2013, even though there was a decline in sorghum growing area from 46 million ha in 1961 to 42 million ha in 2013. Millet production increased from 25 million tonnes in 1961 to 30 million tonnes in 2013, and the area was decreased from 43 million ha in 1961 to 33 million ha in 2013.

Sorghum is grown in two contrasting situations in different parts of the world based on production and utilisation patterns. In the developed world there is intensive, commercialised production, mainly for livestock feed. Hybrid seed, fertiliser and improved water management technologies are used fairly widely, and yields average 3–5 t/ha.

In most of the developing world, there is sharp contrast with the low-input, extensive production systems, where sorghum is grown mainly for food. While improved varieties are being adopted in such systems, particularly in Asia, management practices generally remain less intensive than in the commercialised systems. Fertiliser application rates are low and the adoption of improved moisture conservation technologies is limited. As a result, average yields remained low between 0.5 and 1.0 t/ha in many areas but gradually increasing in spite of area decline in some regions.

Millet production systems in Africa and Asia are generally characterised by extensive production practices and limited adoption of improved varieties. Yield average is still only 0.3–1.0 t/ha. While hybrids are being adopted in parts of Asia, most of the world's millet area remains under traditional varieties. Few farmers apply fertilisers or use improved moisture conservation practices. Therefore, the yield levels remain low for long but increase wherever improved hybrids and management practices are increasingly adopted as in India.

Trends in Area, Production and Productivity of Sorghum and Millets in India

Sorghum

India contributes to about 16% of the world's sorghum production. It is the fourth most important cereal crop in the country. In India, this crop was one of the major cereal staples during the 1950s and occupied an area of more than 18 million ha but has come down to 6.61 million ha in 2013. The decline has serious concern on the cropping systems and the food security of these dry land regions of the country. The increased productivity of sorghum has not been able to compensate the loss in area turning the production to be negative.

Pearl Millet

Pearl millet is a major warm-season cereal grown largely in the arid and semi-arid tropical regions of Africa and Asia with India accounting for the largest area (7.2 million ha). The diversification of cultivar base with mostly dual-purpose hybrids has led to 24 kg/ha/year of grain yield increase during the last few decades as compared to only 5.2 kg/ha/year of yield increase during the pre-hybrid phase of 1950–1965. Development of improved crop cultivars is just one major component of technological interventions to enhance food and nutritional security. Improved crop management technologies with potential to substantially increase pearl millet grain yield have been developed.

Small Millets

The crop-wise data on area, production and yield for individual small millets are not available, except for finger millet. Therefore, the statistical data are given separately for finger millet; other small millets are grouped together. The area where small millets are cultivated in India during the last 6 decades has significantly reduced from 8 million ha during 1949–1950 to around 2.3 million ha during 2012–2013. This is also reflected in the diminishing production, from around 4 million tonnes produced in late 1940s to around 2.5 million tonnes during 2011–2012. The loss of area is very severe in all small millets other than finger millet. However, in the last 15 years, the finger millet also has lost ground and its area has come down from 2.4 million to 1.2 million ha.

Despite the reduction in area, the total production is not much affected. By and large, the low productivity of these crops is largely due to the meagre attention received in

Table 4 Area (million ha), production (million tonnes) and productivity (kg/ha) of sorghum, pearl millet and small millets in India.

Crop/ Year	Category	1955–1956	1965–1966	1975–1976	1985–1986	1995–1996	2005–2006	2012–2013
Sorghum	Area	17.36	17.68	16.09	16.10	11.33	8.68	6.18
	Production	6.73	7.58	9.50	10.20	9.33	7.63	5.33
	Productivity	387	429	591	633	823	880	863
Pearl millet	Area	11.34	11.97	11.57	10.65	9.32	9.58	7.20
	Production	3.43	3.75	5.74	3.66	5.38	7.68	8.74
	Productivity	302	314	496	344	577	802	1214
Finger millet	Area	2.30	2.70	2.63	2.41	1.77	1.53	1.11
	Production	1.85	1.33	2.80	2.52	2.50	2.35	1.59
	Productivity	800	492	1064	1049	1410	1534	1428
Small millets	Area	5.34	4.56	4.67	3.16	1.66	1.06	0.75
	Production	2.07	1.56	1.92	1.22	0.78	0.47	0.43
	Productivity	388	341	412	386	469	443	571

Source: Agricultural Census, Directorate of Economics and Statistics, Department of Agriculture & Cooperation, Government of India.

terms of inputs; which is further compounded by low-value status of grains. The bulk of small millet production in India is of finger millet (80%) and the remaining from kodo millet, little millet, foxtail millet, barnyard millet and proso millet in that order.

In general, the area and production of small millets are coming down. The reasons are many: the low productivity, poor resources base, lack of input, price and procurement support coupled with no alternate food uses, campaigns for value-added oilseeds and pulses and 'urbanisation' of food habits are slowly displacing the small millets to more and more marginal, fertiliser-hungry and water-starved abandoned soils.

Finger Millet

The area cultivating finger millet has fluctuated from 2.30 to 1.1 million ha in different years during 1955–2013 and the production has fluctuated from 1.85 to 1.59 million tonnes. The increase in production is mainly due to the raise in productivity from 800 kg/ha during 1955–1956 to 1428 kg/ha during 2012–2013 (Table 4).

Millets are the main component for food and fodder security in the semi-arid tropics. They do have socio-economic, food/feed, health and environmental impacts on the poor farmers of these regions. Substantial advances made in the improvement of millets have brought in the economic transformation of millions of rural families in these regions. In the light of climate change, millets are extremely vital for tackling the food crisis and providing food security. Any improvement in production, availability, storage, utilisation and consumption of these food crops will significantly contribute to the household food security and nutrition of the inhabitants of these areas.

Millets – Store Houses of Nutrition

The major health concern in most of the developing countries is hidden hunger or micronutrient deficiency. This is more prominent in the arid and semi-arid regions, where people are too poor to be able to afford more nutritious foods. Even while vast segments of resource-poor people suffer from malnutrition, there is a growing incidence of obesity and chronic diseases such as diabetes, cardiovascular diseases, cancer, etc. The reason for these dual types of situations could be due to changing food habits, the absence of millets from diet being one of them. Their presence in the world food basket had been declining over the years. However, there is an increasing recognition of their favourable nutrient composition and utility as health food, in the context of increasing lifestyle diseases. Sorghum and millets offer unique advantage for health being rich in micronutrients particularly minerals and B vitamins. The neutraceutical value of these grains, by virtue of their high dietary fibre and low glycemic index, is receiving increased attention. Their good nutritional value including high levels of quality protein, ash, calcium, iron and zinc, makes millet nutritionally superior to most cereals. Additionally millets are also rich in health promoting phytochemicals and have received attention for their potential role as functional foods.

Being non-glutinous, millets are safe for people suffering from gluten allergy and celiac disease. They are non-acid forming, and hence easy to digest. Epidemiologically lower incidence of diabetes is reported in millet consuming populations (Saleh *et al.*, 2013). The diabetes preventing effect of millets is primarily attributed to the high fibre content. Some antioxidant phenols in millets also tend to have antidiabetic effects. Sorghum is rich in phenolic compounds and antioxidants (Awika *et al.*, 2004).

Among minor millets, foxtail- and barnyard millets have low glycaemic index (40–50) which helps to manage blood glucose levels and prevent diabetes.

Millets being high in fibre, antioxidants and complex carbohydrates are potential candidates for having beneficial effects against diseases such as cardiovascular diseases, cancer, etc. in general. Finger millet is rich in niacin, which helps reduce high cholesterol level. It is very high in calcium (340 mg/100 g, i.e. three times more than milk) (Kannan, 2010) making it important for lactating women and children. Pearl millet and sorghum are rich sources of energy (about 350–360 k cal/100 g), with comparable levels as wheat and rice (Nambiar *et al.*, 2011). Teff contains high level of iron. Finger millet protein is unique among cereals to possess very high levels of sulphur amino acids.

Genetic Resources and Crop Improvement of Millets

As the small millets are indispensable to agriculture in semi-arid tropics, there is increasing realisation of the need to improve the productivity of these crops through modern methods of breeding. The ultimate goal of breeding sorghum and millets remains improvement of grain yield including maximisation of biomass and the harvest index. The major objectives for millet improvement for grain and forage include improved adaptation, increased drought tolerance, ability to put forth quick growth and increased resistance to economically important diseases and pests. Quality aspects of both grain and fodder are also important. Improvement in resistance for important biotic and abiotic stresses forms another important objective in millet improvement. Among the abiotic stresses, drought plays an important role since all the millets are grown rainfed. The major biotic stress being grain moulds, shoot fly and charcoal rot in sorghum, downy mildew in pearl millet and blast in finger millet.

The pollination behaviour of different millet crops range from complete self-pollination to predominant cross-pollination. Majority of the small millets are predominantly self-pollinated crops. The degree of selfing varies from near cleistogamy in kodo millet to marginal outcrossing in other small millets. Sorghum is also a predominantly self-pollinated crop with the cross-pollination varying from 2 to 20% (which puts it under often cross-pollinated crop category) in different places and different varieties, more in loose panicles than in compact ones, and hence has the advantage of possessing complete self-pollination to total outcrossing due to its floral biology, genetic and cytoplasmic genetic male sterility and self incompatibility. Breeding methods relevant to self- as well as cross-pollinated crops are, therefore, applied to breed pure line varieties, hybrids and populations. Pearl millet is predominantly protogynous and hence highly cross-pollinated. The large amount of cross-pollination in pearl millet results in the plants being highly heterozygous. In this respect a field of pearl millet shows considerable genetic variability within a single open pollinated variety. Hence the breeding methods that are followed for cross-pollinated crops are followed for pearl millet improvement, and the main breeding approaches are those that aim towards development of hybrids, composites and synthetics.

The ceiling to yield in sorghum and pearl millet has been raised substantially through the commercial use of hybrids during the last 5–6 decades. In both the crops, gene-cytoplasmic sterility-restorer systems have added a new dimension to yield improvement. Considerable progress has also been made in incorporating resistance to major

diseases and pests. In case of small millets, systematic improvement has not been attempted until recently.

Small millets are highly self-fertilised crops and pure line selection has been primarily used to improve the performance of land races. Hybridisation, however, offers immense potential for combining the desirable features. Contact, hot water and gametocide methods have been used in hybridisation with certain amount of success in these crops. The smallness of the spikelets and their delicate nature have been hindering hand emasculation. There is an urgent need to standardise hybridisation techniques for changing the genetic background of the local cultivars. The discovery of male sterility in foxtail millet in China augurs well for the improvement of this crop. Similar mechanisms and also mechanisms like protogyny which promote cross-pollination need to be looked for in other small millets.

Sorghum and millets possess a wealth of genetic diversity. India has assembled more than 15 000 collections of small millets at Bangalore, the headquarters of the Small Millets Improvement Project. Similarly China maintains a rich source of foxtail millet germplasm; earlier Soviet Union had excellent proso millet collections. Africa has assembled teff in Ethiopia and finger millet in Kenya and Uganda. However, there are many areas in India as well as in other countries still unexplored and there is an urgent need to retrieve the genetic diversity under natural conditions.

Promising germplasm for different traits have been identified in sorghum and millets and those have been used in the millet improvement programmes across the countries. Sorghum has five basic races, viz., bicolor, durra, guinea, caudatum and kafir and their ten derived hybrid races. Useful genes for different traits from these germplasm have been exploited in the sorghum improvement programmes across the globe. The male sterile kafir introduced from America is being utilised for exploitation of heterosis in sorghum. Cultivated pearl millet has four basic races, viz., typhoides, nigritarum, globosum, leonis. The zera zera sorghum from the Sudan–Ethiopian border and the iniadi germplasm of pearl millet from the Togo–Ghana–Burkina Faso–Benin region of western Africa have been most extensively used in sorghum and pearl millet breeding programmes worldwide (Rai *et al.*, 1999).

In the case of small millets, the utilisation has been drastically restricted by the difficulties in artificial hybridisation. Except for finger millet and to some extent foxtail millet, hybridisation and recombination breeding in small millets have not been attempted in India. Improvement in these crops so far has been through single plant selection, evaluation and release of promising germplasm. The Indo-African crosses have provided the real backbone for breaking the grain-yield barriers in the improvement of finger millet. They helped in increasing finger millet productivity by more than 50% (Seetharam, 1982). The finger millet germplasm, especially from Africa, possess genes for blast resistance, robust growth, early vigour, large panicle size, finger number and branching and higher grain density. Similarly accessions possessing high protein and desirable physiological attributes, with high carbon dioxide fixation and low leaf area suitable for rainfed conditions have been identified (Seetharam *et al.*, 1984; Sashidhar *et al.*, 1986).

In kodo millet, raceme morphology allows for the recognition of three cultivated complexes. The most common kodo millets are characterised by racemes with the spikelets arranged in two rows on one side of a flattened rachis, as is also typical of wild *P. scrobiculatum*. Two variations on this spikelet pattern often occur in the same field as the more common phenotype. Hybridisation between cultivated varieties and between weedy and cultivated races is common. This explains the absence of clear racial differentiation, even

after some 3000 years of cultivation. Kodo millet is cleistogamous, but protogynous types have been selected, and crosses made. In the Indian wild types the stigmas protrude from the spikelets. The observation by de Wet *et al.* (1983), on the lack of racial differentiation after 3000 years, suggests that it could be a very interesting crop to work with.

Foxtail millet is commonly classified into a European complex (race moharia) and a Far Eastern complex (race maxima). Race moharia includes cultivars with relatively small and erect inflorescences, while race maxima is characterised by large and pendulous inflorescences. Two inflorescence types of race maxima are recognised by Gritzenko (1960). Plants with small, essentially erect, and compact inflorescences occur in northwestern China and Mongolia. Plants from eastern China, Japan and Korea typically have large, compact and pendulous inflorescences. Cultivars from India are morphologically distinct from those of Europe and the Far East, and are recognised as race indica by Prasada Rao *et al.* (1987). The variability available in foxtail millet for panicle shape, size, arrangement of spikelets, tillering, seed size and colour are very diverse offering great scope for exploitation (Harinarayana and Seetharam, 1981).

Cultivated kinds of *P. miliaceum* are commonly subdivided into five subspecies (Lyssov, 1975). These are here recognised as races without taxonomic validity. Race miliaceum resembles wild *P. miliaceum* in inflorescence morphology. It is characterised by large, open inflorescences with suberect branches that are sparingly subdivided. Race patentissimum with its slender and diffused panicle branches is often difficult to distinguish from race miliaceum. These two races occur across the range of broomcorn millet cultivation from Eastern Europe to Japan. Highly evolved cultivars of broomcorn millet have more or less compact inflorescences. These are classified into races contractum, compactum and ovatum. Cultivars included in race contractum have compact, drooping inflorescences. Those belonging to race compactum have cylindrical shaped inflorescences that are essentially erect. Cultivars with compact and slightly curved inflorescences that are ovate in shape are included in race ovatum.

A different Panicum species (sama) is grown as a cereal in the Eastern Ghats of India (Rangaswami Ayyangar and Achyutha Wariar, 1941). This species, *P. sumatrense* Roth. ex Roem. and Schult., represents the domesticated complex of the weedy *P. psilopodium* Trin. (de Wet *et al.*, 1984). The commonly cultivated kind differs from wild *P. psilopodium* with which it crosses to produce fertile hybrids, primarily in having lost the ability of natural seed dispersal. This race of sama is highly tolerant to heat and drought stress. In the more favourable agricultural habitats of the Eastern Ghats a robust race of sama is grown. The inflorescences of this race are strongly branched and compact.

The wide diversity available for sorghum and millets gives immense scope for genetic improvement of these crops for the traits of interest.

Constraints for the Improvement of Millets

Production of small millets is subject to wide fluctuations, and the area is declining. The major constraints limiting millet production are:

1) These crops are often grown in uneven marginal lands, poor in fertility, shallow and gravelly, with low moisture retention capacity.
2) These crops are grown under rainfed conditions in low-rainfall, arid regions.
3) Improved crop management practices are not adopted by the farmers due to socio-economic constraints.

4) There is no organised programme for production and supply of seeds of improved varieties.
5) There is lack of extension and development support.

Scope for Future Improvement of Millets

Recognising the decline in cultivated area and consumption of millets, attempts have been made to generate demand through multiple uses of millets in the areas of food, feed, forage, energy, industrial and other uses. In this era of extreme climate variability and high dietary induced malnutrition, sorghum and millets with a versatility in multi-purpose use, stress adaptation and nutritive value are becoming more important crops. There is an urgent need for giving high priority to millets to meet with three challenging scenarios. The first is global warming; the second, water scarcity mounting to frightening proportions; and the third, the projected malnutrition that threatens to engulf 70% of the population in the developing countries, particularly the poor and the vulnerable sections. Sorghum and millets have an untapped potential under adverse soil and climatic conditions and survive harsh climatic conditions. This makes them an ideal solution to the challenge of climate change.

Because of their comparative photo-insensitive nature, short growing season and low moisture demand, millets can be very well fitted into multiple cropping systems both under irrigation as well as dry farming conditions. During scarcity years they can provide nutritious grain as well as valuable fodder in a short span of time. Their long storability under ordinary conditions has made them 'famine reserves'. This aspect is perhaps the most important for agriculture in arid and semi-arid tropics where crop production suffers due to the vagaries of the monsoon. There are types to suit a wide range of rainfall situations which can be used for mid-season corrections when rains are delayed.

In order to improve the demand and popularity of sorghum and millet, it is important to popularise the health benefits of these millets, and the crop improvement should focus on different traits (Seetharam *et al.*, 1989) such as:

1) Though traditionally small millets are the constituents of dryland farming system, they respond to irrigation. Therefore, there is an immediate need to select genotypes for better water use efficiency.
2) Breeding of drought-tolerant varieties is important in millets which are essentially rainfed crops confining to semi-arid tropics.
3) Sorghum and millets are low-input crops and often grown in infertile depleted soils. However, they respond remarkably to fertiliser management. This demands the need for identification of genotypes which have high fertiliser use efficiency particularly nitrogen whether it is native or applied.
4) Breeding of dwarf varieties is an objective of intensive cultivation.
5) In small millets progress through hybridisation has been extremely limited, except in finger millet. This has been chiefly due to difficulties in emasculation and pollination, in identification of true hybrids, limited heterosis in intervarietal crosses (Srivastava and Yadav, 1977), and the availability of unexploited genetic resources.
6) Millets are vulnerable to a different spectrum of field pests and diseases. The incorporation of genetic resistance to key pests and diseases offers the best choice in

low-input crops like small millets. Cultural controls like early planting and appropriate cropping systems could also reduce pest and disease incidence. These methods in addition to cheap chemical control methods deserve attention.

7) Millets are the staple food of the poor and the working classes and hence their health depends on the quality of the food consumed. Any improvement made in the nutritive quality of millet grain would indirectly help in bettering the general health of the rural people. So, quality breeding to improve the protein content, mineral composition and amino acid balance should be given due priority. Quality specific genotypes can also be bred in order to widen consumer base to offer a choice of foods and to augment industrial uses of small millets.
8) Development of value-added products from small millets will help to upgrade not only the economic status of growers but also their investment resource base.
9) Millets could also be processed into new foods suitable to infants and invalids alike with necessary fortification.
10) While breeding varieties, attention should be paid to retain the desirable qualities of millets such as good storage quality and high mineral content.
11) As small millets are well protected in glume encasements, the processing of the grain to usable form is not only time consuming but also labour intensive. There is therefore a need to develop post-harvest processing technology in order to reduce human drudgery.
12) Genotypes need to be tailored for maturity – early, mid-late and late, depending on the location-specific requirements of soil, rainfall, temperature, humidity, day length and cropping patterns.
13) Screening of germplasm for malting and popping characteristics and breeding varieties for improved malting and popping characteristics.
14) Diversification of uses of small millets and development of health or specialty foods from millets: diabetic foods, high-fibre foods, weaning foods, flakes, quick-cooking cereals, etc.

The improvement of the yield potential as well as nutritive qualities of these grains can make a valuable contribution towards minimising malnutrition. The availability of considerable genetic variability in these crops makes planned breeding work possible. Better seeds, better inputs and better farm practices can boost millets and sorghum production to significant levels. As the demand for millets is going to increase domestic and international markets for their health and nutritional benefits, there is an urgent need for the promotion of health and nutritional benefits. Promotions of value-added products from millets in international markets could fetch higher foreign exchange. They are the potential food crops of tomorrow's world.

References

Awika, J.M., Rooney, L.W. and Waniska, R.D. (2004) Anthocyanins from black sorghum and their antioxidant properties. *Food Chemistry*, 90, 293–301.

de Wet, J.M.J., Prasada Rao, K.E. and Brink, D.E. (1984) Systematics and domestication of *Panicum sumatrense* (Gramineae). *Journal of Agriculture Traditional et Botanique Applique*, 30, 159–168.

de Wet, J.M.J., Prasada Rao, K.E., Mengesha, M.H. and Brink, D.E. (1983) Diversity in kodo millet (*Paspalum scrobiculatum*). *Economic Botany*, 37, 159.

Doggett, H. (1988) *Sorghum Londres*, Longman Scientific and Technical, London.

Food and Agricultural Organization (FAO) (2014) FAO statistical data base, http://apps.fao.org/

Gritzenko, R.J. (1960) Chumiza (Italian millet) taxonomy (*Setaria italica* (L.) P.B. subsp. Maxima Alef.). *Bulletin of Applied Botany. Genetics and Plant-breeding*, 32, 145–182.

Harinarayana G. and Seetharam, A. (1981) Minor millets genetic resources in India. Paper presented in IBPGR Sorghum and Millets advisory Committee meeting. Dakar, Senegal, October 4–9, 1981.

Ho, P. (1975) *The Cradle of the East*, Chicago University Press, Chicago, IL.

Kannan, S. (2010) Finger millet in nutrition transition: an infant weaning food ingredient with chronic disease preventive potential. *British Journal of Nutrition*, 104, 1733–1734. doi: 10.1017/S0007114510002989

Lyssov, B.H. (1975) Proso (Panicum L.), in *Flora of Cultivated Plants*, Vol. III. Croat Crops (ed. A.S. Krotov), Kolos, Leningrad.

Malleshi, N.G. (1989) Processing of small millets for food And industrial uses, in *Small Millets in Global Agriculture* (eds A. Seetharam, K.W. Riley and G. Harinarayana), Proceedings of first international small millets workshop, Bangalore, India, October 29–November 2, 1986. Oxford & IBH Publishing Co. Pvt. Ltd., New Delhi, pp. 325–340.

Nambiar, V.S., Dhaduk, J.J., Sareen, N. *et al.* (2011) Potential functional implications of pearl millet (*Pennisetum glaucum*) in health and disease. *Journal of Applied Pharmaceutical Science*, 1 (10), 62–67.

Prasada Rao, K.E., de Wet, J.M.J., Brink, D.E. and Mengesha, M.H. (1987) Intraspecific variation and systematic of cultivated *Setaria italica* (Gramineae). *Economic Botany*, 41, 108–116.

Purseglove, J.W. (1972) *Tropical Crops: Monocotyledons*, Vol. 1, Londres, Longman Group Limited, 334 pp.

Rai, K.N., Murthy, D.S., Andrews, D.J. and Bramel-cox, P.J. (1999) Genetic enhancement of pearl millet and sorghum for the semi-arid tropics of Asia and Africa. *Genome*, 42, 617–628.

Rangaswami Ayyangar, G.N. and Achyutha Wariar, U.B. (1941) Samas the little millet (Panicum miliare Lamk.). *Madras Agricultural Journal*, 29, 451–470.

Ross, W.M. and Webster, O.J. (1970) *Culture and Use of Grain Sorghum*, USDA/ARS Agric. Handbook No. 385. US Department of Agriculture, Washington DC.

Saleh, A.S.M., Zhang, Q., Chen, J. and Shen, Q. (2013) Millet grains: nutritional quality and potential health benefits. *Comprehensive Reviews in Food Science and Food Safety*, 12, 281–295.

Sashidhar, V.R., Gurumurthy, B.R., Prasad, T.G. *et al.* (1986) Genotypic variation in carbon exchange rate, functional leaf area and productivity in fingermillet (*Eleusine coracana*). An approach to identify desirable plant types for higher water use efficiency under rainfed conditions. *Field Crops Research*, 13, 133–146.

Seetharam, A. (1982) Conservation of minor millets germplasm in India. MILWAI Newsletter, 1, 14.

Seetharam, A., Aradhya, K.M., Sashidhar, V.R. *et al.* (1984) Protein content in white and brown seeded finger millet genotypes. *Sabrao Journal*, 16, 65–67.

Seetharam, A., Riley, K.W. and Harinarayana, G. (1989) *Small Millets in Global Agriculture*, Inde, Oxford and IBH, New Delhi, 392 pp.

Sorghum and millets in human nutrition, FAO 1995.
Srivastava, D.P. and Yadav, A. (1977) Heterosis in *Panicum miliare* Lam. *Current Research*, 6 (4), 66–67.
The World Bank. (2013) Turn Down the Heat: Climate Extremes, Regional Impacts, and the Case for Resilience. A Report for the World Bank by the Potsdam Institute for Climate Impact Research and Climate Analytics. Washington DC: World Bank.

1

Sorghum, *Sorghum bicolor* (L.) Moench

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1.1 Introduction

Sorghum, *Sorghum bicolor* (L.) Moench, is known under a variety of names: 'great millet' and 'guinea corn' in West Africa, 'kafir corn' in South Africa, 'dura' in Sudan, 'mtama' in Eastern Africa, 'jowar' in India and 'kaoliang' in China (Purseglove, 1972). It is the fifth most important cereal crop grown in the world. It is mostly cultivated by subsistence farmers in the semi-arid tropics of Africa, Asia and Latin America. It is an important staple food crop in the semi-arid areas of Asia and Africa, thus contributing to the vital share of energy, proteins, vitamins and minerals for millions of poor people of these regions, whereas it is used as animal feed in the Americas, China and Australia. In India, the rainy-season sorghum grain is used mainly as animal/poultry feed, while the post-rainy-season sorghum grain is used primarily for human consumption. The crop residue (stover) after the harvest is a valuable source of fodder and fuel in India and Africa. Sorghum also has great potential to supplement fodder resources in India because of its wide adaptation, rapid growth, high green- and dry fodder yields with high ratoonability and drought tolerance (Reddy, Ramesh *et al.*, 2004). Grain sorghum grown primarily for food uses can be divided into milo, kafir, hegari, feterita and hybrids (Purseglove, 1972). There are other classes of sorghums such as sorghos, grass sorghums, broomcorn sorghum and special- purpose sorghum. The crop is grown under harsh environments where other crops fail to grow. The produce is mostly consumed locally and the surplus usually does not have assured price.

1.2 Origin and Taxonomy

Mann *et al.* (1983) hypothesised that the origin and early domestication of sorghum took place approximately 5000 years ago in northeastern Africa. Wendorf *et al.* (1992) reported new evidence that places the origin and domestication at 8000 years before present (BP) in the Egyptian–Sudanese border. Thus, there seems to be no argument against the African origin of sorghum (Kimber, 2000), which is also supported by the largest diversity of the cultivated and wild sorghum in Africa (de Wet, 1977; Doggett, 1988). The great diversity of *S. bicolor* has been created through disruptive selection

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(i.e. selection for extreme types) and by isolation and recombination in the extremely varied habitats of northeast Africa and the movement of people carrying the species throughout the continent (Doggett, 1988). In the Indian Subcontinent, evidence for early cereal cultivation was discovered at an archaeological site in the western parts of Rojdi (Saurashtra) dating back to about 4500 BP (Damania, 2002). The Indian Subcontinent is considered to be the secondary centre of origin of sorghum (Vavilov, 1992).

In 1753, Linnaeus described three species of cultivated sorghum in his *Species Plantarum*, viz., *Holcus sorghum*, *Holcus saccaratus* and *Holcus tricolor*. In 1794, Moench distinguished the genus Sorghum from the genus Holcus, and in 1805, Pearson suggested the name *Sorghum vulgare* for *Holcus sorghum* (L.). In 1961, Clayton proposed the name *Sorghum bicolor* (L.) Moench as the correct name for cultivated sorghum and this is currently being used. Detailed classification of sorghum is given by Snowden (1936). Other classifications proposed since then have been the modifications or adaptations of the Snowden system. Harlan and de Wet (1972) published a simplified classification of sorghum. They divided cultivated sorghum into five basic groups or races: *bicolor*, *guinea*, *caudatum*, *kafir* and *durra*. The wild type and shattercane are considered as the two other spikelet types of *S. bicolor*. Based on the polymorphism of 11 enzymes, sorghum is classified into three enzymatic groups. The first group includes mainly *guinea* varieties of West Africa; the second Southern African varieties of all five races; and the third *durra* and *caudatum* types of Central and East Africa (Ollitrault *et al.*, 1989).

Sorghum is classified under the family *Poaceae*, tribe *Andropogoneae*, subtribe *Sorghinae* and genus *Sorghum* Moench (Clayton and Renvoize, 1986). Garber (1950) and Celarier (1959) divided the genera sorghum into five subgenera: sorghum, chaetosorghum, heterosorghum, parasorghum and stiposorghum. *Sorghum bicolor* was further broken down into three subspecies: *S. bicolor* subsp. *bicolor*, *S. bicolor* subsp. *drummondii* and *S. bicolor* subsp. *verticilliflorum*. The cereal sorghums were found to consist of four wild races and five cultivated races (Harlan *et al.*, 1976). The four wild races of *Sorghum bicolor* that include *arundinaceum*, *virgatum*, *aethiopicum* and *verticilliflorum* are placed in *S. bicolor* subsp. *verticilliflorum*, formerly subspecies *arundinaceum*. Cultivated sorghums are placed under *S. bicolor* subsp. *bicolor* and are represented by diverse agronomic types such as grain sorghum, sweet sorghum, sudangrass and broomcorn (Berenji and Dahlberg, 2004). The cultivated races that are presently conceived are *bicolor*, *guinea*, *kafir*, *caudatum* and *durra*. Intermediates that are caused by hybridisation of these races exhibit characters of both parents (Smith and Frederiksen, 2000). Additionally, there are two weedy sorghums widespread in the temperate zone, viz., Johnsongrass and spontaneous sorghum (shattercane).

1.3 Germplasm Resources and Utilisation

Sorghum genetic resources are conserved at many research centres across the world. At the global level, sorghum germplasm collections consist of approximately 168500 accessions (Reddy *et al.*, 2006). The major organisations/countries which maintain sorghum genetic resources are the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India, the National Plant Germplasm System (NPGS) in United States, Ethiopia, Sudan, South Africa, India and China, primarily because of the large crop improvement programmes (Rosenow and Dahlberg, 2000). ICRISAT with a collection of 37949 accessions from 92 countries (about 22% of global total) represents the

major diversity centres of sorghum. The Indian National Gene Bank holds about 19844 accessions of sorghum (Radhamani *et al.*, 2011).

The promising germplasm lines after evaluation can be directly released as varieties. About 31 sorghum germplasm accessions supplied from the ICRISAT gene bank have been directly released as cultivars in 17 countries. Notable among these is IS 18758, a popular landrace from Ethiopia belonging to the hybrid race *guinea-caudatum* WG *zera zera*. It has been released as a variety in Burundi (as Gambella 1107) and Burkina Faso (as E 35-1) (Reddy *et al.*, 2006). The landrace IS 1054 belonging to the race *durra* and subrace *cernuum* is a ruling post-rainy-season-adapted variety released as M 35-1 in peninsular India. Another landrace, IS 33844, selected from a germplasm collection from Ghane Gaon (in Sholapur, Maharashtra), belonging to the race *durra*, was released in Maharashtra, India. The highly popular high-biomass-yielding forage sorghum variety UP Chari-1, released in India, is a landrace (IS 4776). Germplasms with one or more outstanding traits but with poor agronomic performance are considered for registration, which is an instrument of soft protection. About 47 sorghum germplasm accessions are registered for various traits with NBPGR, India (Table 1.1) (Radhamani *et al.*, 2011).

Developing the core and mini-core collections (10 and 1%, respectively, of the entire collection), representing the total genetic diversity, is the best strategy to promote utilisation of germplasm. A core collection consisting of 2247 accessions has been developed and is being maintained at ICRISAT, Patancheru, India (Grenier *et al.*, 2001). The hierarchical cluster analysis of data of the core collection evaluated 11 qualitative

Table 1.1 Sorghum germplasm registered for potential valuable traits.

Trait	No. of accessions registered
Resistant to yellow sugarcane aphid, *Melanaphis sacchari*	1
Cytoplasmic-nuclear male sterility (CMS), thermo-sensitive with high yield and long panicle	1
Roti and dough quality, high protein (9.63%), stover quality, shoot fly and anthracnose resistant	1
Low hydrocyanic acid (HCN) and multiple resistance	1
Drought tolerant	1
Converted male and female parents of dual-purpose sorghum hybrid, SPH 1148 with high yield	2
Shoot fly resistance and high grain yield	2
Sweet sorghum MS line	15
Medium dwarf sweet sorghum male sterile line with yellow grain colour	2
Grain mould resistance	13
Shoot fly tolerance with multiple resistance to leaf diseases and also agronomic superiority and yield	1
Medium early duration male sterile line	2
Resistance to multiple foliar diseases	4
Good flaking quality	1

Source: Adapted from Radhamani *et al.*, 2011.

and 10 quantitative traits in 21 clusters. From each cluster, about 10% or minimum of one accession was selected to form a mini core that comprised 242 accessions (Upadhyaya *et al.*, 2009).

1.4 Genetics and Cytogenetics

Excellent reviews on the genetics of various traits are found in Doggett (1988), Murty and Rao (1997) and Rooney (2000). Quinby and Karper (1954) have shown that four recessive non-linked brachytic dwarfing genes control height. Quinby *et al.* (1973) have shown that the duration of growth and floral initiation is controlled by four loci; involving both dominant and recessive alleles. Most tropical landraces/varieties are dominant at all four loci, but a recessive allele at Mal locus will cause them to be less photoperiod-sensitive and apparently less responsive to temperature variations. The genetics of resistance to most diseases caused by fungi, bacteria and virus are, in general, simple inheritance of dominant alleles. The genetics of resistance to major diseases of sorghum is given in Table 1.2. Grain mould resistance on the other hand, is complex.

In contrast to diseases, the genetics of insect resistance is complex. Four insects are recognised as important pests throughout Asia, Africa and India: shoot fly; stem borer (*Chilo* spp. and *Busseola* spp.); midge; and head bug (*Calocoris* spp.). Rana *et al.* (1980) reported that the F_1 is almost intermediate between the two parents for shoot fly resistance, however, resistance was found to be partially dominant under low to moderate shoot fly pressures. Resistance to stem borer is conferred by both tolerance and antibiosis, with primary damage explained by additive (A) and A × A interactions, with secondary damage controlled by A and non-additive gene interactions (Rana and Murty, 1971; Jotwani, 1976). Resistance to both midge and head bug are predominantly under the control of additive gene action (Sharma *et al.*, 1994; Ratnadass *et al.*, 2002).

Two types of male sterility are widely used in sorghum improvement programmes: (i) genetic male sterility (GMS) and (ii) cytoplasmic nuclear male sterility (CMS). Genetic male sterility is expressed in sorghum in many ways with several sources of male sterility identified. In all the cases, a recessive allele in homozygous condition (designated with alleles, ms_1–ms_7 and *al*) confers male sterility. Genetic male sterility is

Table 1.2 Genetics of disease resistance in sorghum.

Disease	Genetic nature	Number of alleles
Kernel smut	Incomplete, dominant	3
Head smut	Dominant	—
Milo disease	Susceptibility is partially dominant	1
Anthracnose	Dominant, cytoplasm not significant	1
Rust	Dominant	1
Leaf blight	Susceptibility (in sudangrass) is dominant	1
Staygreen trait (charcoal rot tolerance)	Dominant at least with E 36-1 hybrids	—
Downy mildew	Dominant	>2

Source: From House, 1985; Reddy *et al.*, 1992; Reddy and Singh, 1993; Reddy and Stenhouse, 1993.

discussed in detail in Doggett (1988), Murty and Rao (1997), and Rooney (2000). The discovery of the male sterility resulting from the interaction of cytoplasmic and nuclear genes by Stephens and Holland (1954) laid the foundation and revolutionised the development of hybrid cultivar and hybrid seed production technology. The original source of the cytoplasm was the milo race, which induced male sterility in the nuclear background of the *kafir* race, and is designated as A_1 cytoplasm. Since then, several sources and types of male-sterile inducing cytoplasms (A_1–A_6) have been discovered. In all these cytoplasms, a single/oligo recessive gene in the nucleus and sterile cytoplasm induces male sterility. These male-sterile cytoplasms are differentiated based on the inheritance patterns of their fertility restoration, which is unclear, but dependent on the specific cytoplasm and nuclear combinations. Fertility restoration is controlled by single gene in some combinations (e.g. A_1) but is controlled by two or more oligogenes when the same nuclear genotype interacts with a different cytoplasm (Schertz, 1994).

1.4.1 Cytogenetics

Sorghum bicolor has a haploid chromosome number of 10, and it is classified as a diploid ($2n = 2x = 20$). Most species within *Sorghum* are diploid ($2n = 20$), but several species, most notably *S. halapense*, are tetraploid ($2n = 4x = 40$). Euploid variants such as haploids, triploids and tetraploids occur naturally and can be induced. Autotetraploid sorghums have an increased grain size, which sparked interest in their development for grain production (Doggett, 1962). The initial limitation in autotetraploid development was the high level of sterility observed, however selection for improved fertility was successful, with resulting fertility levels near that of diploids (Doggett, 1962; Luo *et al.*, 1992). However, further research in this direction stalled, resulting in the non-realisation of tetraploid sorghum for grain production. Aneuploids are organisms with more or less than an integral multiple of the haploid chromosome number. The most common form of aneuploidy observed in sorghum is trisomy, followed by translocation. Apomixis in sorghum occurs when the embryo forms by apospory from a somatic cell in the nucellus with up to 25% of the progeny developed apomictically, however, this can occur at a significantly higher percentage (Hanna and Schertz, 1970; Rao and Murty, 1972; Murty and Rao, 1977). In most cases, apospory is the primary mechanism of apomixis in sorghum, although diplospory may occur (Murthy *et al.*, 1979). Apomixis provides a mechanism to perpetuate a high-performing hybrid through self-pollination. Obligate apomixis is necessary to develop such a system, but all the reports of apomixis in sorghum involve only facultative apomixes, and efforts to increase the frequency of apomicts have not been successful (Reddy *et al.*, 1980). To utilise facultative apomixis, the use of 'vybrids' has been proposed (Murthy, 1986).

1.5 Reproductive Biology

The inflorescence of sorghum is the panicle/raceme. Sorghum spikelet development is basipetal – those in the upper region of the panicle develop earlier than those in the lower. The tertiary rachis consists of one or several spikelets. One spikelet of a raceme is always sessile and the other pedicellate, except the terminal sessile spikelet, which is accompanied by two terminal pedicellate spikelets. The number of sessile spikelets in a single inflorescence of cultivated sorghum varies from 2000 to 4000. At flowering, they are green but then

change shades, becoming straw- or cream-coloured buff, yellow, red, brown, purple or almost black at maturity. There are two glumes. The lower glume is enclosed by the upper glume with its membranous margin. The lower glume is usually flat and conforms more or less to the shape of the spikelet. The upper glume is more convex or boat-shaped. The seed may be enclosed by the glume or may protrude from it either partially or completely. There are two lemmae. The lower lemma is elliptical or oblong and equal in length to the glume. The upper lemma is short, ovate and may be awned. There are two lodicules and a palea. The spikelet has two pistils and three stamens. The stigma is fluffy, attached to a short style extending to the ovary. The anthers are attached to long, thread-like filaments (House, 1985). The pedicellate spikelets are narrower and may be smaller or longer or of the size of the sessile spikelets. They are male or neutral, or may rarely have a rudimentary ovary. The lemmae are short and the upper lemma rarely has an awn. Three stamens and two lodicules are found between the lemma and the palea.

Floral initiation in cultivated sorghum starts 30–40 days after germination. About 6–10 days before flowering, the boot forms a bulge in the sheath of the flag leaf. Sorghum usually flowers in 55–70 days in warm climates (House, 1985), depending on the genotype. Two days after the emergence of the inflorescence from the boot, the flowers begin to open. The flowering starts in the sessile spikelets at the tip of the inflorescence and progresses towards the bottom over 4 or 5 days. It takes 6 days for the whole inflorescence to complete flowering. The maximum flowering takes place on the third or fourth day. At flowering, the glumes open, and the three anthers fall free, while the two stigmas protrude, each on a stiff style (House, 1985). As the stamens emerge out of the opening glumes, they rotate and spread outward. The filaments elongate rapidly and the anthers become pendent. When flowering of the sessile spikelets is halfway through on the inflorescence, the pedicellate spikelets start opening from the tip and proceed downwards completing flowering earlier than the sessile spikelets in the inflorescence. The time taken from the commencement of glume-opening to completion of its closing is about 1–2 hours, which varies from cultivar to cultivar. Flowering starts at midnight and continues up to 10 a.m. depending on the genotype and climate. The maximum anthesis is between 6 a.m. and 8 a.m.. Wet and cool weather delays flowering. The anthers dehisce when they are dry, and the pollen grains are ejected into the air and onto the stigma. Sorghum is primarily self-pollinated (cross-pollination is only 2–10%). The florets of some of the very long glumed types do not open for outcrossing to take place, a phenomenon called *cleistogamy*. After pollination the glumes close, though the empty anthers and stigmas still protrude. The pollens retain their viability for 5 h at room temperature. The stigma remains receptive for 10 days. Under normal conditions stigma fertilisation takes place in 2 h. Organ differentiation occurs the following 12 days, and the embryo continues to grow until the seed is mature (Schertz and Dalton, 1980). Seed development is in three stages: milk stage, early or soft-dough stage, and late or hard-dough stage. The sorghum seed is a free caryopsis, also called grain. Seeds are spherical in shape, but somewhat flat on one side with the embryo at the base. They are red, brown, white, yellow or cream coloured with a dull or pearly lustre. The endosperm is usually white, sometimes yellow. The grain matures in 30–35 days after fertilisation. At physiological maturity, a dark brown callus tissue is formed at the base where the seed is attached to the spikelet. This callus tissue stops the translocation of nutrients from the plant to the seed. At physiological maturity, the seed contains 25–30% moisture and is fully viable. For safe storage, seed moisture should be brought down to 10–12%.

1.6 Production Constraints

The yield and yield stability of sorghum are constrained by a diverse array of insect pests, which vary according to the location of cultivation. Foliage pests in the United States include green bug (*Schizaphis graminum*), yellow sugarcane aphid (*Sipha flava*), chinch bug (*Blissus leucopterus*), fall armyworm (*Spodoptera frugiperda*), corn leaf aphid (*Rhopalosiphum maidis*), and Banks grass mite (*Oligonychus pratensis*). Other foliage pests are shoot fly (*Atherigona soccata*), spotted stem borer (*Chilo partellus*), and sugarcane aphid (*Melanaphis sacchari*) (Peterson *et al.*, 1997). Midge (*Contarinia sorghicola*) is a serious head pest common in India, Eastern Africa and Australia, with head bug (*Eurystylus oldi*) being another important pest in India and Western and Central Africa.

Sorghum is host to a large number of pathogens, including fungi, bacteria, viruses and nematodes. These pathogens, individually or in combination, may result in significant economic losses to grain and forage production. Important among diseases include grain mould caused by a complex of fungi in all sorghum growing regions of the world, anthracnose in Western and Central Africa (WCA) and Northern India. Apart from this, *Striga* is an important parasitic weed causing immense losses in all regions in Africa.

Drought stress is a major constraint to sorghum production worldwide. Although sorghum possesses excellent drought resistance compared to most other crops, improving its drought resistance would increase and stabilise grain and food production in low-rainfall, harsh environmental regions. (Rosenow *et al.*, 1997). Soil acidity (and associated Al^{3+} toxicity mostly in Latin America) and salinity (mainly in some parts of India and the Middle East countries) are probably the most important constraints to sorghum productivity in tropical environments, with an estimated 72.4 billion ha (18%) of the worlds soils classed as acidic, and 0.9 billion ha classed as saline and sodic (Vose, 1987; Gourley, Watson, Schaffert *et al.*, 1997). These problematic soils are major constraints for the resource-poor tropical farmers in developing countries.

1.7 Breeding Objectives

The identification of geographic functional regions with a set of constraints has resulted in the gradual shift in breeding strategy from initial wide adaptability to specific adaptations, and to trait-based breeding for threshold traits through the 1980s and 1990s (Reddy, Ramesh *et al.*, 2004). For example, improved post-rainy-season sorghums in India would require in addition to higher grain and fodder yields, tolerance to drought, shoot fly and lodging and grain quality (semi-corneous endosperm grains) suitable for making 'roti' (unleavened bread). On the other hand, in the northern Guinea zone of WCA, improved sorghum lines should have longer maturity, and hard grains with stable resistance to *S. hermonthica*, anthracnose, grain mould, stem borer and head bug. Also, grain quality evident traits such as soft endosperm grains are preferred in Eastern Africa for food product preparations such as injera and kisra and hard endosperm grains preferred in Western Africa for tô preparation are important (Reddy and Stenhouse, 1994).

1.7.1 Grain Sorghum

The main breeding objective in any breeding programme is yield. Poor productivity for grain yield of unimproved sorghum cultivars is related to their low harvest index; numerous biotic stresses including diseases, insect pests, and *Striga*; and abiotic stress factors such as heat, drought and problematic soils. All these factors cannot be addressed with the same priority at any given time by breeding. The relative impact of production constraints on yield loss is the primary criterion in research prioritisation. However, when it comes to genetic enhancement, the probability of success can be affected by a complex interplay of several factors, such as availability of genetic resources, inheritance and stability of the traits desired to be improved, simplicity and effectiveness of screening techniques (reliability and cost-effectiveness), access to test environments and availability of technical manpower and material resources, that also become determinants, sometimes of overriding importance. Breeding for high and stable grain yield with an improved harvest index continues to be the top priority in all sorghum programmes worldwide and it requires exploitation of the available germplasm as it provides vast genetic variability for yield components and adaptation traits, of which only a fraction, even from the cultivated types, has been utilised, understanding of the inheritance of most of the characters and designing suitable and simple evaluation procedures.

1.7.1.1 Breeding for Yield

Breeding methods used for genetic improvement of sorghum are similar to those employed for self-pollinated crops. The main methods used are pureline selection, pedigree breeding, back cross-breeding, random mating populations utilising genetic male sterility and hybrids involving cytoplasmic genetic male sterility. The discovery of genetic male sterility in sorghum opened up opportunities for recombination. Of the several genes reported to induce genetic male sterility, only two alleles were widely used in population improvement, as they are stable over a range of environments (Murty and Rao, 1977; Reddy and Stenhouse, 1994a). This, in combination with various mating systems and reciprocal recurrent selection methods in exploiting additive (A), A×A and some epistatic genetic variations led many breeders to propose/take up the population improvement methods in the 1960s (Comstock and Robinson, 1952; Doggett, 1972; Eberhart, 1972; Maunder, 1972). These breeding enhancements led to the development of several populations in East and West Africa supported by funding from the International Development Research Council (IDRC) (Doggett, 1972; Gardner, 1972). About 19 populations have been developed at ICRISAT–Patancheru using ms_3 and ms_7 genes into which 501 diverse germplasm accessions were introgressed. However most of the sorghum cultivars released globally was derived from the pedigree breeding programme rather than from the population improvement programmes. Pedigree selection is more appropriate for a short specific adaptation and targeted genepool approach is appropriate for a programme that aims at broad geographic mandate (Reddy, Ramesh *et al.*, 2004). Recurrent selection and pedigree breeding are the two most common methods used in the genetic improvement. Random mating is achieved through the application of genetic male sterility. At least seven recessive genes for male sterility have been identified in sorghum, but ms_3 has been used in nearly all the population improvement programmes, because it was the first to be discovered that had few disadvantageous pleiotropic effects. Both varieties and hybrids are commercially grown. The highest-yielding hybrids have about 15–30% grain yield advantage over the best

varieties of comparable maturity. A variety in sorghum is an advanced generation progeny (generally F6–F7 or S5–S6) that is highly homozygous and homogeneous. Thus, a sorghum variety has a stable genotypic structure, with little chance of significant genetic change over time except that due to outcrossing or spontaneous mutation. Commercial hybrids are produced using CMS lines and currently, only one CMS system, designated A1, is predominantly used worldwide (Schertz *et al.*, 1997). All the commercial grain hybrids are single-cross hybrids. Three-way hybrids can be produced, but they are less likely to be adopted in sorghum, because sorghum growers are relatively more conscious of the morphological uniformity of single-cross hybrids, and the seed yield advantage of the male-sterile F1s over male-sterile inbreds is much less.

The 1960s were marked by the ready accessibility of germplasm from the developed world to the developing world, and the beginning of the development of hybrid sorghums using cytoplasmic-nuclear male sterility (Reddy and Stenhouse, 1994a). The development and commercial cultivation of hybrid sorghums led to the improvement in grain yield by over 300% from 1950 to 1990 in the United States. Later improvements were in terms of smaller yield increments, and enhanced disease and insect resistance and grain quality (Rooney and Smith, 2000). Introduction of several seed parents of hybrid grain sorghum from the United States paved the way for hybrid development in Australia with several hybrids being released during 1960s. Tropical germplasm is an important source of dominant alleles for yield and plant height, while temperate germplasm has dominant alleles for earliness/maturity. The use of tropical×temperate crosses has produced several high-yielding varieties with desirable plant height (2–2.5 m) and maturity (100–110 days) (Rao and Rana, 1982). The type of restorer line used in breeding significantly impacts on heterosis, or vigour, in the resulting hybrids. *Guinea* restorer lines contributed to the highest heterosis and grain yield *per se* in hybrids, followed by *caudatum* restorer lines. However, accompanying problems such as clasping of glumes to the grain in hybrids of *caudatum–kafir* male-steriles and *guinea* restorers need to be addressed (Reddy and Prasada Rao, 1993). To circumvent the problem of negative correlation of grain size with number of grains and its associated problem of germination, some breeding programmes have successfully minimised the negative correlation and optimised the grain size by selecting seed parents of hybrids with the highest grain number within some pre-judged minimum range, then selecting the male parents (R-lines) with large grains (without regard for numbers).

1.7.1.2 Breeding for Abiotic Stress Resistance

Drought is the most devastating production constraint that can occur at any crop growth stage. Drought tolerance in sorghum is specific to the growth stage, that is, sorghum genotypes with good tolerance during one of the developmental stages might be susceptible to drought during the other growth stages, making it a complex character to work with. Drought is highly specific and that breeding for drought resistance therefore depends upon the stage of the crop at which the drought occurs, inferring that breeding for the traits that contribute to specific drought resistance should be carried out to realise further productivity gains in the target regions (Reddy, 1986). The mechanisms of drought tolerance in sorghum can be described as escape, avoidance and tolerance (Reddy *et al.*, 2009). Early maturity is a well-known 'drought-escape' mechanism through which the crop completes its life cycle before the onset of severe moisture deficits, and is often associated with reduced yield potential. Short-duration sorghums have lower evapo-transpiration rates due to smaller leaf area and smaller root density compared

to those of long-duration ones (Blum, 1979). To some extent, yield loss can be overcome by increasing the plant density. Drought avoidance is a mechanism for avoiding lower water status or to maintain a relatively higher level of hydration in tissues during drought by maintaining cell turgor and cell volume either through aggressive water uptake by an extensive root system (Manschandi *et al.*, 2006; Hammer *et al.*, 2009), or through reduction of water loss from transpiration and other non-stomatal pathways (Ludlow and Muchow, 1990) such as through the plant cuticle. Most cultivated dryland sorghum genotypes show epicuticular wax values close to the maximum (Jordan *et al.*, 1983). Plants avoid low Leaf Water Potential (LWP) by one or more mechanisms, such as a change in rooting pattern, an increased root growth for maximising water uptake or an adjustment in leaf area for optimisation of the use of absorbed water for the production of dry matter (Seetharama *et al.*, 1982). Sufficient genetic variability was recorded for the root attributes, transpiration efficiency and transpiration regulation (Hammer *et al.*, 1997; Kholová *et al.*, 2010), and canopy development (Borrell, Hammar and Henzell, 2000; Kim *et al.*, 2010). Drought tolerance is a mechanism by which plant maintains metabolism even at low water potential. Dehydration results in irreversible disruption of cellular organisation and metabolism and most crop plants belong to the dehydration-intolerant category. Severe dessication represents a small proportion of the total instances of drought. However, enhancement of dehydration tolerance, which results in continued leaf growth and decreased senescence during mild or moderate drought, could have a positive effect on agricultural production. This trait is considered as the most difficult to improve through conventional plant breeding. Characterisation of the target production region is the first and the crucial step in undertaking a genetic improvement programme aimed at improving yield and yield stability in drought-prone environments (Robertson, 1988).

Thus, while breeding for drought resistance and yield potential, emphasis should be given for traits such as emergence under crust, seedling drought recovery, and grain yield under drought-prone and yield-potential areas for early stage drought; for drought recovery and grain yield under drought-prone and yield-potential areas under mid-season drought; and stay-green, non-lodging and grain yield under drought-prone and yield-potential areas for terminal drought (Reddy, 1986).

1.7.1.2.1 Drought Tolerance

Drought stress is a major constraint to sorghum production worldwide. Although sorghum possesses excellent drought resistance compared to most other crops, improving its drought resistance would increase and stabilise grain and food production in the low-rainfall and harsh environmental regions of the world (Rosenow *et al.*, 1997). Drought resistance is the phenotypic expression of a number of morphological characteristics and physiological mechanisms including drought escape, dehydration avoidance and dehydration tolerance (Ludlow, 1993). Therefore, drought resistance in sorghum is a complex trait affected by several interacting plant and environmental factors.

The response of sorghum to soil moisture stress is largely determined by the stage of growth at which moisture stress occurs, with two distinct responses to drought stress identified. The pre-flowering (mid-season) drought response is expressed when plants are stressed during panicle differentiation prior to flowering, while the post-flowering drought response is expressed when moisture stress occurs during the grain filling stage (Rosenow and Clark, 1995). Two further responses were described by ICRISAT – where emergence under crust and high temperature prevailed in drought-prone environments,

and wherein the lines with long mesocotyl emerge earlier than others; and early stage (120-day-old seedlings) drought recovery where distinct differences among the genotypes were observed (Reddy, 1985).

Symptoms of pre-flowering drought stress susceptibility include leaf rolling, uncharacteristic leaf erectness, leaf bleaching, leaf tip and margin burn, delayed flowering, poor panicle exsertion, panicle blasting and floret abortion and reduced panicle size. Tolerance to pre-flowering drought stress is indicated by the alternative condition in each instance. Since the panicle is directly affected, severe pre-flowering stress can result in drastic reductions in grain yield. Research at ICRISAT–Patancheru, India, screened and identified progenies with high levels of pre-flowering stress recovery which were further selected for grain yield alternatively under mid-season drought and yield potential environments in India. When tested in drought-prone environments in Africa, these lines had greater stability and grain and biomass yield than other varieties. Similarly, promising lines with resistance to seedling emergence under crust and high temperature were also identified (ICRISAT, 1982; 1986; 1987).

Symptoms of post-flowering drought stress susceptibility include premature plant (leaf and stem) death or plant senescence, stalk collapse and lodging, charcoal rot (*Macrophomina phaseolina*) and a significant reduction in seed size, particularly at the base of the panicle. Tolerance is indicated when plants remain green and fill grain normally. Such green stalks also have good resistance to stalk lodging and to charcoal rot. Such cultivars are referred to as having 'stay-green' trait.

Stay-green is an important post-flowering drought-resistance trait, with genotypes possessing stay-green ability maintain a greater green leaf area under post-flowering drought than their senescent counterparts (Rosenow *et al.*, 1997). Recent studies have shown that leaves stay green not only because of small sink demand, but also due to higher leaf nitrogen status and transpiration efficiency resulting in maintenance of photosynthetic capacity and ultimately, higher grain yield and lodging resistance (Borrell and Douglas, 1997; Borrell *et al.*, 1999; Borrell, Hammar and Douglas, 2000; Borrell and Hammer, 2000). Greater green leaf-area duration during grain fill appears to be a product of different combinations of three distinct factors, green leaf area at flowering; time of onset of senescence and subsequent rate of senescence, all of which are independently inherited and easily combined in breeding programmes (Van Oosterrom *et al.*, 1996; Borrell, Hammar and Henzell, 2000). Stay-green hybrids produce significantly greater total biomass after anthesis, retain greater stem-carbohydrate reserves, maintain greater grain-growth rates and have significantly greater yields under terminal drought stress than related but senescent hybrids (Henzell *et al.*, 1997; Borrell *et al.*, 1999; Borrell, Hammar and Douglas, 2000). Excellent sources of resistance to both pre- and post-flowering drought have been identified, and although high levels of both types of resistance are generally not found in the same genotype, some genotypes possess good levels of resistance to both types (Rosenow *et al.*, 1997).

Several physiological traits such as heat tolerance, desiccation tolerance, osmotic adjustments, rooting depth and epicular wax are known to improve drought resistance (Downes, 1972; Sullivan, 1972; Sullivan and Ross, 1979; Turner, 1979; Jordan and Monk, 1980; Kramer, 1980; Jordan and Sullivan, 1982; Peacock and Sivakumar, 1987; Levitt, 1992; Krieg, 1993; Ludlow, 1993; Van Oosterrom *et al.*, 1996; Henzell *et al.*, 1997). Although screening techniques based on these traits for drought resistance have been reported, little if any progress using specific physiological traits has been documented, partly because interaction of various physiological mechanisms involved in drought tolerance is still poorly

understood (Christiansen and Lewis, 1982; Garrity *et al.*, 1982; Seetharama *et al.*, 1982; Blum, 1983; Jordan *et al.*, 1983; Ejeta, 1987; Bohnert *et al.*, 1995). It appears that individual physiological traits identified to date are not sufficiently related to overall drought response or field performance to merit selection based on them (Rosenow *et al.*, 1997).

Field nurseries in dry environments have been used to screen pre- and post-flowering drought response in several countries around the world including Mexico, Sudan and Australia (Ejeta, 1987; Rosenow *et al.*, 1997). Soil type affects screening, with sandy soil or shallow soil best suited for pre-flowering evaluation, and heavier, deeper soils best for evaluating post-flowering stress (Rosenow *et al.*, 1997).

The stay-green trait has been successfully used in Australia to develop post-flowering drought-stress resistance and lodging resistance in parental lines and in commercial hybrids. Conventional breeding for stay-green is primarily based on two sources, B35 and KS19 of Ethiopian and Nigerian origin, respectivley (Henzell *et al.*, 1984; 1992; Henzell and Hare, 1996; Rosenow *et al.*, 1997; Mahalakshmi and Bidinger, 2002). KS19 has been commercially used primarily in the breeding programme of Queensland Department of Primary Industries and Fisheries (QDPIF) while B35 is widely used in both public and private sector breeding programmes in the United States (Henzell and Hare, 1996). B35 has provided the major and best sources of stay-green used in QDPIF programme, and produced the key line QL41 with high levels of stay-green expression. Crosses between QL41 and sorghum midge-resistant lines formed the basis of the female stay-green and midge-resistant genepool in the QDPIF programmes, although less progress has been made in developing such germplasm in the male population (Rosenow *et al.*, 1983; Henzell *et al.*, 1997). Because of this precise requirement for the trait expression, field environments do not offer ideal conditions for selection and therefore, identification of QTL conferring stay-green trait and the molecular markers tightly linked to these QTL will provide powerful tools to enhance drought resistance (Henzell and Hare, 1996; Crasta *et al.*, 1999; Xu *et al.*, 2000).

1.7.1.2.2 Tolerance to Soil Acidity

Tolerance to soil acidity and Al^{3+} toxicity in sorghum is controlled by a few dominant genes under additive and non-additive actions, with heterosis also observed (Flores *et al.*, 1991; Adamou *et al.*, 1992; Zake *et al.*, 1992; Maciel, Andrade Lima de, Duncan *et al.*, 1994; Gourley, Watson, Schaffert *et al.*, 1997). Soil acidity stress factors vary with location, soil depth, rainfall, temperature, effective cation exchange capacity (ECEC), natural content of essential elements, level of toxic ions, p-fixation capacity and amount and quality of organic matter (OM) (Gourley, Watson, Schaffert *et al.*, 1997). These factors combined with a poor correlation of results obtained in nutrient culture for acidity tolerance in field or greenhouse studies are the causes of complexity of breeding for tolerance to soil acidity (Horst, 1985; Marschner, 1991). Nevertheless, much progress has been made since EMBRAPA sorghum for tolerance to acid soils and International Sorghum and Millets (INTSORMIL) sorghum acid-soil breeding project were initiated in Columbia in 1981 (Schaffert *et al.*, 1975).

Many sorghum lines have been identified with good levels and substantial genetic variability in Al^{3+} toxicity tolerance (Andrade Lima de *et al.*, 1992; Maciel, Andrade Lima de, Santos *et al.*, 1994; Gourley, Watson, Schaffert *et al.*, 1997). More than 6000 sorghum genotypes from the world collection were screened at Quilichao, Colombia, with around 8% found to tolerate 65% Al^{3+} saturation, with a few of these genotypes able to produce greater than 2 t/ha of grain (Gourley, 1988). Many of these highly tolerant genotypes from the world collection originated in acid-soil areas in Nigeria, Uganda or Kenya and

were classified as *caudatum* or *caudatum*-hybrid races. The open-panicled *Guinea* race and the hybrid *Guinea bicolor* lines had a higher overall percentage of acid-tolerant sorghum entries than those of other races and hybrids evaluated (Gourley, 1988).

The INTSORMIL and EMBRAPA projects used pedigree-breeding methods to identify Al-tolerant plants, and screened the F_2 plants at 65 and 45% Al saturation, respectively. The resulting tolerant lines had yields between 2.6 and 4.6 t/ha, with the INTSORMIL lines shorter and earlier than the EMBRAPA lines (Gourley, Watson, Schaffert *et al*., 1997). About 170 grain sorghum inbreds with tolerance to Al saturation levels of tropical acid soils developed by pedigree breeding have been released as germplasm by Mississippi Agricultural and Forestry Experiment Station (MAFES) (Gourley, Watson, Goggi *et al*., 1997).

ICRISAT and Centro International de Agriculture Tropical (CIAT) screened large numbers of grain sorghum lines (male-sterile, restorer and forage lines) over four consecutive seasons under varied Al^{3+} concentrations, and identified high-yielding male-sterile lines (MS), restorer lines (R) and forage sorghums tolerant to Al^{3+} that have been distributed to various agencies in the region (ICRISAT, NARS, CIAT, 1997). Evaluation of these high-yielding breeding materials in multiple locations resulted in the identification of many male-sterile lines (MS), restorer lines (R), maintainer lines (B), and forage lines with wide adaptability (regression coefficient between 0 and 1) (Reddy *et al*., 1998; Reddy and Rangel, 2000).

Four of the nearly 200 sorghum hybrids evaluated at Matazul (60% Al^{3+} and 4.6% organic matter), were found to have outstanding tolerance to soil acidity, and they were also less susceptible to leaf diseases, were greener at the time of maturity, and also taller than the control Real 60 (ICRISAT, 2000). Hybrids therefore hold promise for improving the sustainability of the acid savannas (Reddy, Prakasha Rao *et al*., 2004).

1.7.1.2.3 Soil Salinity Tolerance

While there are several studies on the assessment of variability for salinity tolerance in sorghum, studies on genetic basis of this variation is rather limited (Azhar and Mc Neilly, 1989; Haggag *et al.*, 1993; de la Rosa Ibarra and Maiti, 1994; Fernandes *et al*., 1994; Igartua *et al*., 1994; Jiqing Peng *et al*., 1994; Maiti *et al*., 1994; Richter *et al*., 1995). The genetic control of salinity tolerance appears to be complex with both additive and dominant gene effects important in controlling the expression of salt tolerance, however, the effect of dominant genes appear to be most important (Igartua *et al.*, 1994). The relatively high heritability for salt tolerance suggests the possibility of rapid improvement in salinity tolerance using high selection pressures in F_2 populations (Azhar and McNeilly, 1989).

Early screening for salt–stress-tolerant sweet sorghum genotypes can be done *in vivo* by: (i) growing the seedlings on sand in polystyrene containers, and (ii) growing the seedlings in spectrophotometer cuvettes (Montemurro *et al*., 1994). Genotypic response to salt stress is similar in both the methods, and classification of sweet sorghum genotypes for salt tolerance was effectively demonstrated. A third method was suggested by Hassanein and Azab (1990), where seeds of sorghum genotypes were grown in water (control) and NaCl solution (ECE = 12, 16 or 20 mhos/cm).

Biochemical basis of resistance to salinity: The concentration of biochemical components such as proline and hydrocyanic acid (HCN) increase with an increase in salinity levels in resistant genotypes, but not in the susceptible genotypes of sorghum at the seedling stage (Richards and Dennett, 1980; de al Rosa Ibarra and Maiti, 1994). The detailed study of resistance mechanism of these lines would aid in incorporation of resistance in elite agronomic background.

Attempts to breed sorghum for salinity tolerance is rather limited. This is because the major problem when breeding sorghum for abiotic stresses such as salinity is the choice of optimal selection environment/s due to the high levels of both spatial and temporal variation in salinity-affected fields (Richards and Dennett, 1980; Richards *et al.*, 1987; Igartua, 1995). Spatial variation occurs horizontally and vertically on very small scales, and, therefore, most salinity-affected lands are actually comprised of many micro-environments, ranging from low to high salinity in the same field (Igartua, 1995).

Testing genotypes across a broad range of salinity levels shows that genotype×salinity level interactions are commonly large and significant in sorghum, forcing the plant breeder to decide whether to work over the whole target environment (breeding for wide adaptation), or subdivide it into more homogeneous sub-environments (breeding for specific adaptation) (Azhar and Mc Neilly, 1987; Igartua, 1995). This decision depends mainly on the relative sizes of the genotype×year and genotype×location interaction (Austin, 1993). Unfortunately, when working in areas with saline soils, this choice does not exist as the highly variable conditions occur concurrently in the same field. Thus, breeding for saline areas can be compared to wide adaptation.

The target environments, both for breeding for saline soils or for wide adaptation, are actually a population of many possible environments, for which there exists a significant component of genotype×environment interaction (Igartua, 1995). Three environment selection strategies have been proposed: (i) make selection in a stressful environment; (ii) select under optimum growing conditions and (iii) use a combination of both the approaches, that is, select materials that perform well under both stress- and non-stress conditions (Calhoun *et al.*, 1994). The third option appears to be the best as separate selection for distinct environments is not possible, and greater accuracy of selections is achieved over more environments used (Igartua, 1995). However, as testing resources are limited, a sensible compromise seems likely to be combination of a non-stress location, and at least one stress environment (within the range of target environment) between which there is G×E interaction (of cross over type). Selection of breeding populations for salinity tolerance over three salinity levels: low, high and average of the two extreme levels, instead of the whole range of salinity levels, has demonstrated the usefulness of option 3 to select for improved yield in grain sorghum under saline soil conditions (Maas and Hoffman, 1977; Igartua, 1995).

Salinity causes more serious damage to sorghum cultivars in the seedling-emergence stage than in any other stage as revealed through both field and laboratory experiments in China (Jiqing Peng *et al.*, 1994). Therefore, enhancing the salinity tolerance of grain sorghum at the germination-emergence stage should be one of the breeding objectives sought for areas affected by soil salinity (Hassanein and Azab, 1990). The effectiveness of divergent selection for tolerance to salinity at germination-emergence stage in grain sorghum has been demonstrated where subsets of the progenies showing best and least tolerance to salinity were selected and recombined to constitute the next cycle. Evaluation of the original and four subpopulations under saline conditions evaluated in the laboratory and the field for germination-emergence ability revealed the effectiveness of selection in separating the subpopulations (Igartua and Gracia, 1998).

Thus, it appears that while attempts to enhance salinity tolerance of sorghum in saline areas are limited, much progress has been achieved in breeding sorghum for soil acidity tolerance with and without Al^{3+} toxicity. Future breeding programmes should aim at specific adaptations in view of significant genotype×Al^{3+} toxicity interaction variation, and variation in Al^{3+} saturation from location to location. Further, the possibility of

different resistance mechanisms due to varying levels of Al^{3+} saturation necessitates the study of resistance mechanisms and their genetics in selected sorghum lines. Wide adaptation for salinity tolerance is also warranted due to the considerable variability in soil salinity levels both spatially and temporally within field plots.

1.7.1.3 Breeding for Biotic Stress Resistance

Breeding schemes involving simultaneous selection for resistance and grain yield and converting the maintainer selections into male-sterile lines has been used effectively to develop male-sterile lines for resistance to pests and diseases in the shortest possible period of 4 years (Reddy, Prakasha Rao *et al*., 2004). Breeding for insect resistance targets multiple traits. For stem borer resistance, the independence of antibiosis and the difference in patterns of inheritance of resistance to flower and peduncle damage and dead heart formation must be considered. The traits foliar and stem damage, and the percentage of dead hearts were targeted with stem-borer-resistant genotypes identified (Singh and Rana, 1994). For shoot fly, the most important factor is to select for resistant germplasm in the season for which the material is intended (Jayanthi, 1997). In selecting for resistance and increased yield, a multiple selection approach is employed with resistance selected on a family basis, and then selecting individuals within the resistant family for yield (ICRISAT, 1995). In combining resistance characters that are simply inherited with grain yield, multiple crosses (three- or four-way) are as effective as single crosses. However, the selection for resistance of quantitatively inherited traits, such as resistance to stem borer or shoot fly, is not effective in four-way crosses (Reddy, 1993).

Extensive use of the zera zera group of converted sorghums has made major contribution to disease resistance, yield potential and grain quality of the US hybrid sorghum (Rosenow and Dalhberg, 2000). On a global scale, breeding for grain mould in sorghum has been accorded the highest priority. However, the success rate has been disappointing, because grain mould is caused by a complex of parasitic fungi (species of *Fusarium*, *Curvularia*, *Phoma* and *Colletotrichum*) that damage endosperm and saprophytic fungi (species of *Aspergillus* and *Cladosporium*) that affect the pericarp. Mould-resistance sources are mostly red or brown grain types, which are associated with high tannins and (or) phenolic compounds such as flavan-4-ols. A few good resistance sources with red grain types have been found in tannin-free backgrounds (Bandyopadhyay *et al*., 1988). In white grain sorghums, moderate levels of resistance are available only in hard endosperm backgrounds. Associations such as these have deterred the incorporation of mould resistance into early-maturing and large-seeded white grain sorghums with high grain yield. Other biotic constraints have received relatively low priority in the semi-arid tropical regions of Asia and Africa. These can be grouped into two categories. The first category includes anthracnose (*Collitotrichum graminicola* (Ces.) Wils.), leaf blight (*Exserohilum turcicum* Leo and Sug.) and leaf spot (*Cercospora sorghi* Ellis and Everhert), diseases of sorghum; midge (*Stenodiplosis sorghicola* Coquillett)) and head bugs (*Calocoris* and *Eurystylus* species) insect pests of sorghum; and the root parasite *Striga hermonthica* (Del.) Benth. of sorghum. For these, good resistance sources and effective screening techniques have been developed (Sharma *et al*., 1991; 1993; Thakur *et al*., 1992; 1993; Ejeta *et al*., 1997). However, these have been shown not to have as large an impact on yield, on as large a geographical scale, as grain mould. Crop losses due to *S. hermonthica* can be considerably reduced in both crops through the use of trap and catch crops, and through various cultural practices (Lagoke *et al*., 1991). The second category includes stem borers (species of *Busseola*, *Eldana*, *Sesamia* and *Chilo*) shoot

fly (*Atherigona soccata* Rodani) and ergot (*Claviceps africana*, Frederickson, Mantle and de Milliano) of sorghum for which confirmed sources of good resistance are not available and (or) the trait inheritance is too complex to permit its effective utilisation in breeding. This category has received little attention in breeding programmes in Asia and Africa.

1.7.1.3.1 Resistance to Foliar, Stem and Head Feeding Insects

The lack of elite insect-resistant varieties and hybrids is due to low resistance levels when transferred into agronomically improved sorghum. When resistance is high, progenies are agronomically undesirable (Nwanze *et al*., 1995). In addition, resistance to some insects is quantitatively inherited and difficult to incorporate into elite, high-yielding varieties or hybrids (Pederson *et al*., 1997).

Population, pedigree and/or backcross breeding methods are adopted to develop insect-resistant sorghum genotypes. If resistance is evaluated using the techniques developed by entomologists in collaboration with plant breeders such as in the greenhouse (as for green bug), only resistant genotypes are taken to the field for further selection or crossing (Pederson *et al*., 1997). On the other hand, if resistance evaluation is done in the field, resistant genotypes should be identified before pollination to expedite development of improved plant populations. The appropriate method to use will be specific to a particular research programme, the genetics of resistance, research objectives and the needs of collaborators (Pederson *et al*., 1997).

Development of improved germplasm and/or varieties resistant to shoot fly, stem borer and midge are the examples for the success of conventional breeding programmes in Africa and India (Sharma, 1993). Low levels of resistance to shoot fly have been incorporated into a few promising cultivars, and although several improved shoot fly-resistant male-sterile lines have been developed by involving these improved varieties and restorers in back-cross programme, hybrid parents with improved agronomic characters such as greater seed size coupled with shoot fly-resistance are needed to produce post-rainy-season hybrids in India. Until now, pedigree and backcross breeding have been used (supported by artificial screening) at ICRISAT–Patancheru to breed hybrid parents resistant to shoot fly and adapted to the rainy-season-production systems from a broad range of germplasm accessions and several breeding lines. Use of wild sorghums, *S. versicolor* and *S. arundinacium* to obtain qualitatively different sources of resistance is the future objective. Absolute resistance to shoot fly was noticed in wild relatives *S. dimidiatum and S. australiense*, with efforts currently underway to exploit and introgress these using molecular markers.

Several midge-resistant varieties and hybrid parents have been developed at ICRISAT–Patancheru using pedigree selection and backcross techniques; however, these are mostly based on single source of resistance that loses its resistance at the high altitudes and low temperatures of Eastern Africa. An immediate objective would be to incorporate midge resistance expressed at low temperatures into agronomically improved cultivars. In Western and Central Africa, advanced midge-resistant lines bred at Patancheru are crossed to locally adapted elite materials to obtain improved midge-resistant cultivars.

Breeding efforts for resistance to stem borer by ICRISAT in India and western and central Africa are focused on *C. partellus* and *B. fusca*, with several stem-borer-resistant male-sterile lines, pollinators, and varieties developed. In Western and Central Africa, a random mating population with sources of resistance to *B. fusca* and adapted

high-yielding lines are being developed and pursued through recurrent selection procedures. To make necessary genetic improvement in insect resistance, breeders and other scientists will need to incorporate molecular biological tools into their programmes to a greater extent (Peterson *et al*., 1997).

1.6.1.3.2 Breeding for Disease Resistance

Disease management through genetic manipulation has been the most effective means of reducing losses in many crop species. However, managing all diseases by genetic means is neither feasible nor possible (Thakur *et al*., 1997).

Breeding for host-plant resistance is one of several methods of protecting the crop. Therefore, before a resistance breeding programme begins, it must be clearly determined that: (i) the disease is of sufficient economic importance, (ii) sufficient information is available on the nature of host-pathogen system and on screening techniques, (iii) well-defined sources of resistance are available and (iv) the expected economic output will occur within a given time.

Breeding for disease resistance in sorghum began about three decades ago (Mukuru, 1992; Rosenow, 1992). Crop improvement employed diverse exotic germplasm to improve both grain yield and the agronomic characters of local cultivars. Choice of parents is the first crucial step in any hybridisation and selection programme. Usually an agronomically good, high-yielding cultivar is crossed to other parents with disease resistance, good grain quality, local adaptation, etc. Appropriate weight should be given to the maturity period, height, grain quality and status of resistance to various stress factors of the parents involved in the cross. The genetic basis of resistance should suggest the selection procedure (Thakur *et al*., 1997). Disease control through host genetic manipulation is difficult and has been slower for charcoal rot and grain mould, in which gene effects are small, compared to downy mildew, anthracnose and leaf blight, in which gene effects are large (Thakur *et al*., 1997).

Pedigree breeding with selection for resistance based on families and agronomic desirability within the selected families of single crosses, and frequently in three-way crosses has resulted in disease-resistant, high-yielding hybrid parents. It has been found that a third parent in the cross can supplement useful traits/recessive genes and increase their frequency in the segregating populations without seriously affecting agronomic eliteness. Specific improvement for resistance to a simple disease (e.g. rust) can be obtained by back-cross breeding. Pedigree-breeding selection procedures to accumulate favourable alleles for multiple resistance factors for diseases such as grain mould, downy mildew, charcoal rot, etc. were used at ICRISAT–Patancheru, and considerable progress has been made in transferring resistance to individual diseases into several high-yielding sorghum lines for grain mould, downy mildew, rust, leaf blight and anthracnose.

Current breeding methods at ICRISAT–Patancheru, India, include both pedigree and population improvement for grain mould resistance breeding. Pedigree selection using artificial screening for grain mould resistance has resulted in improved high-yielding lines and hybrid parents with white grain types. A random mating population with white grains and *guinea* type panicle and glume traits is under improvement at ICRISAT–Patancheru. Male-sterile lines with white, red and brown grain colours and with resistance to grain mould have also been developed. The possible roles of anti-fungal proteins that inhibit the growth of grain mould fungi are being investigated at ICRISAT–Patancheru and Texas A&M University in the United States. Several

male-sterile lines resistant to anthracnose (*Colletotrichum graminicola*) have been developed at ICRISAT–Patancheru, India, following pedigree selection and back-cross methods.

With the advent of modern molecular techniques, however, significant advances have occurred in molecular characterisation of resistance genes and identification of markers for tagging. Present-day breeding for disease resistance is a collaborative effort of pathologists, molecular biologists and breeders working across locations and regions (Thakur *et al*., 1997).

1.7.1.3.3 Breeding for Striga Resistance

Witchweed (*Striga* spp.) is endemic to subtropical regions and comprise about 36 species, of which around 31 occur in Africa (Raynal-Roques, 1987). Five species of *Striga* attack cultivated cereals: *Striga hermonthica* (Del.) Benth, *S. aspera* (Willd) Benth, *S. forbesii* Benth, *S. asiatica* (L) Kuntze and *S. densiflora* Benth (Doggett, 1984). Only three species are of widespread economic importance in Africa: *S. asiatica* and *S. hermonthica*, which attack cereals, and *S. gesnerioides* that parasitise legumes, principally cowpea (*Vigna unguiculata*) (Doggett, 1988).

Striga asiatica occurs mainly in Southern and Central Africa while *S. hermonthica* predominates in the semi-arid zones of tropical Eastern, Central and Western Africa where it attacks food crops such as sorghum, pearl millet (*Pennisetum glaucum*), maize (*Zea mays*), upland rice (*Oryza sativa*), sugarcane (*Saccharum officinarum*), as well as several wild grasses (Tarr, 1962; Doggett, 1988). *Striga hermonthica* and *S. asiatica* are obligate parasitic weeds of sorghum with significant economic importance. The yield losses from damage are often significant with estimates varying from 10 to 70% depending on crop cultivator and degree of infestation (Doggett, 1988). Crop losses due to *Striga* infestation are often higher in Africa than in India. The *Striga* parasite produces large numbers of tiny seeds that remain viable in the soil for many years, germinating only when a host root grows in close proximity, and once established in the fields, it is virtually impossible to eradicate, making this parasite extremely difficult to control (Doggett, 1988).

Host plant resistance is the most practical and economically feasible means for reducing crop losses due to *Striga* and is central to an integrated control approach. *Striga* resistance is defined as the capacity of a host plant to support fewer emerged *Striga* plants and to yield more grain than a susceptible crop plant grown under similar infestation (Ejeta *et al*., 1997). Characterisation of source germplasm, development of simple and efficient screening techniques and a well-planned selection strategy for yield and other traits of importance in subsistence agriculture are the bare essentials for embarking on breeding for *Striga* resistance. Given the widespread *Striga* problem, and the opportunities for natural and deliberate selection in environments where the host and parasite have co-evolved, there has been surprisingly low genetic variability for *Striga* resistance in sorghum germplasm (Ejeta *et al*., 1997).

Pedigree breeding selections for agronomic and grain quality traits in early-generation breeding progenies, with selection for *Striga* resistance defered until homozygous progenies are derived after several generations of selfing. This is necessary because, selecting for field-*Striga* resistance in unreplicated segregating progenies on per plant basis is uninformative. Seed parents (with genes for *Striga* resistance) were developed following pedigree breeding and used to develop resistant hybrids at ICRISAT–Patancheru and Purdue University.

Recurrent selection schemes involve a population-improvement approach using a cyclical selection scheme in a carefully synthesised random-mating population to pyramid genes for *Striga* resistance from several sources into one common background. A random-mating sorghum population has been developed at Purdue University (Ejeta and Bulter, 1993b).

1.7.1.4 Breeding for Grain Quality

The starch content of whole sorghum is about 70%, and its protein content is about 11% (flour weight basis), which is higher than in maize (Klopfenstein and Hoseney, 1995). The digestibility of sorghum protein is relatively poor, because cross-linked prolamine levels are relatively higher in sorghum which are known to be extremely low in the essential amino acid lysine, rich in leucine and with low protein digestibility (i.e. lowered when the grain is cooked) (Deosthale *et al*., 1972; Maclean *et al*., 1983; Rao, Mehta *et al*., 1984; Magnavaca *et al*., 1993). The digestibility problem is further complicated by the presence of polyphenols as condensed tannins in some brown grain sorghums (those with a testa). Sorghum is usually rich in glutamic acid, leucine, alanine, proline and aspartic acid, with the level of amino acid highly positively correlated with protein content (Waggle and Deyoe, 1966). Similar protein content of immature and mature grain coupled with higher content of lysine, aspartic acids and glycine and much lower glutamic acid, proline and leucine makes immature grain more nutritionally balanced than mature grain in terms of amino acid composition (Deyoe *et al*., 1970). The proteins albumin and globulin, glutein and prolamins are best, intermediate and poorest proteins in terms of nutrition (Virupaksha and Sastry, 1969; Wall and Blessin, 1970).

Considerable variability has been reported for protein content as well as essential amino acid levels such as: lysine, methionine, tryptophan, histidine, arginine, aspartic acid, threonine, serine, glutamic acid, proline, glycine, alanine, cystine, valine, methionine, isoleucine, tyrosine and phenylalanine (Virupaksha and Sastry, 1968; 1969; Deosthale *et al*., 1970; Reich and Atkins, 1971; Mali and Gupta, 1974; Nanda and Rao, 1975a; 1975b).

While the protein content of sorghum grain is governed by additive gene action, essential amino acids such as lysine and methonine are controlled by both additive and non-additive gene action. Another essential amino acid, tryptophan appears to be governed by non-additive gene action (Nanda and Rao, 1975a; 1975b; Rana and Murty, 1975; Singhania *et al*., 1979; Nayeem and Bapat, 1984; Chinna and Phul, 1986; Mallick *et al*., 1988). While the high-lysine natural mutant gene (hl) is a monogenic recessive (Singh and Axtell, 1973), lysine content is inherited as a single gene with partial dominance in p-721 Q, a chemically induced high-lysine mutant of sorghum (Mohan, 1975; Axtell *et al*., 1979). Similarly, protein digestibility in a sorghum line, p-851171 derived from p-721 Q is inherited as a simple Mendelian trait (Oria *et al*., 2000; Axtell, 2001).

The identification of naturally high-lysine Ethiopian sorghum mutants from the world sorghum collection, a chemically induced high-lysine mutant, and the recent identification of a sorghum line with high protein digestibility levels surpassing that of maize, facilitated the prospects for combining high nutritional quality and grain yield (Singh and Axtell, 1973; Mohan, 1975; Oria *et al*., 2000). The two high-lysine Ethiopian lines, IS 11758 and IS 11167, have exceptionally high-lysine contents, are photoperiod-sensitive, tall, late and have shrivelled or dented seeds. Their acceptance is limited due to many problems associated with their opaque kernel characteristics, reduced grain yield, slow drying in the field, increased susceptibility to moulds and insects and the tendency

of the seed to crack when mechanically harvested (Rao, Mehta *et al*., 1984; Ejeta and Axtell, 1990). Similarly, the chemically induced high-lysine strain p-721 Q has soft kernel and floury endosperm with reduced yielding ability (Rao, Rana *et al*., 1984; Asante, 1995; Axtell, 2001).

Earlier attempts to select agronomically desirable recombinants with dwarf- to medium plant height, early maturing and relatively photoperiod-insensitive with superior protein quality, from various cross combinations of the very tall, late, photoperiod-sensitive Ethiopian high-lysine parents were not fruitful (Rao *et al*., 1983b). Although it was possible to select plump, corneous grain types with the high-lysine trait, as breeding continued and generations advanced, there was a reduction in the frequency of plants with high levels of lysine. Selection during 1994 from a high-lysine population developed at Purdue University had 0.30–0.49% lysine (flour basis), compared to normal sorghum cultivars that contain about 0.24% lysine with grain yield in this group ranging from 3 to 4 t/ha (Hamaker and Axtell, 1997). Establishment of a negative correlation between protein and lysine content in several segregating generations of Ethiopian high lysine × agronomically superior varieties forced the breeders to improve lysine at moderate protein levels (Rao *et al*., 1983a; Rao, Rana *et al.*, 1984).

Ejeta and Axtell (1990) were able to select modified endosperm of p-721 opaque (high lysine mutant) with vitreous kernels similar to normal types. But, vitreous phenotypes have been detected in advanced generation (F_6) of breeding. However, crosses between p-721 Q (high protein digestibility) and other elite lines resulted in improved yields (Axtell *et al*., 1979). The recent identification of sorghum line, p-851171, (a derivative of p-721 Q) with protein digestibility levels surpassing that of maize raises the hopes of improving protein digestibility in sorghum (Oria *et al*., 2000). However, to date, no studies have examined the association between protein digestibility and lysine concentration in crosses involving p-85117 (Axtell, 2001).

Recent development of a rapid protein digestibility assay for identifying highly digestible sorghum lines will help in screening large number of breeding lines for protein digestibility (Aboubacar *et al*., 2002). Sorghum germplasm with high protein digestibility as high as or higher than maize or other staple cereals have been identified through Purdue/INTSORMIL research. In addition, lines having vitreous kernels with good food grain and processing properties have been identified and are available for breeding programmes at Purdue University (Axtell, 2001).

Whole-grain digestibility of sorghum is sometimes a problem; however, local processing techniques convert sorghums into digestible foods. Development of highly digestible sorghum is desirable, but in many environments, the highly digestible sorghums are predigested by moulds and insects in the field and have quite low yields. Therefore, highly digestible types may be limited to production in extremely dry environments where the grain is not subjected to humidity after maturity. It is difficult to improve digestibility without enhancing the susceptibility of the grain to deterioration, thus, efforts to enhance digestibility of sorghum must be done with care. Waxy sorghums have improved digestibility for ruminants and possibly swine, but that improvement is accompanied by poor seedling emergence and viability. Current waxy sorghum hybrids have lower grain yields, however hetero-waxy hybrids, where one parent is waxy and one non-waxy, provide high-yielding hybrids with improved digestibility (Rooney *et al*., 2003).

Contrary to the belief of many scientists and nutritionists that all sorghums contain tannins, sorghums without a pigmented testa do not contain tannins (Bulter, 1990a).

The tannin (brown) sorghums have a very definite pigmented testa (caused by combination of dominant B_1-B_2-S-genes) with levels of condensed tannins which may offer resistance to birds and grain mould (Tipton *et al*., 1970; Mc Millian *et al*., 1972; Bulter, 1990b; Rooney *et al*., 2003). The rate of pre-harvest germination is significantly lower for most high-tannin sorghums (Harris and Burns, 1970; Chavan *et al*., 1980; Asante, 1995). The level of tannins in high-tannin sorghums is enough to cause significant anti-nutritional effects, especially if the diet is inadequate in protein (Bulter, 1990b). Adding extra protein to the ration overcomes the effects of the tannins. The tannin sorghums decrease feed efficiency by about 10% when fed to livestock. The tannin sorghums have high anti-oxidant activities and may be a very important source of nutraceuticles. Thus, we might someday use the sorghums with a pigmented testa and dominant spreader gene as potent, more efficient sources of anti-oxidants than fruits or berries (Rooney *et al*., 2003). Thus, it appears that tannins have more beneficial than harmful effects, and hence the problem of tannins can be addressed by identification and development of sorghums in which beneficial effects are retained, while anti-nutritional effects are eliminated.

Two micronutrients, iron (Fe) and zinc (Zn) and pro-vitamin A (β-carotene) are recognised by the World Health Organization (WHO) as limiting. Deficiency for Fe, Zn and β-carotene is highest in South Asia, Southeast Asia and sub-Saharan Africa. These are also the regions where sorghum is cultivated and consumed as food by large number of people.

Considering the prospects of large genetic variability and presumably simpler genetic inheritance for Zn and Fe, as evidenced from other cereals like rice, wheat and maize, levels of these mineral nutrients can be further improved through concerted breeding efforts (Banziger and Long, 2000; Gregorio *et al*., 2000). A fairly good variability coupled with additive genetic inheritance and moderate heritability of β-carotene levels brightens the prospects of improving this trait in sorghum (Nanda and Rao, 1974; 1975a; 1975b). Further, positive association of β-carotene with grain yield offers opportunities for combining high yield with enriched β-carotene in sorghum (Nanda and Rao, 1975a, 1975b). ICRISAT–Patancheru has initiated sorghum improvement for improved Zn, Fe and β-carotene levels.

1.7.2 Forage Sorghum

Single-cut forage sorghums grow upto 3 m tall and have large stem diameter. These sorghums produce silage of a lower quality than corn. However, incorporation of brown midrib (BMR) trait can improve the digestibility. Sudangrass has finer stems, produces numerous tillers and is leafier than single-cut forage sorghums. They produce very few seed, and regrowth rate is high. Furthermore, sudangrass accumulates less of the poisonous compound prussic acid (HCN) than forage sorghums.

Sorghum × *sudangrass hybrids*: Hybrids of forage sorghum and sudangrass have the highest yield potential if adequate rainfall is received or irrigation is provided. The forage should reach 24 inches before grazing. At this stage, sorghum×sudangrass hybrids will generally have total digestible nutrients (TDN) values in excess of 53–60% and crude protein (CP) concentrations of 9–15%. Varieties with the BMR trait are usually preferred for grazing. Research in Texas has indicated that BMR varieties may improve animal gains by as much as 5–8% relative to non-BMR varieties. In the southeastern United States, sorghum×sudangrass hybrids are commonly used as a forage crop for

stocker cattle and brood cows following a winter or spring crop. Sorghum×sudangrass forage crops are designed for multiple harvests and can be used as hay, silage, pasture or green chop. Unfortunately, these hybrids dry very slowly, even if an impeller (flail) or roller-crimper conditioner is used during crop harvest. Consequently, hay production from these species is at greater risk of rain damage or being allowed to get too mature before hay harvesting is possible.

Forage is defined as 'food for animals especially when taken by browsing or grazing' (Webster, 1986). Sorghum grown for forage in the tropics is often tall (2–3 m) but can be the very same dwarf hybrid grown for grain production and may or may not include grain fraction of the plant (Pedersen and Fritz, 2000). However, from a definition point of view, the forage sorghum includes cultivars ranging from silage sorghum hybrids, to varieties, to *S. sudanense* ($2n = 10$) and sorgo-sudangrass hybrids to sudangrass varieties ($2n = 10$) and hybrids (Kalton, 1988). The uses of forage sorghum varies; in India it is commonly used as green fodder in northern states, and as stover after the grain harvest in southern states (House *et al*., 2000); whereas in the United States they are primarily used as silage, and to a limited extent, as pasture and hay for livestock (Kalton, 1988).

Forage sorghums make efficient use of soil moisture by resorting to a semi-dormant state during stress, with a rapid response to moisture and a wide range of adaptability (Hanna and Cordona, 2001). They also make efficient use of soil fertility by producing higher number of tillers and biomass and thus take advantage of growing conditions (Ahlrichs *et al*., 1991). Owen and Moline (1970) proposed a general classification of the forage sorghums based upon their use: (i) pasture using Columbus grass (*S. almum*); (ii) pasture and green chop or hay using Johnson grass (*S. halepense*, $2n = 40$), sudangrass (*S. sudanense*, $2n = 10$) or sudangrass hybrids; (iii) green chop or hay using sorghum–sudangrass hybrids; (iv) silage using sorgos and canes and (v) dual-purpose (i.e. for production of grain and stover) using grain sorghums or single- or two-gene dwarf sorghums.

Genetic improvement of forage sorghums has often been a secondary objective of grain sorghum breeding programmes. Until 1988, the primary objective of most forage breeding programmes was forage yield (Kalton, 1988). However, after 1988, efforts were directed towards improving quality traits. Although most forage quality traits like *in vitro* dry matter digestibility (IVDMD), crude protein (CP), neutral detergent fiber (NDF) and acid detergent fiber (ADF) appear to be quantitatively inherited, several simply inherited qualitative traits such as plant height, maturity, juiciness, sweetness, plant colour, stay-green trait, etc., have significant impact on forage quality (Bramel-Cox *et al*., 1995; Pederson, 1997). Improvements in forage quality hold the greatest opportunities in improving forage sorghum (Hanna and Cordona, 2001).

Owen and Moline (1970) concluded that the stage of maturity was the most important factor influencing the quantity and quality of forage produced. From heading to the ripe-seed stage, forage sorghums generally declined in protein content, crude fiber and ash. An increase in lignin content followed by variable sugar content was observed with stage of maturity in grain sorghum. The sudangrass and sorghum–sudangrass hybrids were the most affected by maturity, with reduced protein content.

Four basic height genes are related to the dwarfing of the sorghum plant (Quinby and Karper, 1954). It has been shown that dwarf sorghums containing one, two or three of these dwarfing genes have no difference in leaf percentage; however, the percentage stalk versus head was significantly affected. The one-dwarf type had 75% stalks and 7% heads, the two-dwarf type had 56% stalks, 23% heads, and the three-dwarf type had 36% stalks and 43% heads (Gourley and Lusk, 1978).

The usefulness of forage incorporated into diets of ruminants and forage used as biomass for biological conversion to liquid fuels, is limited by the quantity of lignin present (Cherney *et al*., 1991). Hence, there is worldwide interest in improving the quality of forage through breeding to reduce or alter lignin content by incorporating BMR trait in plants (Cherney, 1990). Brown-midrib, a single gene trait, has greatest forage quality, and Kalton (1988) recognised that great improvement was possible with increased incorporation of BMR trait into all types of forage sorghum. Brown-midrib mutants were discovered in maize in 1924 by Jorgenson (1931), and the trait was later induced in sorghum (Porter *et al*., 1978). Lignin concentrations in BMR mutants are consistently lower than their normal counterparts in sorghum. While *in vitro* digestibility of BMR genotypes has been consistently higher than normal, their *in vitro* rate of digestion does not appear to be consistently affected. Brown mid-rib mutants, differing in quantity and quality of lignin from normal genotypes, offer an opportunity to increase the overall digestion of plant fibre which is a major constituent of forage crops, comprising 30–80% of their dry matter (Cherney *et al*., 1991). Several sorghum lines with high biomass were selected for the BMR trait at ICRISAT, with several white-grained B-lines, a red-grained B-line and two red-grained varieities identified.

Stay-green is another simply inherited trait that is known to improve forage quality. Whether sorghum is grown for dual-purposes (grain and stover) or forage, incorporation of the 'stay-green' trait is a boon for improving the quality of fodder. Stay-green, governed by a recessive allele, not only slows down senescence, but also arrests the decline in protein content of the ageing leaves (Humphreys, 1994). It is also known to contribute to terminal drought and charcoal rot resistance (Rosenow and Clark, 1995). Several stay-green hybrid parental lines have been developed at ICRISAT–Patancheru with their information available from the webpage: http:/www.icrisat.org/text/research/grep/homepage/sorghum/breeding/main.htm

Kalton (1988) proposed that an ideal silage sorghum would include traits such as red seed, yellow endosperm, absence of testa layer, BMR, tan plant colour, juicy stalk, moderate- to low hydro cyanic acid (HCN), high IVDMD, good protein content and good leafiness and green leaf retention. However, incorporating all of these, along with high yield and agronomic acceptability into hybrids would be an ambitious effort by forage sorghum breeders.

ICRISAT has developed a strong forage sorghum improvement programme that has developed a diversified set of hybrid parents, grain and dual-purpose varieties, and a population improvement programme to improve sudangrass sorghums. Breeding has focussed on high biomass, grain yield and stem-sugar content, BMR lines, grain types that tiller under stress conditions such as drought and stem borer resistance (Reddy *et al*., 1994). This programme has resulted in the production of several lines with high tiller numbers, and the identification of sweet-stalk lines, useful for developing ratoon and multicut sweet sorghum, dual-purpose and forage varieties and hybrids.

1.7.3 Sweet Sorghum

Sweet sorghums have a great potential for ethanol production by virtue of their high stem-sugar concentrations, with a brix value up to 24% (Reddy, Ramesh *et al*., 2004). Ethanol extracted from sweet sorghum has superior quality, less sulphur content, high octane rating and automobile friendly (up to 25% blending). Bagasse obtained after juice extraction has higher biological value and rich in micronutrients and is used as

feed or for power cogeneration. At ICRISAT, it was found that the representative internode for Brix estimation is third in B-lines, fifth in varieties and fourth in hybrids. Sweet-stalk sorghum hybrids in rainy season out yield the non-sweet stalk hybrids both for stalk sugar and grain yield. There is no decrease in sugar yield if sweet sorghum is harvested at maturity instead of at flowering time. As there is season specificity in sweet sorghum, cultivars should be specific to season of cultivation. Sweet sorghum cultivars grown in vertisols (black soils) give maximum sugar and grain yields per hectare than those grown in alfisols. The feed stock supply can be extended by using cultivars with different maturity durations, extension of planting time and seasons, planting in wider areas, establishment of decentralised crushing units and widening the harvest window. Harvest window can be increased by more than 4 days if the panicle is harvested at physiological maturity and water is given to the standing stalks. It will also give increased sugar yield per hectare. The overall sugar yield will go down with the delay in crushing of harvested stalks.

The BMR mutant sorghum, pearl millet and maize lines have significantly lower levels of lignin content (51% less in stems and 25% less in leaves). Research at Purdue University showed 50% higher yield of the fermentable sugars from stover of certain sorghum BMR lines after enzymatic hydrolysis. Therefore, the use of BMR cultivars would reduce the cost of biomass-based ethanol production. ICRISAT is developing BMR sorghum hybrid parents (involving the genes *bmr* 1, *bmr* 3 and *bmr* 7) useful for developing high-biomass BMR hybrids.

1.8 Sorghum Improvement Across Diverse Parts of the World

1.8.1 Sorghums of India

In India, sorghum is grown during both *kharif* (rainy) and *rabi* (post-rainy/winter) seasons for multiple uses as a food, feed, fodder and a fuel crop. The cultivar requirements for these two seasons are quite diverse due to different agro-climatic conditions (Rana *et al*., 1997). During rainy season, sorghum at the maturity stage is often caught in rains and the grain quality is affected due to grain moulds. Hence, the grain is mainly utilised as feed. However, *rabi* (post-rainy) sorghum is primarily used as food owing to its good grain quality and also serves as a main source of fodder especially during dry seasons when fodder from other sources are not available. Rabi sorghum is grown under receding soil moisture conditions during winter season and without irrigation after the cessation of rains.

1.8.1.1 Rainy / kharif Sorghum

Before the advent of hybrid technology, the varieties were tall, late in flowering, photoperiod sensitive, low in harvest index and locally preferred. Modifications of excessive height and maturity period have been possible through the introduction of early maturity and dwarfing genes from the temperate germplasm of US origin. The optimum genotype was characterised by a height of 175–180 cm and flowering at 68–70 days with reduced leaf numbers. These intermediate types between temperate and tropical parents, as a bridge population, offered further opportunities for rapid recombination. These types with optimal dry matter production per unit time and distribution and

growth rhythms used water efficiently and formed the basis of improving rainy-season sorghum in India for yield and stability. However, reduction in duration of maturity coinciding with occasional rains resulted in grain deterioration following grain mould attack rendering the grain less preferred for human consumption and marketing. Rana *et al*. (1978) utilised hard grain, low water absorption and tan plant background as a selection criterion to breed for grain mould resistance. Tan plant pigment has also been useful in furnishing resistance to more prevalent leaf diseases (Rana *et al*., 1976).

In the early 1960s, the Indian Council of Agricultural Research, with Rockefeller Foundation assistance, initiated research on hybrid sorghum. ICAR then initiated the All India Coordinated Sorghum Improvement Project (AICSIP) in 1969. This programme organised the research of National Agricultural Research Systems (NARS) and conducted multi-location testing for improved characteristics of hybrids and varieties, working with state agricultural universities, research institutes, ICRISAT and experiment stations. The first sorghum hybrid, CSH 1 (Coordinated Sorghum Hybrid), was bred in India and officially released for commercial cultivation in 1964. The first set of sorghum hybrids was released in the mid-1960s. These were followed by the release of more popular hybrids, like CSH 5 and CSH 6 in the mid-1970s and CSH 9 in the early 1980s, augmenting the spread of sorghum high yielding varieties (HYVs) and open-pollinated varieties and boosting productivity. The gains in productivity, however, were countered by the decline of planted area. Sorghum production levels increased slowly from 6 million tons during the 1950s to a maximum of 11 million tons in the early 1980s. It started declining thereafter, and currently stands around 9.2 million tons. The hybrids played a major role in pushing up productivity and production, particularly in the case of *kharif* sorghum (NRCS, 2007). In view of seed production problems and stagnating yield levels, the need for diversification of hybrid parents was felt. As a result, a high-yielding hybrid, CSH16, was developed from new MS line 27A and the R-line C43. This hybrid showed improvement in grain mould-tolerance as the grain-mould-resistant genes from Ethiopian germplasm line IS 23549 were introduced to its male parent (Audilakshmi *et al*., 2003). CSH 1, CSH 5, CSH 6, CSH 9, CSH 14 and CSH 16 show dramatic increases in productivity. From CSH 5 and CSH 6, with a yield potential of 3.4 t/ha, yield potential was raised to 4 t/ha in CSH 9 and to more than 4.1 t/ha in CSH 16 and CSH 23 (NRCS, 2007).

Varietal improvement was achieved by introducing temperate and tropical germplasm. The first variety, CSV 1 is a direct introduction of line IS 3924 from the United States. By crossing temperate and tropical germplasm, the varieties CSV 2 and CSV 3 were developed. CSV 5 was another variety derived from a cross between Indian local and US line IS 3687. It showed resistance for *Striga*. The variety, CSV 10, which became popular for higher fodder value was developed from a cross between Texas elite variety SC 108 and the Indian elite variety CS 3541. CSV 13, yet another high-yielding variety with medium height was developed from multiple cross having exotic and local parentage. Another variety, CSV 15 was developed from the segregating population derived from the cross between SPV 462 and CSV 13. It is a dual-purpose variety having grain yield comparable to that of hybrid CSH 5 and fodder yield comparable to CSH 10.

1.8.1.2 Post-rainy / winter Sorghum

Unlike in the case of *kharif* sorghum, where 90% of the area is dominated with hybrids, *rabi* sorghum varieties have better preference over hybrids for reasons of adaptability and grain quality. Most of the *rabi* sorghum varieties are only of *durra* type where as

kharif sorghum cultivars belonged to *Caudatum* and *Kafir* races (Reddy *et al*., 2003). Natural selection and domestication over thousands of years have resulted in the development of numerous varieties highly local in their adaptation. The variety M 35-1 has been ruling most of the *rabi* tracts since 7½ decades. Most of the present-day improved varieties are the result of pure-line selection practised among the local/ popular varieties. The popular varieties have lustrous, bold and globular grain distinct, the traits highly preferred by farmers. Some of the popular landraces emerged in various regions include Giddi Maldandi, Yennigar jola, Bilichigan, Fulgar white, Fulgar yellow, Kanki Nandyal, Hagari and Dagadi types from Karnataka, Barshi joot, Saoner, Ramkhe, Aispuri, Maldandis (M 35-1, M 47-3 and M 31-2) and Dagadi types of Maharashtra (Deshpande *et al*., 2003). Notable among the varieties developed from NARS during the early period and which are still under cultivation are the co-series in Tamil Nadu; the Nandyal, Guntur and Ankapalle series of Andhra Pradesh; and the PJ *rabi* series of Maharashtra. Focussed breeding on *rabi* sorghum was initiated in the early 1970s which over the years led to the release of several state and central release varieties. At the national level, the variety CSV 7R was released in 1974, CSV 8R in 1979, Swati in 1984, CSV 14R in 1992, Sel 3 in 1995, Phule Yashoda in 2000, CSV 18 in 2005, CSV 22 in 2007 and CSV 26 in 2012 and CSV 29 in 2013. Several varieties were released at the state level, which included Mukti, Parbhani Moti/ SPV 1411 from Parbhani centre, NTJ 2 and NTJ 3 from the Nandyala station of Andhra Pradesh state (Lakshmaiah *et al*., 2004). Sorghum programme of Karnataka state released varieties DSV 4 and DSV 5. The Maharashtra state sorghum improvement programme released varieties like Swati, Selection 3, CSV 216/ Phule Yashoda/ SPV 1359, RSLG 262/ Phule Maulee, Phule Anuradha, Phule Revati, Phule Vasudha, Phule Chitra and Phule Suchitra. The released post-rainy sorghum varieties, CSV 8R, CSV 14R, CSV 18 and Swathi, were better received than the post-rainy hybrids such as CSH 7R and CSH 8R.

Among the yield component traits, long panicles, number of grains per panicle, 100-seed weight contributed for grain yield, and most of these traits have high heritability enabling the plant breeder to improve these traits through simple selection (Patil *et al*., 2014). The gap between flag leaf sheath and panicle base should be minimum to have good grain filling and the glume coverage on grains is to be less for higher threshability (Reddy *et al*., 2009). The high-yielding crosses should have at least one good general combiner and the average general combining ability (gca) effect of both the parents showed significant positive relationship with yield (Rani and Rao, 2008). Several varieties such as CSV 7R, CSV 8R and CSV 14R were developed using selections from segregating populations derived from the crosses among Indian locals, M 35-1 and IS 2644 with American germplasm lines. Productivity of *rabi* sorghum depends not only on the moisture availability but also on the soil types under which it is grown and the genotypes (Jirali *et al*., 2007). Much of the post-rainy-season sorghum is grown on residual and receding soil moisture on shallow and medium–deep soils. Under shallow soils, the genotypes were shorter, flowered and matured early while in medium–deep soils, mean leaf area, grain number and 1000 grain mass, grain and fodder yields were higher (Rafiq *et al*., 2003). Breeding varieties suitable for varying soil depths was emphasised at Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India. The variety RSLG 262/Phule Maulee was released for shallow to medium soils of Maharashtra in 1999; Phule Chitra (SPV 655×RSLG 112) was released for medium soils in 2006; Phule Vasudha (RSLG

206×SPV 1247) was released for deep soils in 2007; and Phule Anuradha (RSLG 539×RSLG 1175) was released for shallow soils in 2008. The reduction in grain yield under shallow soils was found to be due to reduction in LAI, TDM, grain number per panicle and 1000-grain weight.

The released *rabi* hybrids could not progress well as compared to the varieties. However, studies indicated appreciable levels of heterosis for grain yield and other agronomic traits by Rana *et al.* (1997). Large heterotic response for grain yield and harvest index was accompanied by susceptibility to stalk rot and shoot fly susceptibility (Rao, 1982). Increase in number of seeds per panicle branch in short compact-headed varieties (tropical) and increase in the panicle branches in the long-panicle type (temperate) by introgression of genes from African germplasm result in yield heterosis (Rana and Murty, 1978). The combining ability of compact-headed Indian landraces was found to be relatively poorer than very long panicle types of exotic origin as poor combining of genes responsible for primary axis length and those contributing to girth resulted in lack of marked heterosis for ultimate grain yield (Rao, 1970). Pollinators and female lines from exotic germplasm contributed to poor grain quality. The derivatives *durra–caudatum* (*zera zera*) crosses as pollinators developed for post-rainy-season, and CMS lines developed for *kharif* season from *kafir–caudatum* (*zera zera*) crosses did not attract the attention of farmers as they lacked grain lustre, size and shape and fodder yield comparable to M 35-1, despite their superiority under late sowings in post-rainy-season with yield heterosis of 45–64%.

With the view of introgressing many of the desirable attributes of landraces, landrace pollinator-based hybrids were developed. Though they exhibited moderate levels of shoot fly resistance and desirable grain-quality traits, they lacked lodging resistance and had moderate yielding ability (Reddy *et al*., 1983). Most of the landraces, including M 35-1, showed segregation for fertility restoration/sterility maintenance ability indicating the need to select for restoration ability within the landraces. This also explains the partial restoration observed when bulk pollen of M 35-1 was used by many workers. Upto 100% better-parent heterosis using landraces as pollinators over the A-lines 104A and M 31-2A were obtained (Sajjanar *et al*., 2011). Fertility restoration by landraces was poorer on *durra*-derived A_1 CMS lines than on *caudatum*-derived A_2 CMS lines. When both A_1 and A_2 CMS lines were based on *caudatum*, fertility restoration was higher on A_1 than A_2. This finding has a bearing on developing CMS lines involving *caudatum*-based germplasm lines adapted to post-rainy-season and testing for fertility restoration in hybrids. The hybrids involving *caudatum*-based female parents and *durra*-based landraces showed high heterosis for grain yield but grain quality was poor. *Milo* hybrids exhibited superiority over *maldandi* hybrids for most of the characters in desired direction (Pattanashetti *et al*., 2005). There is season specificity in breeding for shoot fly resistance and the studies by Jayanthi (1997) have shown that shoot fly resistance in both the parents or at least in seed parents in order to realise higher frequency of shoot-fly-resistant hybrids in post-rainy-season. As rabi sorghum is cultivated in winter season, the anthesis period is exposed to low night temperatures. When minimum temperatures go below 10°C during flowering, hybrids that are otherwise male fertile show male sterility as evidenced by partial to complete absence of seed set under bagging. Therefore, greater attention is required to ascertain the differences among the landraces for their ability to restore fertility in hybrids, especially under low temperatures, normally observed in post-rainy-season. By eliminating temperature sensitivity (in relation to development) in both male and female parents,

greater success could be achieved in breeding hybrids for post-rainy-season. However, male sterile lines bred from landraces adapted to post-rainy-season, showed temperature-induced restorer inefficiency. Also, the hybrids developed from landraces crossed to female lines derived from M 35-1 did not show high heterosis. While the use of the *durra* race directly introduces high sensitivity to low temperatures, the direct use of *guineas* in developing hybrid parents, produce hybrids with clasped glumes, an undesirable trait. Hence, *durra* (bold grain lines) and *guinea* (grain-mould-resistant restorers) materials have to be introgressed into high-yielding *caudatum* background to enhance the yield potential of elite sorghum B-lines. Reddy *et al*. (2014) observed significant and positive correlation between low temperature during flowering and germinability and viability of pollen. Among the hybrid parents, R-lines exhibited stability for many characters across the dates of sowing, while B-lines were less stable, indicating the need for the development of stable B-lines for *rabi* season. Leaf sugary melady (Chikta) occurs when morning humidity is between 54 and 74% and minimum temperatures below 18°C. The disease was characterised by an extensive leaf chlorosis followed by oozing of sugars. It was first observed at the flag leaf stage (2%) and it increased until harvest (72%). A steep increase in disease incidence was observed from full bloom (7%) to the hard dough phase (51%). Due to oozing of sugars, the last few leaves (11th, 12th and 13th [flag leaf]) stuck to each other, not allowing the inflorescence to emerge from the boot. The affected plants attracted a variety of insects and supported an extensive bacterial and fungal colonisation. SPV-504 demonstrated least incidence of the disorder sugary disease (*chikta*).

Charcoal rot caused by the pathogen *Macrophomina phaseolina* is a major disease of sorghum grown in arid regions. Sorghum is vulnerable to charcoal rot when it undergoes stress from flowering to grain-filling period. Warm, moist followed by hot, dry growing conditions are favourable for disease development. Resistance to charcoal rot was found to be polygenic, moderate to lowly heritable and partially dominant (Rana *et al*., 1982). Tenkouano *et al*. (1993) reported that charcoal rot resistance is controlled by two dominant genes that are modified by a third locus. Non-senescence is a delayed leaf and plant death-resistance mechanism in sorghum that circumvents the detrimental effects of reduced soil moisture combined with high temperatures during post-anthesis growth. They also noted that charcoal rot and non-senescent phenotypes were controlled by independent loci even though these traits are often associated. They also concluded that non-senescence alone cannot account for, and should not be used as the sole breeding criterion for, resistance to charcoal rot in sorghum.

1.8.1.3 International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)

ICRISAT was established in 1972 at Patancheru, Andhra Pradesh, India, with sorghum as one of its five mandate crops. Improvement for yield potential and resistance to drought, *Striga*, grain mould, downy mildew, charcoal rot, shoot fly, stem borer, midge and head bug and wide adaptability received major attention up to 1980. Genetic male-sterility facilitated populations and pure-line varieties were the target cultivars during the initial years. In resistance breeding programmes, emphasis was given to developing and standardising screening techniques and identification and breeding of improved resistance sources. The initial emphasis on red grain types up to 1975 was gradually shifted to white grain types by the end of the 1970s. During the 1980s, major emphasis was given to regional adaptation and breeding for resistance to biotic stresses (grain

moulds and insect pests only) in white grain background. Breeding for resistance to drought, downy mildew, charcoal rot and *Striga* was discontinued, while development and improvement of male-sterile lines for grain yield and food-quality traits were initiated. Initially, several open-pollinated populations were introduced from the US, West African and East African programmes and were reconstituted with selection. Several of the hybrid seed parents derived from some of these populations are being extensively used for the development of high-yielding hybrids in China. Later on, several high-yielding good grain inbred-lines and *zera zera* landraces (*caudatum*) were extensively involved in breeding at ICRISAT Asia Center (IAC), and *guinea* local landraces along with *caudatum* derived lines at ICRISAT West African Center (Reddy and Stenhouse, 1994). During 1985–1989, major thrust was given for specific adaptation and trait-based breeding for resistance traits. A total of 92 high-yielding A-/B-lines, including 17 early-maturity lines and 75 medium maturity lines, were developed during this period. By late 1980s, many national agricultural research systems (NARS) had enhanced crop improvement programmes aimed at specific adaptation. Thus, the global sorghum improvement programme reoriented itself to develop materials suited for 12 productive systems (PS) in Asia, six in Western Africa, six in Eastern and Southern Africa and five in Latin America. As a result of this reorientation, at ICRISAT's Asia Center (IAC), strategic research on the development of screening techniques, breeding concepts and methods and intermediate products for utilisation in partnership with NARS programmes was given emphasis during 1990–1994. A total of 567 trait-based A-/B-lines (487 A1, 51 A2, 17 A3 and 12 A4 CMS systems-based) were developed during 1989–1998. Besides these, 57 high-yielding A-/B-lines were also developed. In addition, an extensive programme of breeding new *Milo* cytoplasm male-sterile lines for earliness, introgression with *durra* and *guinea* races, incorporating bold and lustrous grain characters and resistance to *Striga*, shoot fly, stem borer, midge, head bug, grain mould, downy mildew, anthracnose, leaf blight and rust was carried out (ICRISAT, 1993). With a major objective of trait-specific breeding, novel populations or trait-specific genepools for bold grain and highly productive tillering were developed. Test crosses involving post-rainy-season 'landraces' as pollinators were examined for their fertility restoration ability under cool nights and for productivity in post-rainy-season. Variability for restoration was quite significant indicating the possibility of selection within hybrids (Reddy and Stenhouse, 1994). Lines with high Fe and Zn content in the grains were identified and the variation for these micronutrients did not appear to be significantly influenced by the environment.

Sweet sorghum research has been given major emphasis at ICRISAT. The sweet-sorghum-based ethanol technology has become a reality with the establishment of Rusni Distilleries near Hyderabad, India, in collaboration with ICRISAT's Agri Business Incubator (ABI). It has become a model for such distilleries all over the world. In collaboration with International Centre for Biosaline Agriculture (ICBA), Dubai and Agriculture Research Station (ARS), Gangavathi, Karnataka, India, ICRISAT has identified promising lines under saline conditions. Similarly, improved lines have been developed for fodder quality and quantity and Al^{3+} tolerance. From 1995 onwards, a partnership mode of conducting research to develop improved intermediate products at ICRISAT, Patancheru, India, and finished products (varieties and hybrids) at other ICRISAT locations in Africa were being emphasised. ICRISAT, working in partnership with NARS, partners helped in release of 200 cultivars in several countries in Asia (53), Africa (112) and Latin America (35).

1.8.2 Sub-Saharan Africa

A high proportion of the population (25%) of sub-Saharan Africa lives in semiarid regions (Sanders *et al*., 1996). The major emphasis of technological change in the semiarid region over the last three decades has been new cultivars (Ahmed *et al*., 2000). Regional sorghum breeding approach began at different periods in three regions – East and Central Africa (ECA), South African Development Community (SADC) and West and Central Africa (WCA) with the objective of tackling different production constraints specific to different regions. ICRISAT has been improving sorghum through its programme in Western and Southern Africa over two decades. In the last 35 years, the area harvested to sorghum in Africa has nearly doubled, but yields averaging 800 kg/ha have not increased. Sorghum research in sub-Saharan Africa has been successful in diffusing a large number of new cultivars onto farmers' fields. The last two decades of research have resulted in the release of over 40 sorghum cultivars (Ahmed *et al*., 2000).

1.8.3 Western and Central Africa (WCA)

The first West Africa breeding research on sorghum started in 1931 using an experiment station created in 1921 at Bambey, Senegal (Atokple, 2010). ICRISAT's involvement in sorghum breeding in WCA began in 1979, and the centre has made extensive sorghum improvement efforts in WCA targeting the unique requirements of the diverse array of production systems in the SAT (Obilana, 2004). The local landraces are mostly two types – guinea race and durra-caudatum – in WCA. Initial efforts were targeted to improve the local landrace germplasm by selection within the landraces or in the segregating progenies derived from crosses among themselves and release them as varieties to farmers. Later on, new germplasm, namely zera zeras (caudatum race) were introduced, and several lines were developed by selection in the segregating progenies involving introduced caudatums and local guineas. In the more recent years, therefore, efforts are being made to develop guinea-based hybrid parents to develop guinea hybrids. As guineas have good food quality attributes and adaptation to local drought conditions, the guinea-based hybrids are expected to have good acceptability and good adaptation to moisture stress environments prevalent in the region (Camara *et al*., 2006). While guinea landrace-based A-lines are tall, photoperiod sensitive, and possess typical guinea grain and panicle architecture, the inter-races cross derivatives-based A-lines are dwarf, basically photoperiod insensitive and possess relatively small grain. The development of new A-lines (on A1 CMS system) continues with sterilisation of guinea-core collection accessions from Burkina Faso, Senegal, Gambia, Sudan, Uganda and Malawi by the ICRISAT programme and interracial lines by IER (Olembo *et al*., 2010).

1.8.4 Eastern and Southern Africa (ESA)

In the beginning, most of the breeding programmes placed emphasis on introductions, evaluating them and then selecting adapted lines. Later, programmes embarked on hybridisation followed by evaluation and selection in segregating populations. The main focus was on earliness, increasing grain yield and disease and pest resistance. Varieties such as Framida and Red Swazi were released with wide appeal. Governments in Southern Africa pooled their resources together and established Sorghum and Millet Improvement Programme (SMIP) in the early 1980s. The programme was managed by

ICRISAT. In early 1983, significant efforts were made through the regional programme SMIP to acquire new and enhanced germplasm from all possible sources. About 10200 exotic germplasms of sorghum were acquired and evaluated at the regional centre at Matopos. As a result of concerted efforts of SMIP, International Sorghum/Millet Collaborative Research Support Program (INTSORMIL), United States, and ICRISAT–Patancheru, India, several hybrid parental lines were developed. Sorghum yields averaged 1.8 t/ha in South Africa since 1980 despite the six drought years after 1980 and the 1991–1992 drought. This contrasts with the 0.8 t/ha in the rest of sub-Saharan Africa. The success of the intensive production pattern of sorghum in Sudan and South Africa is similar to the success of cotton in Francophone Africa and maize technologies in the Sudano-Guinean zone of the Sahel. In these higher-rainfall regions, new cultivar introductions were combined with crop-management improvements, including increases in fertilisation, density and pest control (Ahmed *et al*., 2000).

1.8.5 Latin America

In Latin America, sorghum is produced on intermediate to large farms except in some inland valleys and eroded mountain slopes of Central America utilising hybrids imported from the United States and cultivars developed in the regions. In Guatemala, El Salvador, Honduras, Nicaragua and Haiti, a large part of the production is on small subsistence holdings often less than one hectare in size where farmers use photoperiod-sensitive landraces intercropped with maize and beans using traditional production practices. The damages due to downy mildew, anthracnose, grain mould, stem borer and midge among the biotic stresses and soil acidity and alkalinity, drought and cold temperature among the abiotic stresses are the major yield constraints apart from the lack of early-maturing, tropically adapted cultivars with high yield potential and tolerance to major stresses in the region. ICRISAT initiated the Latin America and Caribbean Program in 1976 by stationing its staff at International Wheat and Maize Improvement Center (CIMMYT), Mexico. The programme was aimed at developing early, dwarf and bold grain varieties for fertile soils in both the highlands and lowlands of Central America. The programme was later transformed as Latin American Sorghum Improvement Program (LASIP) in 1990. LASIP had a comparative advantage in the development of tropically adapted improved germplasm that was resistant/tolerant to major production constraints for foodgrade cultivars in Latin America. Several varieties were released and adopted based on ICRISAT-bred improved germplasm. Due to funding constraints, LASIP was discontinued in 1993. However, considering the interest shown by Latin American NARS, a programme for improving sorghum for acid soil tolerance was initiated in 1996 with funding support from Inter American Development Bank (IADB). The INTSORMIL programme identified 20 acid soil tolerant lines in the 1980s (Gourley, 1991), but they were susceptible to leaf diseases. At its centres in India and Africa, ICRISAT has developed diverse sets of high-yielding sorghum breeding lines useful as base materials for testing in acid soils of Latin America. Since 1996, ICRISAT, International Center for Tropical Agricultural (CIAT) and the national programmes of Brazil, Colombia, Honduras and Venezuela have jointly implemented an IADB-funded project on 'A research and network strategy for sustainable sorghum production systems for Latin America'. The major objectives of this project include: (i) to assemble, multiply and evaluate grain and forage sorghum breeding lines for tolerance to acid soils and resistance to foliar diseases, (ii) to develop a research network of scientists

working on this crop in the region and train them in sorghum research and (iii) to test the most promising genotypes in the target production systems.

1.8.6 China

Modern sorghum breeding in China began in the 1920s, and heterosis breeding has been the main method of breeding since 1965 in China. The major objectives of sorghum improvement research in China include: grain yield, multiple resistance to abiotic (low temperature and drought) and biotic (aphids and head smut) stresses, grain quality, grain feed and forages for livestock. The increase in yield due to utilisation of hybrids is estimated at 30–40%, with the remaining improvement being due to better cultivation conditions (Zhen Yang, 1997). Low temperature is an important stress factor, especially for northeastern China in both the seedling and grain filling stages. Some cold-tolerant local varieties have been identified using low temperature seedling treatment (Zheng Yang, 1997). New male-sterile lines and restorers with resistance to drought are being developed by selecting for rapid seedling-emergence rates in water-limited areas (Zheng Yang, 1997). Most Chinese sorghum varieties lack genetic resistance to aphids. Several new male-sterile lines with high degree of resistance have been developed by the Sorghum Research Institute (SRI), Liaoning Academy of Agricultural Sciences (LAAS) (Zheng Yang, 1997). Sorghum head smut caused by the fungus, *Sphacelotheca reliana* is a serious disease. There are three different physiological races of the pathogen in China. Resistance to head smut is controlled by both major genes of two or three pairs and some minor genes (Yang Zhen and Yang Xiaoguang, 1993). Among 10083 germplasm accessions screened, 39 showed immunity to race 2, while 3 accessions have shown resistance to race 3. Chinese Kaolings are an excellent source of good grain quality types such as Xiang Yanai and Zhen Zhubai. However, they are not used directly in heterosis breeding due to low combining ability and poor restoration. Nutritive composition of hybrid sorghum grain is poor and the traditional fragrance of original local varieties needs to be recovered in high-yielding background (Zheng Yang, 1997). Since sorghum is the main raw material of compound feeds for livestock and poultry, breeding for feed quality has been one of the major objectives of sorghum breeding in China (Shi Yuxue *et al*., 1992). Most forage sorghums can be classified as dual purpose in China, with the grain for human consumption and stover for other purposes. At present, the focus is on breeding for high biomass coupled with good nutritional value and low HCN content (Zhen Yang, 1997). In China, sweet sorghum is primarily used for silage preparation. With the introduction of improved sweet sorghum varieties such as Rio, Roma, Ramada and Wray from several countries, a systematic sweet sorghum breeding programme was initiated in LAAS in 1985. As a result, two sweet sorghum hybrids, Liaosiza No.1 and Liaosiza No.2 were developed and released during 1989 and 1995, respectively.

1.9 Future Prospects

As sorghum is grown under marginal and harsh environments, the options to shift to other lucrative crops are limited. Investments should flow towards breeding varieties incorporating the quality attributes preferred by end users. Breeding efforts for value-added characteristics like tolerance to drought, grain mould, charcoal rot, shoot fly, stem borer and striga should continue as their yield loss due to these factors is to the

tune of 30–50%. The second priority is to breed varieties to increase the shelf life of grain and reduce the undesirable attributes in the grain like reducing fat content and phenol compounds, followed by improving/keeping quality of the flour and exploring the health benefits and nutraceutical value. Industrial demand for grain-based alcohol is also expected to propel a double-digit growth rate. Investment in research should be directed towards increasing productivity of *rabi* sorghum which would help in bringing down the prices and make it affordable for lower-income consumers. In order to improve productivity of *rabi* sorghum, besides targeting improved varieties, targeting on the key recommended technologies, management practices like drilling of fertiliser along with seed, seed treatment, deep sowing, wide row spacing, optimum plant population, integrated pest management (IPM) and integrated nutrient management (INM) is crucial. In addition, the biotic and abiotic problems such as resistance to shoot fly, aphid, charcoal rot, drought and cold are important for adaptation in *rabi* season. Consumer acceptability is towards bold, round and lustrous grain and higher flour recovery. Thus, research efforts on *rabi* sorghum should address the above problems on priority in order to augment productivity rendering sorghum as a profitable crop benefiting the small and marginal farmers in SAT areas. Exploring non-conventional uses and extrusion products is another important area for future investment in these crops. Incentives should be provided to food industry to use *rabi* sorghum for novel processed food products (snacks, bread, biscuits, flakes, papad, rava, etc.) and also traditional processed products. Enriching nutritional value in zinc and iron content should be continued.

Much of the millets in the rural areas are processed at household level by following a tedious method involving considerable drudgery. So, there is vast scope to transfer information regarding modern technologies and benefits of value addition to the farmers. Providing backward and forward linkages for value chain using innovative value addition in domestic and international markets is required. Capacity building for social capital formation among farmers and consumers regarding their cooperation for millet cultivation and consumption considering their nutraceutical properties is quintessential. Field level findings suggests that there is scope to arrest the declining demand for sorghum in urban centres by promoting value added and ready to eat products as they are in much demand in hotels and restaurants. Though consumers are aware of the health benefits of sorghum in their dietary requirement, unavailability of processed products as in the case of wheat have contributed to decline in consumption of sorghum. Hence, keeping in view the potential benefits of sorghum, research efforts should be focused on releasing varieties to cater to needs of processing sector for better value-added products and to meet the demands of the growing urban population.

References

Aboubacar, A., Axtell, J.D., Huang, C.P. and Hamaker, B.R. (2002) A rapid protein digestibility assay for identifying highly digestible sorghum lines. *Cereal Chemistry*, **78**, 160–165.

Adamou, M., Gourley, L.M., Watson, C.E. *et al*. (1992) Evaluation of combining ability of acid soil tolerant sorghum germplasm in Niger, in *Agronomy Abstracts*. American Society of Agronomy Minneapolis, MN, November 1–6, p. 88.

Ahlrichs, S.L., Duncan, R.R., Ejeta, G.E. *et al.* (1991) Pearl millet and sorghum tolerance to aluminum in acid soil, in *Plant Soil Interactions at Low pH* (ed. R.J. Wright), Kluwer Academic Publishers, The Netherlands, p. 197.

Ahmed, M.M., Sanders, J.H. and Nell, W.T. (2000) New sorghum and millet cultivar introduction in Sub-Saharan Africa: impacts and research agenda. *Agricultural Systems*, **64**, 55–65.

Andrade Lima de, M.M., Maciel, G.A., Tabosa, J.N. *et al.* (1992) Advanced grain sorghum trial for aluminium tolerance. *Sorghum Newsletter*, **33**, 58.

Asante, S.A. (1995) Sorghum utility and utilization. *African Crop Science Journal*, **3**, 231–240.

Atokple, I.D.K. (2010) Sorghum and millet breeding in West Africa in Practice. CSIR-Savanna Agricultural Research Institute, PO Box 52, Tamale, Ghana. http://www.afripro.org.uk/papers/Paper14Atokple.pdf (accessed on 30 January, 2010).

Austin, R.B. (1993) Augmenting yield-based selection, in *Plant Breeding Principles and Prospects* (eds M.D. Hayward, N.O. Bosemark and I. Romagosa), Chapman and Hall, London, pp. 391–405.

Axtell, J.D. (2001) Breeding sorghum for increased nutritional value, INTSORMIL Sorghum/Millet collaborative support program (CRSP), 2001 Annual Report, pp. 67–73.

Axtell, J.D., Van Scoyoc, S.W., Christensen, P.J. and Ejeta, C. (1979) Current status of protein quality improvement in grain sorghum, in *Proceedings of an international symposium on seed protein improvement in cereals and grain legumes*, IAEA, Vienna, published by IAEA, Austria, pp. 357–366.

Azhar, F.M. and McNeilly, T. (1987) Variability for salt tolerance in *Sorghum bicolor* (L.) Moench under hydroponic condition. *Journal of Agronomy and Crop Science*, **159**, 269–277.

Azhar, F.M. and McNeilly, T. (1989) Heritability estimates of variation for NaCl tolerance in *Sorghum bicolor* (L.) Moench seedlings. *Euphytica*, **43**, 69–72.

Bandyopadhyay, R., Mughogho, L.K. and Rao, K.E.P. (1988) Sources of resistance to sorghum grain molds. *Plant Disease*, **72**, 504–508.

Banziger, M. and Long, J. (2000) The potential for increasing the iron and zinc density of maize through plant-breeding. *Food and Nutrition Bulletin*, **21**, 397–400.

Berenji, J. and Dahlberg, J. (2004) Perspectives of sorghum in Europe. *Journal of Agronomy and Crop Science*, **1905**, 332–338.

Blum, A. (1979) Genetic improvement of drought resistance in crop plants: a case for sorghum, in *Stress physiology in crop plants* (eds H. Mussell and R.C. Staples), John Wiley & Sons, Inc., New York, USA, pp. 429–445.

Blum, A. (1983) Genetic and physiological relationships in plant breeding for drought resistance. *Agricultural Water Management*, **7**, 195–202.

Bohnert, H.J., Nelson, D.E. and Jensen, R.G. (1995) Adaptations to environmental stresses. *Plant Cell*, **7**, 1099–1111.

Borrell, A.K., Bidinger, F.R. and Sunitha, K. (1999) Stay-green associated with yield in recombinant inbred sorghum lines varying in rate of leaf senescence. *International Sorghum and Millets Newsletter*, **40**, 31–33.

Borrell, A.K. and Douglas, A.C.L. (1997) Maintaining green leaf area in grain sorghum increases nitrogen uptake under post-anthesis drought. *International Sorghum and Millets Newsletter*, **38**, 89–92.

Borrell, A.K. and Hammer, G.L. (2000) Nitrogen dynamics and the physiological basis of stay-green in sorghum. *Crop Science*, **40**, 1295–1307.

Borrell, A.K., Hammar, G.L. and Henzell, R.O. (2000) Does maintaining green leaf area in sorghum improve yield under drought? II. Dry matter production and yield. *Crop Science*, **40**, 1037–1048.

Borrell, A.K., Hammar, G.L. and Douglas, A.C.L. (2000) Does maintaining green leaf area in sorghum improve yield under drought? I. Leaf growth and senescence. *Crop Science*, **40**, 1026–1037.

Bramel-Cox, P.J., Kumar, K.A., Hancock, J.D. and Andrews, D.J. (1995) Sorghum and millets for forage and feed, in *Sorghum and Millets: Chemistry and Technology* (ed. D.A.V. Dendy), American Association of Cereal Chemists, St. Paul, MN, pp. 325–364.

Bulter, L.G. (1990a) Tannins and other phenols, effects on sorghum production and utilization, *INTSORMIL Annual Report*, A Technical Research Report of the grain sorghum/pearl millet Collaborative Research Support Program (CRSP), pp. 140–144.

Bulter, L.G. (1990b) The nature and amelioration of the anti nutritional effects of tannins in sorghum grain, in *Sorghum Nutritional Quality* (eds G. Ejeta, E.T. Mertz, L. Rooney *et al.*) *Proceedings of the International Conference on Sorghum Nutritional Quality*, February 26–March 1, 1990, Purdue University, W. Lafayette, Indiana, pp. 191–205.

Calhoun, D.S., Gebeyehu, C., Miranda, A. *et al.* (1994) Choosing evaluation environments to increase grain yield under drought conditions. *Crop Science*, **34**, 673–678.

Camara, Y., Bantilan, M.C.S. and Ndjeunga, J. (2006) Impacts of sorghum and millet research in West and Central Africa (WCA): a synthesis and lessons learnt. Working Paper Series No. 22. Sahelian Center, International Crops Research Institute for the Semi-Arid Tropics, BP, Niamey, Niger, 48 pp.

Celarier, R.P. (1959) Cytotaxonomy of the Andropogonea. III. Sub-tribe Sorgheae, genus, Sorghum. *Cytologia*, **23**, 395–418.

Chavan, J.K., Kadam, S.S. and Salunkhe, D.K. (1980) Changes in tannin free amino acids, reducing sugars, and starch during seed germination of low and high tannin cultivars of sorghum. *Journal of Food Science*, **46**, 638–639.

Cherney, J.H. (1990) Normal and brown-midrib mutations in relation to improved ligno cellulose utilization, in *Microbial and Plant opportunities to improve lignocellulose utilization by ruminants* (eds D.E. Akin and L.G. Lungdahl), Elsevier, Amsterdam, pp. 205–214.

Cherney, J.H., Cherney, D.J.R., Akin, D.E. and Axtell, J.D. (1991) Potential of brown-midrib, low lignin mutants for improving forage quality. *Advances in Agronomy*, **46**, 157–198.

Chinna, B.S. and Phul, P.S. (1986) Heterosis and combining ability studies for protein, lysine and tryptophan in sorghum (*Sorghum bicolor* (L) Moench). *Genetica Agraria*, **40**, 405–414.

Christiansen, M.N. and Lewis, C.F. (1982) *Breeding Plants for Less Favourable Environments*, John Wiley & Sons, Inc., New York.

Clayton, W.D. and Renvoize, S.A. (1986) Genera Graminum grasses of the world. Kew Bulletin Additional Series XIII, Royal Botanic gardens, Kew, 338–345.

Comstock, R.E. and Robinson, H.F. (1952) Genetic parameters, their estimation and significance. *Proceedings of Sixth International Grasslands Congress*, 284–291.

Crasta, O.R., Xu, W.W., Rosenow, D.T. *et al.* (1999) Mapping of post-flowering drought resistance traits in grain sorghum: association between QTL influencing premature senescence and maturity. *Molecular General of Genetics*, **262**, 579–588.

Damania, A.B. (2002) The Hindustan centre of origin of important plants. *Asian Agricultural History*, **6** (4), 333–341.

de la Rosa Ibarra, M. and Maiti, R.K. (1994) Morphological and biochemical basis of resistance of glossy sorghum to salinity at seedling stage. *International Sorghum and Millets Newsletter*, **35**, 118–119.

de Wet, J.M.J. (1977) Domestication of African cereals. *African Economic History*, **3**, 15–32.

Deosthale, Y.G., Mohan, V.S. and Rao, V. (1970) Varietal differences in protein, lysine and leusine content of grain sorghum. *Journal of Agricultural and Food Chemistry*, **18**, 644–646.

Deosthale, Y.G., Nagarajan, V. and Vesweswar Rao, K. (1972) Some factors influencing the nutrient composition of sorghum grain. *Indian Journal of Agricultural Sciences*, **42**, 100–108.

Deshpande, S.P., Borikar, S.T., Ismail, S. and Ambekar, S.S. (2003) Genetic studies for improvement of quality characters in *rabi* sorghum using landraces. *ISMN*, **44**, 6–8.

Deyoe, C.W., Shoup, F.K., Miller, G.D. *et al.* (1970) Amino acid composition and energy value of immature sorghum grain. *Cereal Chemistry*, **47**, 363–368.

Doggett, E. (1988) *Sorghum*, John Wiley & Sons, Inc., New York, USA.

Doggett, H. (1962) Tetraploid hybrid sorghum. *Nature*, **196**, 755–756.

Doggett, H. (1972) The important sorghum in East Africa, in *Sorghum in Seventies* (eds N.G.P. Rao and L.R. House), Oxford and IBH Publishing Co., New Delhi, pp. 47–59.

Doggett, H. (1984) Striga: its biology and control – an overview, in *Striga: Biology and Control* (eds E.S. Ayensu, H. Doggett, R.D. Keynes *et al.*), ICSU Press, Paris, France, p. 27.

Downes, R.W. (1972) Effect of temperature on the phenology and grain yield of sorghum bicolor. *Journal of Agricultural Research*, **23**, 385–394.

Eberhart, S.A. (1972) Techniques and methods for more efficient population improvement in sorghum, in *Sorghum in Seventies* (eds N.G.P. Rao and L.R. House), Oxford and IBH, New Delhi, pp. 195–213.

Ejeta, G. (1987) Breeding sorghum hybrids for irrigated and rainfed conditions in Sudan, in *Food Grain Production in Semi-Arid Africa*, Proceedings of International Drought Symposium, May 19–23, 1986, Nairobi, Kenya, p. 121.

Ejeta, G. and Axtell, J.D. (1990) Development of hard endosperm high lysine sorghum lines, in *Sorghum Nutritional Quality* (eds Ejeta *et al.*), Proceedings of an International Conference, W. Lafayette, IN. Feb 26–1st March 1990, Purdue University, West Lafayette, IN, pp. 126–141.

Ejeta, G. and Bulter, L.G. (1993b) Host-parasite interactions throughout the *Striga* life cycle and their contributions to *Striga* resistance. *African Crop Science Journal*, **1**, 75–80.

Ejeta, G., Bulter, L.G., Hess, D.E. *et al*. (1997) Breeding for *Striga* resistance in Sorghum. Proceedings of International Conference on Genetic Improvement of Sorghum and Pearl Millet, September, 22–27, 1996, Lubbock, Texas, INTSORMIL and ICRISAT, pp. 504–516.

Fernandes, M.B., Castro, J.R., de Fernandes, V.L.B. *et al.* (1994) Evaluation of forage sorghum cultivars in salt affected soils of Rio Grande do Norte, Brazil. *Pesquisa Agropecuaria Brasileira*, **29**, 25–261.

Flores, C.I., Clark, R.B., Pedersen, J.F. and Gourley, L.M. (1991) Leaf mineral element concentrations in sorghum (*Sorghum bicolor*) hybrids and their parents grown at varied Aluminium saturations on an ultisol, in *Plant Soil Interactions at Low pH* (eds R.J. Wright, V.C. Baligar and R.P. Murrmann), Kluwer academic Publishers, Dordrecht, The Netherlands, pp. 1095–1104.

Garber, E.D. (1950) Cytotaxonomic studies in the genus Sorghum. *University of California Publication of Botany*, **23**, 283–361.

Gardner, C.O. (1972) Development of superior populations of sorghum and their role in breeding program, in *Sorghum in Seventies* (eds N.G.P. Rao and L.R. House), Oxford and IBH Publishing Co., New Delhi, pp. 180–183.

Garrity, D.P., Sullivan, C.Y. and Ross, W.M. (1982) Alternative approaches to improving grain sorghum productivity under drought stress, in *Drought Resistance in Crops with Emphasis in Rice*, International Rice Research Institute, Manila, Philippines, pp. 339–356.

Gourley, L.M. (1988) Breeding sorghum for acid soils of the humid tropics, in *Africaland – Land Development and Management of Acid Soils in Africa II* (ed. M. Lathan), Inter Board for Soils Research and Management (IBSRAM) Bangkok, Thailand, pp. 261–273.

Gourley, L.M. (1991) Breeding sorghum for tolerance to infertile acid soils. International Sorghum and Pearl Millet Program (INTSORMIL) Annual Report 1991. Lincoln, Nebraska, USA: INTSORMIL, pp. 91–98.

Gourley, L.M. and Lusk, J.W. (1978) Genetic parameters related to sorghum silage quality. *Journal of Dairy Science*, **61**, 1821–1827.

Gourley, L.M., Watson, C.E., Goggi, A.S. *et al.* (1997) Grain sorghum inbreds tolerant to tropical acid soils released as germplasm. *International Sorghum and Millets Newsletter*, **38**, 93–94.

Gourley, L.M., Watson, C.E., Schaffert, R.E. *et al.* (1997) Genetic resistance to soil chemical toxicities and deficiencies. International Conference on Genetic Improvement of Sorghum and Pearl Millet, September 22–27, 1996, Lubbock, Texas. INTSORMIL and ICRISAT, pp. 461–480.

Gregorio, G.B., Senadhira, D., Htut, H. and Graham, R.D. (2000) Breeding for trace mineral density in rice. *Food and Nutrition Bulletin*, **21**, 382–386.

Grenier, C., Hamon, P. and Bramel-Cox, P.J. (2001) Core collection of sorghum: I. Stratification based on ecogeographical data. *Crop Science*, **41**, 234–240.

Haggag, M.E., Shafey, S.A. and Mousa, M.E. (1993) Variation in salinity tolerance among forage sorghum – Sudan hybrids. *Journal of Agricultural Sciences, Mansoura University*, **18**, 1597–1608.

Hamaker, B.R. and Axtell, D. (1997) Nutritional quality of sorghum, in Proceedings of the International Conference on Genetic Enhancement of Sorghum and Pearl Millet, September 22–27, 1996, Lubbock, Texas, INTSORMIL and ICRISAT, p. 531.

Hammer, G.L., Dong, Z.S., McLean, G. *et al.* (2009) Can changes in canopy and/or root system architecture explain historical maize yield trends in the US corn belt? *Crop Science*, **49**, 299–312.

Hammer, G.L., Farquhar, G.D. and Broad, I.J. (1997) On the extent of genetic variation for transpiration efficiency in sorghum. *Australian Journal of Agricultural Research*, **48**, 649–655.

Hanna, W.W. and Cordona, S.T. (2001) Pennisetums and sorghum in integrated feeding systems in the tropics, in *Tropical Forage Plants: Development and Use* (eds A.S. Rios and W.D. Pitman), CRC Press, Boca Raton, Florida, pp. 193–200.

Hanna, W.W. and Schertz, K.F. (1970) Inheritance and trisome linkage of seedling characters in *Sorghum bicolor* (L.) Moench. *Crop Science*, **10**, 441–443.

Harlan, J.R. and de Wet, J.M.J. (1972) A simplified classification of cultivated sorghum. *Crop Science*, **12**, 172–176.

Harlan, J.R., de Wet, J.M.J. and Stemler, A.B.L. (eds) (1976) *Origins of African Plant Domestication*, Mouton, The Hague.

Harris, H.B. and Burns, R.E. (1970) Influence of tannin content on pre-harvest and seed germination in sorghum. *Agronomy Journal*, **62**, 835–836.

Hassanein, A.M. and Azab, A.M. (1990) Test for salt tolerance in grain sorghum. *Bulletin of Faculty of Agriculture, University of Cairo*, **41**, 265–276.

Henzell, R.G., Brengman, R.L. Fletcher, D.S. and McCosker, A.N. (1992) Relationship between yield and non-senescence (stay green) in some grain sorghum hybrids grown under terminal drought stress, in Proceedings of the Second Australian Sorghum Conference, February 4–6, 1992, Gatton, QLD Australian Institute of Agricultural Science, Melbourne, Occasional Publication No. 68, pp. 355–358.

Henzell, R.G., Dodman, R.L., Done, A.A. *et al.* (1984) Lodging, stalk rot and root rot in sorghum in Australia, in *Sorghum Root and Stalk Rots: A Critical Review* (ed. Mughogho, L.K), Proceedings of Consultative Group Discussion of Research Needs and Strategies for Control of Sorghum Root and Stalk RotDdiseases, Bellagio, Italy, November 27–December 2, 1983. ICIRISAT, Patancheru, AP, India, pp. 225–236.

Henzell, R.G., Hammar, G.I., Borrell, A.K. *et al.* (1997) Research on drought resistance in grain sorghum in Australia. *International Sorghum and Millets Newsletter*, **38**, 1–8.

Henzell, R.G. and Hare, B.W. (1996) Sorghum breeding in Australia: public and private endeavors, in Proceedings of the Third Australian Conference, February 20–22, 1996, Tamworth, NSW Australian Institute of Agricultural Science, Melbourne, Occasional Publication No. 93, pp. 159–171.

Horst, W.J. (1985) Quick screening of Cowpea (*Vigna unguiculata*) genotypes for aluminium tolerance in an aluminium-treated acid soil. *Zeitschrift fuer pflanzenernaehr Bodenkd*, **148**, 335–348.

House, L.R. (1985) *A Guide to Sorghum Breeding*, 2nd edn, International Crops Research Institute for the Semi-Arid Tropics, Patancheru, AP, India.

House, L.R., Gomez, M., Murty, D.S. *et al.* (2000) Development of some Agricultural industries in several African and Asian countries, in *Sorghum: Origin, History, Technology and Production* (eds C.W. Smith and R.A. Frederiksen), John Wiley & sons, Inc., New York, pp. 131–190.

Humphreys, M.O. (1994) Variation in carbohydrate and protein content of rye grasses: potential for genetic manipulations, in *Breeding for Quality* (eds D. Reheul and A. Ghesquiere), Proceedings of 19th Eucarpia Fodder Crops Section Meeting, Brugge, Belgium, Rijksstation plantenveredeling, merelberke, Belgium.

ICRISAT (International Crops Research Institute for the Semi-Arid Tropics) (1982) *Annual Report 1981*, ICRISAT, Patancheru, AP, p. 37.

ICRISAT (International Crops Research Institute for the Semi-Arid Tropics) (1986) Annual Report 1985, ICRISAT, Patancheru, AP, p. 30.

ICRISAT (International Crops Research Institute for the Semi-Arid Tropics) (1987) Annual Report 1986, ICRISAT, Patancheru, AP, p. 22.

ICRISAT (International Crops Research Institute for the Semi-Arid Tropics) (1993) Sorghum: diseases, insect pests, in *Cereals Program, ICRISAT Annual Report 1992*, ICRISAT, Patancheru, AP, India (semi-formal publication), p. 16.

ICRISAT (International Crops Research Institute for the Semi-Arid Tropics) (1995) Restorers, in *ICRISAT Asia Region Annual Report 1992*, ICRISAT, Patancheru, AP, India, p. 75.

ICRISAT (International Crops Research Institute for the Semi-Arid Tropics) (2000) *A research and network strategy for sustainable sorghum production systems for Latin America, Ninth Season Report, January 2000–June 2000*, Patancheru, AP, India. ICRISAT (Limited distribution)

ICRISAT, NARS, CIAT (1997) A research and network strategy for sustainable sorghum production systems for Latin America, Third Report (semi-formal publication) ICRISAT (International Crops Research Institute for semi-arid Tropics), Patancheru, AP, India, p. 57.

Igartua, E. (1995) Choice of selection environment for improving crop yields in saline areas. *Theoretical and Applied Genetics*, **91**, 1016.

Igartua, E. and Gracia, M.P. (1998) Divergent selection for salinity tolerance at the germination-emergence stage in grain sorghum. *Maydica*, **43**, 161.

Igartua, E., Gracia, M.P. and Lasa, J.M. (1994) Characterization and genetic control of germination emergence responses of grain sorghum to salinity. *Euphytica*, **76**, 185.

Jayanthi, P.D.K. (1997) *Genetics of shoot fly resistance in sorghum hybrids of cytoplasmic male sterile lines*, Ph.D. Thesis, Acharya N.G. Ranga Agricultural University, Hyderabad, Andhra Pradesh, India.

Peng, J., Lill, H., Li, J. and Tan, Z. (1994) Screening Chinese sorghum cultivars for tolerance to salinity. *Sorghum and Millets Newsletter*, **35**, 124.

Jirali, D.I., Biradar, B.D. and Rao, S.S. (2007) Performance of *rabi* sorghum genotypes under receding moisture conditions in different soil types. *Karnataka Journal of Agricultural Sciences*, **20**, 603–604.

Jordan, W.R., Dugas, W.A. and Shouse, P.J. (1983) Strategies for crop improvement for drought prone regions. *Agricultural Water Management*, **7**, 281–299.

Jordan, W.R. and Monk, R.L. (1980) Enhancement of the drought resistance of sorghum: progress and limitations, in Proceedings, Thirty-fifth Corn and Sorghum Research Conference, American Seed Trade Association, Chicago, IL, USA.

Jordan, W.R. and Sullivan, C.Y. (1982) Reaction and resistance of grain sorghum to heat and drought, in Sorghum in the eighties, ICRISAT, Proceedings of International Sorghum Workshop, 2–7 Nov 1981, Hyderabad, India, pp. 131–142.

Jorgenson, L.R. (1931) Brown-midrib in maize and its linkage relations. *Journal of American Society of Agronomy*, **23**, 549–557.

Jotwani, M.G. (1976) Host plant resistance with special reference to sorghum. *Proceedings of the National Academy of Sciences*, **46**, 42.

Kalton, R.R. (1988) Overview of forage sorghums, *Proceedings of the 43rd Annual Corn and Sorghum Research Conference*, Chicago, 8–9 Dec 1988, Washington, DC: American Seed Trade Association **43**, 1–12.

Kholová, J., Hash, C.T., Kakkera, A. *et al.* (2010) Constitutive water conserving mechanisms are correlated with the terminal drought tolerance of pearl millet [*Pennisetum glaucum* (L.) R. Br.]. *Journal of Experimental Botany*, **61**, 369–377.

Kim, H.K., Luquet, D., van Oosterom, E. *et al.* (2010) Regulation of tillering in sorghum: genotypic effects. *Annals of Botany*, **106**, 69–78.

Kimber, C. (2000) Origins of domesticated sorghum and its early diffusion to India and China, in *Sorghum: Origin, History, Technology, and Production* (eds C.W. Smith and R.A. Frederickson), John Wiley & Sons, Inc., New York, pp. 3–98.

Klopfenstein, C.F. and Hoseney, R.C. (1995) Nutritional properties of sorghum and the millets, in *Sorghum and Millets: Chemistry and Technology* (ed. D.A.V. Dendy), American Association of Cereal Chemists, St. Paul, MN, pp. 125–168.

Kramer, P.J. (1980) Drought, stress and the origin of adaptations, in *Adaptation of Plants to Water and High Temperature Stress* (eds N.C. Turner and P.J. Karmer), Wiley-Interscience, New York, USA, pp. 7–20.

Krieg, D.R. (1993) Stress tolerance mechanisms in above ground organs, pp. 65–79, in Proceedings of a workshop on adaptation of plants to soil stresses, August 1–4, 1993, Lincoln, NE, INTSORMIL Publication No, pp. 94–2.

Lagoke, S.T.O., Parkinson, V. and Agunbiade, R.M. (1991) Parasitic weeds and control methods in Africa, in *Combating Striga in Africa* (ed. S.K. Kim). Proceedings, International Workshop organised by IITA, ICRISAT and IDRC, August 22–24, 1988, IITA, Ibadan, Nigeria, pp. 3–14.

Lakshmaiah, K., Jayalakshmi, V. and Sreenivasulu, M.R. (2004) Nandyal Tella Jonna 4, a high yielding sorghum variety identified. *Agricultural Science Digest*, **24** (4), 289–291.

Levitt, J. (1992) *Responses of Plants to Environmental Stresses*, Academic Press, New York.

Ludlow, M.M. (1993) Physiological mechanisms of drought resistance, in *Proceedings of Symposium on Application and Prospects of Biotechnology* (eds T.J. Mabry, H.T. Nguyen and R.A. Dixon), November 5–7, 1992, Lubbock, Texas, USA. IC2 Institute, University of Texas, Austin, pp. 11–34.

Ludlow, M.M. and Muchow, R.C. (1990) A critical evaluation of traits for improving crop yields in water-limited environments. *Advances in Agronomy*, **43**, 107–153.

Luo, Y.W., Yen, X.C., Zhang, G.Y. and Liang, G.H. (1992) Agronomic traits and chromosomal behavior of autotetraploid sorghums. *Plant Breeding*, **109**, 46–53.

Maas, E.V. and Hoffman, G.S. (1977) Crop salt tolerance: current assessment. *Journal of the Irrigation and Drainage Division (ASCE)*, **103** (IR2), 115–134.

Maciel, G.A., Andrade Lima de, M.M., Duncan, R.R. *et al.* (1994) Combining ability of Aluminium tolerance in grain sorghum lines. *International sorghum and Millets Newsletter*, **35**, 73–74.

Maciel, G.A., Andrade Lima de, M.M., Santos, J.P.O. *et al.* (1994) Screening new grain sorghum introductions for aluminium tolerance. *International Sorghum and Millets Newsletter*, **35**, 117–118.

Maclean, W.C., Lopez de Romana, G. and Graham, G.G. (1983) The effects of decortication and extrusion on the digestibility of sorghum by preschool children. *Journal of Nutrition*, **113**, 2171.

Magnavaca, R., Lakins, B.A., Schaffert, R.C. and Lopes, M.A. (1993) Improving protein quality of maize and sorghum, in *International Crop Science I* (eds D.R. Buxton, R.A. Shibles, B.A. Forsberg *et al.*), Crop Science Society of America, Inc., Madison, Wisconsin, USA, pp. 649–653.

Mahalakshmi, V. and Bidinger, F.R. (2002) Evaluation of stay-green sorghum germplasm lines at ICRISAT. *Crop Science*, **42**, 965–974.

Maiti, R.K., de la, R. and Laura, A. (1994) Evaluation of several sorghum genotypes for salinity tolerance. *International Sorghum and Millets Newsletter*, **35**, 121.

Mali, P.C. and Gupta, Y.P. (1974) Chemical composition and protein quality of improved Indian varieties of *Sorghum Vulgare* pers, *Indian Journal of Nutrition and Dietetics*, **11**, 289–295.

Mallick, A.S., Gupta, M.P. and Pandey, A.K. (1988) Combining ability of some quality traits in grain sorghum [*Sorghum bicolor* (L) Moench]. *Indian Journal of Genetics*, **48**, 63–68.

Mann, J.A., Kimber, C.T. and Miller, F.R. (1983) The origin and early cultivation of sorghums in Africa. *Texas Agriculture Experimental Station Bulletin*, **1454**, 1–21.

Manschandi, A.M., Christopher, J., de Voil, P. and Hammer, G.L. (2006) The role of root architectural traits in adaptation of wheat to water-limited environments. *Functional Plant Biology*, **33**, 823–837.

Marschner, H. (1991) Mechanisms of adaptation of plants to acid soils. *Plant and Soil*, **134**, 1–20.

Maunder, A.B. (1972) Objectives and approaches to grain and forage sorghum improvement in the Americas, in *Sorghum in Seventies* (eds N.G.P. Rao and L.R. House), Oxford and IBH Publishing Co., New Delhi, pp. 60–100.

Mc Millian, W.W., Wiseman, B.R., Burns, R.E. *et al.* (1972) Bird resistance in diverse germplasm of sorghum. *Agronomy Journal*, **64**, 821–822.

Mohan, D. (1975) *Chemically induced high lysine mutants in Sorghum bicolor (L.)* Moench, Thesis, Purdue University, West Lafayette, IN, pp. 110.

Montemurro, F., Rigoldi, M.P., Sunseri, F. and Vanadia, S. (1994) Early screening methodologies for selecting salt stress tolerant sweet sorghum [*Sorghum bicolor* (L.) Moench]. *Rivista di Agronomia*, **28**, 179–183.

Mukuru, S.Z. (1992) Breeding for grain mold resistance, in *Sorghum and Millet Diseases, A second World Review* (eds W.A.J. de Milliano, R.A. Frederiksen and G.D. Bengston), ICRISAT, Patancheru, AP, India, pp. 273–285.

Murthy, U.R. (1986) Apomixis: achievements, problems and future prospects, in *Advanced Methods in Plant Breeding*, Oxford and IBH, New Delhi, India.

Murthy, U.R., Schertz, K.F. and Bashaw, E.C. (1979) Apomictic and sexual reproduction in sorghum. *Indian Journal of Genetics and Plant Breeding*, **39**, 271–278.

Murty, V.R. and Rao, N.G.P. (1977) Sorghum, in *Genetics, Cytogenetic and Breeding of Crop Plants* (eds P.N. Bahl, P.M. Salimath and A.K. Mandal), Oxford and IBH Publishing Co. Pvt. Ltd, pp. 197–239.

Nanda, G.S. and Rao, N.G.P. (1974) Gene action for vitamins in grain sorghum. *Crop Improvement*, **1**, 53–60.

Nanda, G.S. and Rao, N.G.P. (1975a) Gene action for content of amino acid in grain sorghum. *Indian Journal of Genetics*, **35**, 395–398.

Nanda, G.S. and Rao, N.G.P. (1975b) Genetic analysis of some exotic x Indian crosses in sorghum. *IX. Nutritional quality and its association with grain yield. Indian Journal of Genetics*, **35**, 131–135.

Nayeem, K.A. and Bapat, D.R. (1984) Heterosis and heterobeltiosis for grain yield and quality in sorghum [*Sorghum bicolor* (L.) Moench]. *Indian Journal of Agricultural Sciences*, **23**, 306–310.

NRCS (National Research Centre for Sorghum) (2007) *Perspective plan: Vision 2025*. NRCS, Rajendra Nagar, Hyderabad, India.

Nwanze, K.F., Seetharama, N., Sharma, H.C. and Stenhouse, J.W. (1995) Biotechnology in pest management: improving resistance to sorghum to insect pests. *African Crop Science Journal*, **3**, 209–215.

Obilana, A.B. (2004) Sorghum breeding research in Africa, in *Sorghum Genetic Enhancement – Research Process, Dissemination and Impacts* (eds M.C.S. Bantilan, U.K. Deb, C.L.L. Gowda *et al*.) International Crops Research Institute for the Semi-Arid Tropics, Patancheru, AP, India, pp. 105–138.

Olembo, K.N., M'mboyi, F., Kiplagat, S. *et al.* (2010) *Sorghum breeding in Sub-Saharan Africa: Success Stories*, African Biotechnology Stakeholders Forum (ABSF), Nairobi, Kenya, p. 40.

Ollitrault, P., Arnaud, M. and Chantereau, J. (1989) Polymorphisme enzymatique des sorghos. IIOrganisation génétique et évolutive des sorghos cultivés. *L' Agro Trop*, **44** (3), 211–222.

Oria, M.P., Hamaker, B.R. and Axtell, J.D. (2000) A highly digestible sorghum cultivar exhibits a unique folded structure of endosperm protein bodies. *Proceedings of National Academy of Sciences*, **97** (10), 5065–5070.

Owen, F.G. and Moline, W.J. (1970) Sorghum for forage, in *Sorghum Production and Utilization* (eds J.S. Wall and W.M. Ross), AVI Publication Co., Westport, CT, pp. 382–415.

Patil, J.V., Sanjana Reddy, P., Prabhakar *et al.* (2014) History of post-rainy-season sorghum research in India and strategies for breaking the yield plateau. *Indian Journal of Genetics and Plant breeding*, **74**(3), 271–285.

Pattanashetti, S.K., Biradar, B.D. and Salimath, P.M. (2005) Comparative performance of *Milo v/s Maldandi* based rabi sorghum hybrids in the Transitional Zone of Karnataka. *Karnataka Journal of Agricultural Sciences*, **18**, 655–659.

Peacock, J.M. and Sivakumar, M.V.K. (1987) An environmental physiologist approach to screening for drought resistance in sorghum with particular reference to sub-Saharan Africa, *Proceeding of the International Drought Symposium* (ed. S.M. Menyonga), Kemyatta Conference Centre, Nairobi, Kenya, May 19–23, 1986.

Pederson, J.F. (1997) Breeding sorghum and pearl millet for forage and fuel, in *Proceedings of International Conference on Genetic Improvement of Sorghum and Pearl Millet*, Lubbock, Texas, September 22–27, 1996, INTSORMIL and ICRISAT, pp. 539–548.

Pedersen, J.F. and Fritz, J.O. (2000) Forages and Fodder, in *Sorghum: Origin, History, Technology and Production* (eds W.C. Smith and R.A. Frederiksen), John Wiley & Sons, Inc., New York, pp. 797–810.

Peterson, G.C., Reddy, B.V.S., Youm, O. *et al.* (1997) Breeding for resistance to foliar- and stem-feeding insects of sorghum and pearl millet, in *Proceedings of the International Conference on Genetic Improvement of Sorghum and Pearl Millet*, Lubbock, Texas, September 22–27, 1996, INTSORMIL and ICRISAT, pp. 281–302.

Porter, K.S., Axtell, J.D., Lechtenberg, V.L. and Colenbrander, V.F. (1978) Phenotype, fiber composition, and in vitro dry matter disappearance of chemically induced brown midrib (bmr) mutants of sorghum. *Crop Science*, **18**, 205–208.

Purseglove, J.W. (1972) *Sorghum bicolor* (L.) Moench, in *Tropical Crops. Monocotyledons*, Longman Group Limited, London, pp. 261–287.

Quinby, J.R., Hesketh, J.D. and Voigt, R.L. (1973) Influence of temperature and photoperiod on floral initiation and leaf number in sorghum. *Crop Science*, **13**, 243–246.

Quinby, J.R. and Karper, R.E. (1954) Inheritance of height in sorghum. *Agronomy Journal*, **46**, 212–216.

Radhamani, J., Pandey, A., Srinivasan, K. and Tyagi, V. (2011) Conserving millet genetic resources in India. *Proceedings of the Indian National Science Academy*, **77** (4), 295–304.

Rafiq, S.M., Madhusudhana, R. and Umakanth, A.V. (2003) Heterosis in post-rainy season sorghum under shallow and medium–deep soils. *International Sorghum and Millets Newsletter*, **44**, 17–21.

Rana, B.S., Anahosur, K.H., Jaya-Mohan Rao, V. *et al.* (1982) Inheritance of field resistance to sorghum charcoal rot and selection for multiple disease resistance. *Indian Journal of Genetics*, **42**, 302–310.

Rana, B.S., Jotwani, M.G. and Rao, N.G.P. (1980) Inheritance of host plant resistance to sorghum shoot fly, in *Insect science and its application*, IC1PE, 4–8 May, Nairobi, Kenya.

Rana, B.S. and Murty, B.R. (1971) Genetic analysis of resistance to stem borer in sorghum. *Indian Journal of Genetics*, **31**, 521–529.

Rana, B.S. and Murty, B.R. (1975) Heterosis and components of genetic variation for protein and lysine content in some grain sorghums. *Theoretical and Applied Genetics*, **45**, 225–230.

Rana, B.S. and Murty, B.R. (1978) Role of height and panicle type in yield heterosis in some grain sorghums. *Indian Journal of Genetics and Plant Breeding*, **38**, 126–134.

Rana, B.S., Rao, V.J.M. and Rao, N.G.P. (1978) Genetic analysis of some exotic x Indian crosses in sorghum. XVIII. Breeding for resistance to grain deterioration. *Indian Journal of Genetics*, **38**, 322–332.

Rana, B.S., Swarnalata, K. and Rao, M.H. (1997) Impact of genetic improvement on sorghum productivity in India, in *Proceedings of an International Conference on the Genetic Improvement of Sorghum and Pearl Millet*, held at Lubbock, Texas, September 22–27, 1996. International Sorghum and Millet Research (INTSORMIL) – International Crops Research Institute for the Semi-arid Tropics (ICRISAT), pp. 142–165.

Rana, B.S., Tripathi, D.P. and Rao, N.G.P. (1976) Genetic analysis of some exotic x Indian crosses in sorghum. XV. Inheritance of resistance to sorghum rust. *Indian Journal of Genetics*, **36** (2), 244–249.

Rani, K.J. and Rao, S.S. (2008) Mid parental gca – a better prediction of hybrid performance in rabi sorghum. *Research on Crops*, **9**, 652–656.

Rao, N.G.P. (1970) Genetic analysis of some exotic × Indian crosses in Sorghum I. Heterosis and its interaction with seasons. *Indian Journal of Genetics*, **30**, 347–361.

Rao, N.G.P. (1982) Transforming traditional sorghum in India, in *Sorghum in the Eighties* Vol. 1, (eds L.R. House, L.K. Mughogho and J.M. Peacock), Proceedings of the International Symposium on Sorghum, November 2–7, 1981, ICRISAT, Patancheru, AP, India, pp. 39–59.

Rao, V.J.M., Deosthale, Y.G., Rana, B.S. *et al.* (1983a) Genetic analysis of some exotic x Indian crosses in sorghum, XXXI Nutritional quality in grain sorghum: variability for protein, lysine and leucine. *Indian Journal of Genetics*, **43**, 380–382.

Rao, V.J.M., Deosthale, Y.G., Rana, B.S. *et al.* (1983b) Genetic analysis of some exotic x Indian crosses in grain sorghum XXXII, Nutritional quality in grain sorghum: behaviour of crosses involving between high lysine sorghum and agronomically superior types. *Indian Journal of Genetics*, **43**, 383–394.

Rao, V.J.M., Mehta, S.L. and Rao, N.G.P. (1984) Breeding sorghums for high protein content and quality. *Indian Journal of Genetics*, **44**, 305–313.

Rao, N.G.P. and Murthy, U.R. (1972) Further studies on obligate apomixis in grain sorghum. *Sorghum bicolor* (L.) Moench. *Indian Journal of Genetics*, **32**, 379–383.

Rao, N.G.P. and Rana, B.S. (1982) Selection in temperate and tropical crosses of sorghum, in *Sorghum in the Eighties*, Vol. 1, (eds L.R. House, L.K. Mughogho and J.M. Peacock), Proceedings of the International Symposium on Sorghum, November 2–7, 1981, ICRISAT, Patancheru, AP, India, pp. 403–420.

Rao, V.J.M., Rana, B.S., Reddy, B.B. and Rao, N.G.P. (1984) Genetic upgrading of protein quality in sorghum, in *Nutritional and Processing Quality of Sorghum* (eds D.K. Salunkhe, J.K. Chavan and S.J. Jadhav), Oxford and IBH Publishing Co., New Delhi, pp. 67–90.

Ratnadass, A., Chantereau, J., Coulibaly, M.F. and Cilas, C. (2002) Inheritance of resistance to the panicle-feeding bug (*Eurystylus oldi*) and the sorghum midge (*Stenodiplosis sorghicola*) in sorghum. *Euphytica*, **123**, 131–138.

Raynal-Roques, A. (1987) The genus *Striga* (Scrophulariaceae) in western and central Africa – a survey, in *Parasitic Flowering Plants* (eds H. Weber, Chr and W. Forstreuter), proceedings of the 4th ISPFP, Phillips University, Marburg, Germany, pp. 675.

Reddy, B.V.S. (1985) Breeding grain sorghums for adaptation to specific drought situations. RELATORIO FINAL DE CONSULTORIA. IICA/EMBRAPA/IPA. January 1984 to March 1985, pp. 1–83.

Reddy, B.V.S. (1986) Genetic improvement for drought resistance in sorghum: a plant breeder's view point, in *Genetic Improvement of Drought Resistance*, Proceedings of a Discussion Series of the Drought Research Seminar Forums, ICRISAT, Patancheru, India, pp. 28–32.

Reddy, B.V.S., Hash, C.T., Stenhouse, J.W. *et al.* (1994) Crop improvement for livestock crop residue feed at ICRISAT Asia Center, in *Proceedings of a Workshop on Crop Improvement and its Impact on the Feeding Value of Straw and Stovers of Grain Cereals in India, November 21, 1994*, ICAR, New Delhi, pp. 85–92.

Reddy, B.V.S., Mughogho, L.K. and Jambunathan, R. (1992) Breeding grain mold resistance seed parents and hybrids. Cereals Program – Annual Report, 1991, ICRISAT, Patancheru, AP, India, pp. 28–29.

Reddy, B.V.S., Prakasha Rao, Deb, U.K. *et al*. (2004) Global sorghum genetic enhancement processes at ICRISAT, in *Sorghum Genetic Enhancement: Research Process, Dissemination and Impacts* (eds M.C.S. Bantilan, U.K. Deb, C.L.L. Gowda *et al*.), Patancheru, AP, India: International Crops research Institute for the Semi-Arid tropics, pp. 65–102.

Reddy, B.V.S. and Prasada Rao, K.E. (1993) Varietal Improvement: Genetic Diversification in Cereals Program, ICRISAT Annual Report 1992, ICRISAT, Patancheru, AP, India (semi-formal publication), pp. 48–51.

Reddy, B.V.S., Ramesh, S. and Sanjana Reddy, P. (2004) Sorghum breeding research at ICRISAT: Goals, strategies, methods and accomplishments. *International Sorghum and Millets Newsletter*, **45**, 5–12.

Reddy, B.V.S., Ramesh, S., Sanjana Reddy, P. and Ashok Kumar, A. (2009) Genetic enhancement for drought tolerance in sorghum. *Plant Breeding Reviews*, **31**, 189–222.

Reddy, B.V.S. and Rangel, A.F. (2000) Genotype (G) x Environment (E) interactions in sorghum in acid-soils of the oriental Llanos of Colombia, in *A Research and Network Strategy for Sustainable Sorghum and Pearl Millet Production Systems for Latin America* (eds B.V.S. Reddy, C. Hernán; O. Rodomiro), Proceedings of the workshop, November 24–26, 1998, Villavicencio, Meta, Colombia. Patancheru, Andhra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) and Cali, Colombia: Centro International de Agricultura Tropical (CIAT), pp. 46–51.

Reddy, B.V.S., Rangel, A.F. and Iglesaias, C. (1998) Latin American Sorghum Project: some results, in *Proceedings of the First International Symposium on Sorghum*, Rio Bravo, Tamaulipas, Mexico, CIAT, Columbia, May 27–30, 1998, pp. 70–79.

Reddy, B.V.S., Rudrappa, A.P., Prasada Rao, K.E. *et al*. (1983) Sorghum improvement for *rabi* adaptation: approach and results. Presented at the All India Coordinated Sorghum Improvement Project Workshop, April 18–22, 1983, Haryana Agricultural University, Hisar, India. Hisar, Haryana, India: All India Coordinated Improvement Project.

Reddy, B.V.S., Sanjana, P. and Ramaiah, B. (2003) Strategies for improving post-rainy-season sorghum: a case study for landrace hybrid breeding approach, Paper presented in the workshop on Heterosis in Guinea Sorghum, Sotuba, Mali, 10–14 March 2003.

Reddy, B.V.S. and Singh, S.D. (1993) Sorghum Anthracnose, Inheritance of Resistance, Cereals Program – Annual Report, 1992, ICRISAT, Patancheru, AP, p. 17.

Reddy, B.V.S. and Stenhouse, J.W. (1993) Hybrid Development and Testing, Cereals Program-Annual Report 1992, ICRISAT, Patancheru, AP, pp. 45–48.

Reddy, B.V.S. and Stenhouse, J.W. (1994a) Sorghum improvement for semi-arid tropics region; past current and future research thrusts in Asia. *PKV Research Journal*, **18**, 155–169.

Reddy, B.V.S. and Stenhouse, J.W. (1994b) Improving post-rainy-season sorghum, a case for landrace hybrids approach, An invited paper presented at All India Co-ordinated Sorghum Improvement Project – (AICSIP) workshop held at Pantnagar, Uttar Pradesh, April 18–20.

Reddy, C.S., Schertz, K.F. and Bashaw, E.C. (1980) Apomictic frequency in sorghum R 473. *Euphytica*, **29**, 223–226.

Reddy, G.V., Upadhyaya, H.D. and Gowda, C.L.L. (2006) Current status of sorghum genetic resources at ICRISAT: their sharing and impacts. *International Sorghum and Millets Newsletter*, **47**, 9–13.

Reddy, J.N. (1993) Combining ability and heterosis of stover yield in sorghum [*Sorghum bicolor* (L.) Moench]. *Orissa Journal of Agricultural Research*, **6**, 164–166.

Reddy, P.S., Patil, J.V. and Krishna, T.P. (2014) Response of diverse groups of sorghum (*Sorghum bicolor* (L.) Moench) genotypes to low temperature stress at anthesis. *Indian Journal of Genetics*, **74** (4), 444–449.

Reddy, V.G., Upadhyaya, H.D. and Gowda, C.L.L. (2006) Current status of sorghum genetic resources at ICRISAT: their sharing and impacts. *SAT e-journal*, **2** (1), 1–5.

Reich, V.H. and Atkins, R.E. (1971) Variation and interrelationship of protein, oil content and seed weight in grain sorghum. *Iowa State Journal of Science*, **46**, 13–22.

Richards, R.A. and Dennett, C.W. (1980) Variation in salt concentration in a wheat field, University of California Co-operative Extension. *Soil and Water*, **44**, 8–9.

Richards, R.A., Dennett, C.W., Qualset, C.O. *et al.* (1987) Variation in yield of grain and biomass in wheat, barley and triticale in a salt-affected field. *Field Crops Research*, **15**, 277–287.

Richter, C., Heiligtag, B., Gertling, M. and Abdullahzadeh, A. (1995) Salt tolerance of different varieties of *Sorghum bicolor* and *Vicia faba*. *Tropenlandwirt*, **96**, 141–152.

Robertson, G.W. (1988) Possibilities and limitations of rainfall analysis for predicting crop available water, in *Drought Research Priorities for the Dryland Tropics* (eds F.R. Bidinger and C. Johansen), ICRISAT, Patancheru, India, pp. 3–14.

Rooney, W.L. (2000) Genetics and Cytogenetics, in *Sorghum: Origin, History, Technology and Production* (eds C.W. Smith and R.A. Frederiksen), John Wiley & Sons, Inc., New York, pp. 261–307.

Rooney, L.W., Hamker, B. and Botorou, Q. (2003) Grains in West Africa: processing and product marketing through value added supply chain management, A concept note paper presented in the expert meeting on alternative uses of sorghum and pearl millet in Asia, July 1–4, 2003, ICRISAT, Patancheru, AP, India.

Rooney, W.L. and Smith, C.W. (2000) Techniques for developing new cultivars, in *Sorghum: Origin, History, Technology and Production* (eds C.W. Smith and R.A. Frederiksen), John Wiley & Sons, Inc., New York, pp. 329–347.

Rosenow, D.T. (1992) Using germplasm from the world collection in breeding for disease resistance, in *Sorghum and Millet Diseases: A Second World Review* (eds W.A.J. de Milliano, R.A. Frederiksen and G.D. Bengston), ICRISAT, Patancheru, AP, India, pp. 319–324.

Rosenow, D.T. and Clark, L.E. (1995) Drought and lodging resistance for quality sorghum crop, in *Proceedings of the 50th Annual Corn and Sorghum Industry Research Conference, Chicago, IL., December 6–7, 1995*, American Seed Trade Assoc., Washington, DC, pp. 82–97.

Rosenow, D.T. and Dahlberg, J.A. (2000) Collections, conversion and utilization of sorghum, in *Sorghum: Origin, History, Technology and Production* (eds C.W. Smith and R.A. Frederiksen), John Wiley & Sons, Inc., New York, USA, pp. 309–328.

Rosenow, D.T., Dahlberg, J.A., Peterson, G.C. *et al.* (1997) Registration of fifty converted sorghums from the sorghum conversion program. *Crop Science*, **37**, 1397–1400.

Rosenow, D.T., Quinsenberry, J.A., Wendt, W.C. and Clark, L.E. (1983) Drought-tolerant sorghum and cotton germplasm. *Agricultural Water Management*, **7** (1–3), 207–222.

Sajjanar, G.M., Biradar, B.D. and Biradar, S.S. (2011) Evaluation of crosses involving *rabi* landraces of sorghum for productivity traits. *Karnataka Journal of Agricultural Science*, **24**, 227–229.

Sanders, J.H., Shapiro, B.I. and Ramaswamy, S. (1996) *The Economics of Agricultural Technology in Semi-arid Sub-Saharan Africa*, Johns Hopkins University Press, Baltimore, MD.

Schaffert, R.E., McCrate, A.J., Trevisan, W.L. *et al.* (1975) Genetic variation in *Sorghum bicolor* (L.) Moench for tolerance to high levels of exchangeable aluminium in acid soils of Brazil, in *Proceedings of Sorghum Workshop*, University of Puerto Rico, Mayaguez, Puerto Rico, pp. 151–160.

Schertz, K.F. (1994) Male sterility in sorghum: its characteristics and importance, in *Use of Molecular Markers in Sorghum and Pearl Millet Breeding for Developing Countries* (eds J.R. Witcombe and R.R. Duncan), Proceedings of an ODA Plant Sciences Research Conference, March 29–April 1, 1993, Norwich, UK, Overseas Development Administration (ODA), UK, pp. 35–37.

Schertz, K.F. and Dalton, L.G. (1980) *Sorghum, in Hybridization of Crop Plants*, American Society of Agronomy – Crop Science Society of America, Madison, USA, pp. 577–588.

Schertz, K.F., Sivaramakrishnan, S., Hanna, W.W. *et al.* (1997) Alternate cytoplasms and apomixis of sorghum and pearl millet, in *Proceedings of an International Conference on the Genetic Improvement of Sorghum and Pearl Millet, held at Lubbock, Texas, September 22–27, 1996*, International Sorghum and Millet Research (INTSORMIL) – International Crops Research Institute for the Semi-arid Tropics (ICRISAT), pp. 213–223.

Seetharama, N., Reddy, B.V.S., Peacock, J.M. and Bidinger, F.R. (1982) Sorghum improvement for drought resistance, in *Drought Resistance in Crops with Emphasis on Rice*. International Rice Research Institute, Los Banos, Laguna, Manila, Philippines, pp. 317–338.

Sharma, G.C., Abraham, C.V., Vidyasagar, P. and Stenhouse, J.W. (1994) Gene action for resistance in *Sorghum bicolor* (L.) Moench to sorghum midge, (*Contarinia Sorghicola*). *Crop Science*, **36**, 259–265.

Sharma, H.C. (1993) Host plant resistance to insects in sorghum and its role in integrated pest management. *Crop Protection*, **12**, 11–34.

Sharma, H.C., Agrawal, B.L., Abraham, C.V. *et al.* (1993) Identification and utilization of resistance to sorghum midge, *Contarinia sorghicola*. Coq. *Crop Protection*, **12**, 343–350.

Sharma, H.C., Taneja, S.L., Leuschner, K. and Nwanze, K.F. (1991) Techniques to screen sorghum for resistance to insects. International Crops Research Institute for the Semi-arid Tropics (ICRISAT) Information Bulletin No. 32. ICRISAT, Patancheru, India.

Yuxue, S., Yue, C. and Yang, Z. (1992) Approaching a series of problems on Sorghum production in Liaoning province. *Liaoning Agricultural Science*, **6**, 42–45.

Singh, B.V. and Rana, B.S. (1994) Influence of varietal resistance on disposition and larval development of stalk borer, *Chilo Partellus* Swinhoe and its relationship to field tolerance in sorghum. *Insect Science and its Application*, **5**, 287–296.

Singh, R. and Axtell, J.D. (1973) High lysine mutant gene (hl) that improves protein quality and biological value of grain sorghum. *Crop Science*, **13**, 535.

Singhania, D.L., Deosthale, Y.G. and Rao, N.G.P. (1979) A study of gene action for protein and lysine content in sorghum (*Sorghum bicolor* [L.] Moench). *Indian Journal of Heredity*, **11**, 25–34.

Smith, C.W. and Frederiksen, R.A. (2000) *Sorghum: Origin, History, Technology, and Production*, John Wiley & Sons, New York.

Snowden, J.D. (1936) *The Cultivated Races of Sorghum*, Allard and Co, London, UK.

Stephens, J.C. and Holland, R.F. (1954) Cytoplasmic male-sterility for hybrid sorghum seed production. *Agronomy Journal*, **46**, 20–23.

Sullivan, C.Y. (1972) Mechanisms of heat and drought resistance in grain sorghum and methods of measurements, in *Sorghum in Eighties* (eds N.G.P. Rao and L.R. House), Oxford and IBH publishing Co., New Delhi, India, pp. 247–263.

Sullivan, C.Y. and Ross, W.M. (1979) Selecting for drought and heat resistance in grain sorghum, in *Stress Physiology in Crop Plants* (eds H. Mussell and R.C. Staples), Wiley-Interscience, New York, USA, pp. 263–281.

Tarr, S.A.J. (1962) *Diseases of Sorghum, Sudan Grass and Broom Corn*, Commonwealth Mycological Institute, Kew, Surrey, UK, pp. 380.

Tenkouano, A., Miller, F.R., Frederiksen, R.A. and Rosenow, D.T. (1993) Genetics of non-senescence and charcoal rot resistance in sorghum. *Theoretical and Applied Genetics*, **85**, 644–648.

Thakur, R.P., Frederiksen, R.A., Murty, D.S. *et al.* (1997) Breeding for disease resistance in sorghum, in *Proceedings of International Conference on Genetic Improvement of Sorghum and Pearl Millet, September 22–27, 1996*, INTSORMIL and ICRISAT, Lubbock, Texas, pp. 303–315.

Thakur, R.P., King, S.B., Rai, K.N. and Rao, V.P. (1992) Identification and utilization of smut resistance in pearl millet. International Crops Research Institute for the Semi-arid Tropics (ICRISAT) Research Bulletin No. 16. ICRISAT, Patancheru, India.

Thakur, R.P., Rai, K.N., King, S.B. and Rao, V.P. (1993) Identification and utilization of ergot resistance in pearl millet. International Crops Research Institute for the Semi-arid Tropics (ICRISAT) Research Bulletin No. 17. ICRISAT, Patancheru, India.

Tipton, K.W., Floyd, E.H., Marshall, J.G. and McDevit, J.B. (1970) Resistance of certain grain sorghum hybrids to bird damage in Louisiana. *Agronomy Journal*, **62**, 211–213.

Turner, N.C. (1979) Drought resistance and adaptation to water deficits in crop plants, in *Stress Physiology in Crop Plants* (eds H. Mussell and R.C. Staples), Wiley & Sons, Inc., New York, pp. 343–372.

Upadhyaya, H.D., Pundir, R.P.S., Dwivedi, S.L. *et al.* (2009) Developing a mini core collection of sorghum for diversified utilization of germplasm. *Crop Science*, **49** (5), 1769–1780.

Van Oosterrom, E.J., Jayachandran, R. and Bidinger, F.R. (1996) Diallel analysis of the stay-green trait and its components in sorghum. *Crop Science*, **36**, 549–555.

Vavilov, N.I. (1992) *The Origin and Geography of Cultivated Plants*, Cambridge University Press, Cambridge.

Virupaksha, T.K. and Sastry, L.V.S. (1968) Studies on the protein content and amino acid composition of some varieties of grain sorghum. *Journal of Agricultural and Food Chemistry*, **16**, 199–203.

Virupaksha, T.K. and Sastry, L.V.S. (1969) Alcohol soluble proteins of grain sorghum. *Cereal Chemistry*, **46**, 284–293.

Vose, P.B. (1987) Genetic aspects of mineral nutrition – progress to date, in *Genetic Aspects of Plant Mineral Nutrition* (eds W.H. Gabelman and B.C. Loughman), Martinus Nijhoff Publishers, Dordrecht, The Netherlands, pp. 3–13.

Waggle, D.H. and Deyoe, C.W. (1966) Relationship between protein level and amino acid composition of sorghum grain. *Food Stuffs*, **38**, 18–19.

Wall, J.S. and Blessin, C.W. (1970) Composition of sorghum plant and grain, in *Sorghum Production and Utilization* (eds J.S. Wall and W.M. Ross), AVI publishing Co., Westport, CT, pp. 118–166.

Webster (1986) *Webster's Ninth New Collegiate Dictionary*, Merriam-Webster, Spring Field, MA.

Wendorf, F., Close, A.E., Schild, R. *et al.* (1992) Saharan exploitation of plants 8,000 years bp. *Nature*, **359**, 721–724.

Xu, W.W., Subudhi, P.K., Crasta, O.R. *et al.* (2000) Molecular mapping of QTL conferring stay-green in grain sorghum (*Sorghum bicolor* L. Moench). *Genome*, **43**, 461–469.

Yang, Z. and Yang, X. (1993) Research on genetics of resistance to No.3 physiological race of head smut in sorghum. *Liaoning Agricultural Science*, **4**, 38–50.

Zake, V.M., Watson, C.E. Jr. and Gourley, L.M. (1992) Performance of grain sorghum hybrids on infertile, acid soils in Kenya, in *Proceedings of Workshop on Adaptation of plants to soil stresses*, Lincoln, N.E. August 1–4, 1993, INTSORMIL Publication No. 94-2, Lincoln, N.E. pp. 80–99.

Yang, Z. (1997) Sorghum breeding research in China. *International Sorghum and Millets Newsletter*, **38**, 15–18.

2

Pearl Millet, *Pennisetum glaucum* (L.) R. Br.

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2.1 Introduction

Pearl millet, *Pennisetum glaucum* (L.) R. Br., is the sixth important cereal crop after rice, wheat, maize, barley and sorghum. It is a C4 species with a very high photosynthetic efficiency and dry-matter production. It is cultivated in 30 million hectares (m ha) in more than 30 countries in five continents viz., Asia, Africa, North America, South America and Australia, supporting more than 100 million people – the poorest of the poor (Yadav *et al*., 2013). The major pearl-millet-producing countries are Senegal, Mali, Burkina Faso, Niger, Nigeria, Chad, Sudan and India. It is also grown in Oceania and the Americas, predominantly as a forage and/or mulch component of minimum tillage-based cropping systems. India is the largest producer of this crop, both in terms of area (9.1 million ha) and production (7.3 million t), with an average productivity of 780 kg ha^{-1} during the last 5 years. In Western and Central Africa (WCA), open-pollinated varieties of pearl millet are cultivated in 16 million ha with a production of 11.5 million t and productivity of 800 kg ha^{-1}. India accounts for above 80% of the 12 million ha in Asia under pearl millet cultivation (Rai *et al*., 1999). The crop is well adapted to drought-prone areas, low soil fertility and high temperature situations. It is a predominantly cross-pollinated crop with 75–80% out-crossing. The grain yields largely under subsistence farming are low (500–700 kg ha^{-1}). Low soil fertility, rain-fed farming characterised by erratic and inadequate rainfall (annual precipitation as low as 300 mm), negligible external inputs, continued use of mostly unimproved cultivars with a low harvest index (<20%) and the prevalence of diseases and insect pests being the major causes of low productivity. Under these conditions, yields of maize become too uncertain, and pearl millet stands out as the most reliable food cereal. Pearl millet, in general, occupies the drier parts of the semi-arid tropics and extends into the arid zone, where soils tend to be sandier, the growing season shorter and drought stress more frequent.

With regard to nutritional quality, it is equivalent to maize and superior to sorghum in protein content and quality, protein-efficiency ratio, metabolisable energy levels and does not contain tannins. Though it is deficient in essential amino acids, it contains 35% more lysine than sorghum (Rooney and McDonough, 1987). It contains 5–6% oil (Jambunathan and Subramanian, 1988) and is a rich source of iron and zinc. Apart from being a main staple, its use for poultry feed is on the increase. It is also an important

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source of fodder and the only source of feed in dry months (Hash *et al*., 2003). The presence of all required nutrients make it suitable for large-scale utilisation in the manufacture of various food products such as traditional meals, baby foods, snack foods and dietary foods in both grain and flour form. Both grain and stover of pearl millet have a better mineral profile than many other cereals. Beside its nourishment qualities, the bioavailability of various minerals such as Ca and P and trace elements such as Zn, Fe, Cu and Mn is low because of the presence of some inherent anti-nutritional factors, for example, phytate, and polyphenols in grain; and oxalic acid in fodder and forage, which are undesirable. However, several processing techniques such as dehulling, milling, malting, blanching, acid treatment, dry heat treatment and par-boiling have been developed which enhance the food value and shelf-life of pearl millet products and improve the availability of starch, protein and minerals. Decreasing or degrading of phytic acid is very advantageous, due to its influence on nutrition.

The use of pearl millet is increasing in brewing industry, in poultry and animal feed, as fodder and as roofing material. Use of pearl millet is also increasing in traditional foods and snacks such as porridge, chapatti, *khichri*, *laddoo*, *mathi*, etc.; baked products such as cake, *nan khatai*, biscuits, etc.; extruded products such as sev and sweet vermicelli; flakes and pops and many more. The National Dairy Research Institute, Karnal, has recently developed and launched pearl millet *lassi*, made from pearl millet flour. Pearl millet is also being used in preparing various types of health foods and food ingredients as it contains a relatively higher proportion of insoluble dietary fibre, which causes slow release of sugar, thus making the food products based on them especially suitable for those suffering from or prone to diabetes. Despite all these advantages, it is considered to be an inferior food crop due to lack of nutritional awareness, processing and economic incentives to farmers. Its per capita consumption is declining, whereas production is increasing, and this leads to high volatility in its prices and farmers' incomes.

India produces more than half the world's pearl millet (FAOSTAT, 2006), and has been the centre of research efforts since the 1960s when the availability of cytoplasmic-genetic male-sterile lines brought a succession of hybrids. Since the mid-1960s, when hybrid pearl millets were first introduced in India, average grain yields nearly doubled, despite the shift to more marginal production environments. The All India Coordinated Pearl Millet Improvement Project (AICPMIP) was started in 1967 in Pune, Maharashtra, and later moved to Mandor (Jodhpur), Rajasthan. The first pearl millet hybrid HB 1 (developed by Punjab Agriculture University, Ludhiana) was released in 1965, making pearl millet one of the earliest public-bred hybrid crops marketed in India. During 1974–1975, a heavy attack of downy mildew reduced pearl millet production dramatically, to 3.3 million t – a decrease of 57% from previous years. The second series of millet hybrids was released during 1974–1975 (PBH 10 and 14) and proved more tolerant than the previous cultivars, but they also broke down quickly. The two other hybrids released during the mid-1980s, BJ 104 and BK 560, were known for their short duration and drought resistance. With the improved adoption levels, they slowly brought back the production up to 6 million t. However, these cultivars also suffered downy mildew attack, and the Government of India withdrew them both from commercial use in 1986 (Pray and Ribeiro, 1990). Popular public hybrids such as HHB 67 (released by Haryana Agricultural University in 1989) delivered increased production levels from the early 1990s until now – with current production at 9 million t. Now hybrids cover more than 50% of the total national pearl millet area of 10 million hectares (Thakur *et al*., 2003).

2.2 Origin and Taxonomy

2.2.1 Taxonomy

Taxonomists place the genus Pennisetum in the tribe Paniceae, close to the genus Cenchrus on the basis of spikelets that are arranged in groups surrounded by an involucre. The genus consists of five sections – Gymnothrix, Brevivalvula, Penicillaria, Heterostachya and Eu-Pennisetum. All the species of Pennisetum having penicillate anther tips and pinnate involucral bristles were included in the section Penicillaria (Leeke, 1907). According to Brunken (1977), Pennisetum includes two reproductively isolated species. These are *Pennisetum purpureum* Schumach, a tetraploid (2*n*=28) perennial species which occurs throughout the wet tropics of the world; and *Pennisetum americanum* (L.) Leeke, a diploid (2*n*=14), native to semi-arid tropics of Africa and India. The species americanum contains three subspecies. The subspecies americanum includes a wide array of cultivated pearl millets. The name *Pennisetum americanum* is not taxonomically valid (de Wet, 1987), and the name was revised to *Pennisetum glaucum* (L.) R. Br. The taxonomical classification currently adopted is:

Family:	*Poaceae*
Subfamily:	*Panicoideae*
Tribe:	*Paniceae*
Subtribe:	*Panicinae*
Section:	*Penicillaria*
Genus:	*Pennisetum*
Species:	*glaucum*

The genepool system of classification was suggested by Harlan and de Wet (1971). In this system, the total array of variation within maximum genetic reach is partitioned into primary, secondary and tertiary genepools. The primary genepool includes all those taxa that naturally cross with the cultivated species and includes all variations of cultivated *P. glaucum*, the wild progenitor violaceum (monodii) and the weedy form stenostachyum. The secondary genepool (SGP) includes all those species that can be crossed with the crop species but one has to overcome barriers such as poor chromosome pairing. Napier grass, *Pennisetum purpureum* Schum., is a member of SGP. *P. Schweinfurthii*, which has *n*=7 chromosomes, may also belong to SGP as it was possible to cross it with pearl millet. The tertiary genepool (TGP) includes all those species that can be crossed with pearl millet but the hybrids are lethal, completely sterile, or anomalous. Hanna (1987) grouped all species of Pennisetum other than *P. purpureum* into TGP.

2.2.2 Origin

Vavilov (1949/1950) in his classic work on 'origin of crops' suggested the Ethiopian centre of domestication for pearl millet. However, later Ethiopia is considered as the product of post-domestication introduction. Pearl millet was considered as one of the

several Western African crops domesticated by the Mande people near the head waters of the river Niger between 5000 and 4000 BC (Murdock, 1959; Baker, 1962). The greatest morphological diversity occurs today in Western Africa, south of Saharan desert and north of the forest zone (Murty *et al*., 1967; Clement, 1985; Anand Kumar and Appa Rao, 1987). Taking these facts into consideration, Harlan (1971) and Harlan *et al*. (1975) suggested a diffuse belt stretching from western Sudan to Senegal as the centre of origin. Pearl millet originated in Western Africa some 4000 years ago, then reached Eastern Africa, and from there spread to Southern Africa and India some 2000 years ago. India is considered the secondary centre of diversity.

Based on seed shape, cultivated pearl millet has been classified into four basic races (*typhoides*, *nigritarum*, *globosum* and *leonis*) (Brunken, 1977), although intermediates between any two of these basic types also exist. The race typhoides is the most variable among the four races and is also most widely distributed. It occurs from Senegal to Ethiopia, from northern to southern Africa. It is the only basic race found outside Africa, and the predominant race grown in India (Appa Rao, Mengesha *et al*., 1986d; Appa Rao, Mengesha, Sibale *et al*., 1986; Appa Rao *et al*., 1987a) and Southern Africa (Appa Rao, Mazhani *et al*., 1986; Appa Rao, Mengesha, Sibale *et al*., 1986). The race nigritarum is found from western Sudan to northern Nigeria. Race globosum is the most common race in the central Nigeria, Niger, Ghana, Togo and Benin (Bono, 1973). The race leonis is indigenous to Sierra Leone. The greatly elongated characteristic of the grain may be an adaptation to the relatively high rainfall regions of Sierra Leone.

2.3 Genetic Resources

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) has assembled 21191 germplasm accessions of cultivated pearl millet and its wild species from 49 countries, of which more than one-third is from India. Apart from this ICRISAT has assembled 671 accessions of 23 different species of Pennisetum. A collection of over 2700 accessions, representing cultivated, weedy and wild relatives is maintained by the Services Scientifiques Centraux of ORSTOM at Bondy, France. The Institute Senegalaise de Recherches Agricoles (ISRA) at Bambey, Senegal, has over 2400 accessions. Besides, 500 accessions are conserved in Canada, 32 in Italy, 291 in Malawi, 36 in Pakistan, 32 in Tunisia and 24 in Zambia (Acheampong *et al*., 1984; Mengesha *et al*., 1989). The SADC Plant Genetic Resources Centre (SPGRC) near Lusaka, Zambia, began conserving germplasm from SADC countries.

Pearl millet being an allogamous crop, the recessive alleles are maintained in population in heterozygous condition and exposed on inbreeding. During the course of germplasm evaluation, a number of traits were identified. They include two new dwarfing genes (Appa Rao, Mengesha *et al*., 1986b), three glossy genes (Appa Rao *et al*., 1987b), two mid-ribless genes (Appa Rao *et al*., 1988a) in which there was a reduction of vascular bundles, eight early-maturing syocks (Appa Rao *et al*., 1988b), sweet stalk sources with high sugar content (Appa Rao *et al*., 1982) and chlorophyll-deficient mutants (Appa Rao *et al*., 1984). Germplasm is also a good source of genes for fertility restoration and sterility maintenance (Appa Rao, Mengesha *et al*., 1986c). The brown midrib pearl millet genetic stock was found to be associated with high digestibility (Gupta *et al*., 1983).

Genus *Pennisetum* is polybasic with x=5, 7, 8 and 9. In the x=5 type, $2n$=10 was observed in *P. ramosum* only. In the x=7 type, $2n$=14 was observed in *P. glaucum*, *P. violaceum*, *P. mollissimum*, and *P. schweinfurthii* while $4x$=28 was observed in *P. purpureum*. In the x=8 type, $2x$=16, and $4x$=32 were observed in *P. mezianum*. In the x=9 type, $2x$=18 and $3x$=27 were observed in *P. hohenackeri* and $3x$=27 in *P. setaceum*. Tetraploid number $4x$=36 was observed in *P. mecrorum*, *P. divisum*, *P. cenchroides*, *P. clandestinum*, *P. pedicellatum* and *P. orientate*, while $5x$=*45* was observed in *P. villosum*. The species *P. squamulatum* and *P. polystachyon* showed $6x$=54 chromosomes, while the highest chromosome number (68) was observed in the species *P. macrostachyum* only. The species *P. schweinfurthii* is valued for its large grains and waxy coating, *P. purpureum* for forage and *P. clandestinum* as pasture, *P. setaceum* and *P. villosum* as ornamentals, and *P. hohenackeri* for thatching and rope making (ICRISAT, 1989).

2.3.1 Genetic Diversity

The first attempt to analyse genetic diversity in pearl millet was by Murty *et al.* (1967) and Upadhyay and Murty (1970) using the Rockefeller Foundation collection assembled at New Delhi, India. They found that major variability occurs in Africa and that accessions from India showed low but distinct diversity. Variation pattern seems to be associated with agro-climatic conditions where early-maturing forms were found in low rainfall areas, especially in the fringes of deserts. Genetic diversity was observed for seed characters, physical and structural characteristics (McDonough and Rooney, 1987), for protein content and quality (Godawat and Kaul, 1981), drought resistance (Blum and Sullivan, 1986), disease resistance (Deshmukh *et al*., 1978; Basavaraju *et al*., 1981; Thakur *et al*., 1988; Thakur *et al*., 1992; Singh *et al*., 1993), insect resistance (Merkle *et al*., 1983), enzymes (Subba Rao *et al*., 1988; Lagudah and Hanna, 1990; Tostain, 1992), mitochondrial DNA (Chowdhury and Smith, 1988) and nucleotide polymorphism (Gaut and Clegg, 1993).

Assessment of diversity in 21594 pearl millet accessions from 50 countries for 23 morphoagronomic traits revealed large variability for days to flowering (33–159 days), plant height (30–490 cm), tillers/plant (1–35), panicle length (5–135 cm), and 1000-seed weight (1.5–21.3 g). The phenotypic diversity index ranged from 0.427 (tiller number) to 0.772 (endosperm structure) with a mean of 0.528 (Upadhyaya *et al*., 2007). About 335 accessions of *Pennisetum glaucum* subsp. *monodii* originating from 13 countries were evaluated and assessed for diversity and geographical gaps. A wide variation was observed in the collection for total tillers per plant (16–609), productive tillers per plant (12–368), leaf length (21.3–58.8 cm) and leaf width (8.1–33.1 mm), indicating high fodder-yield potential of the collection (Upadhyaya *et al*., 2014).

2.3.2 Germplasm Utilisation

Selection by plant breeders within pearl millet landraces, which have far greater intrapopulation variability, has produced improved OPVs, but these have had limited gains in productivity. These improved landraces have been used by more traditional farmers.

Pearl millet germplasm has been widely used in developing composites, which include a wide range of germplasm and improved breeding lines, mostly from Western and Southern Africa (Rai and Anand Kumar, 1994). Pearl millet composites were primarily intended for breeding OPVs. Most programmes dedicated to breeding hybrid parents

have used pedigree breeding. This approach continues to be successful, although the genetic base of hybrids and hybrid parents has narrowed considerably, and broadening the genetic base of elite hybrid parents by expanded use of new germplasm is essential for long-term progress in hybrid development.

Iniadi germplasm from the Togo–Ghana–Burkina Faso–Benin region of Western Africa is being most extensively used in pearl millet breeding programmes worldwide (Andrews and Anand Kumar, 1996). Typical characteristics of this germplasm are large-sized grain (15–18 g per 1000) of globular shape and dark grey colour with bright outer exposed surface, starchy endosperm, compact and conical panicles, relatively less photoperiod-sensitive, earliness (70–85 days to mature), rapid grain-filling (23–25 days relative to 25–32 days for others), good downy mildew-resistance, and good combining ability for grain yield. A majority of hybrids in India include some degree of *Iniadi* germplasm in their parental lines, and almost all the hybrids under advanced testing in the United States include a great deal of it. This germplasm is being increasingly introgressed which may result in disrupting heterotic patterns, if any, in improved breeding materials and, hence, reduces the probability of producing high-yielding hybrids in the future.

Photoperiod-sensitive germplasm accessions have been little used in breeding programmes outside their area of adaptation. This is because (i) the trait needs have been largely met from within the vast less-sensitive group, of which only a small fraction has been used so far, and (ii) the high attrition rate in segregating generations derived from sensitive×insensitive crosses has led to few successful outcomes. Some of the promising germplasm lines for various traits are given in Table 2.1.

Table 2.1 Promising pearl millet accessions for agronomic and economically important traits.

Character	Germplasm accession	References
Vigour (score)	IP 1024, IP 3467, IP 3986, IP 4021, IP 13523	Khairwal *et al*., 2007
Days to 50% flowering (earliness)	OPY 197, IP 4006, IP 550, IP 3549, IP 4066, IP 9496 and IP 9426	Khairwal *et al*., 2007: Manga, 2015
Days to maturity	OPY 197, IP 3549, SNV 26	Khairwal *et al*., 2007
Plant height (cm) (Tall)	IP 1497, IP 947, IP 3541, IP 3749, IP 3616, IP 19190, IP 19405, IP 13150 and IP 5452	Khairwal *et al*., 2007; Manga, 2015
Productive tillers per plant	RMFB-35, RMFB-34, IP 13645, IP 15273 and IP 17493	Khairwal *et al*., 2007; Manga, 2015
Total tillers per plant	IP 6148 and IP 15257	Manga, 2015
Nodes per plant		
Sheath length (cm)	Dhodsar (Sunda Ram), Jhakrana, Sulkania and SR 54	Manga, 2015
Blade length (cm)	Dhodsar (Sunda Ram), Jhakrana, Sulkania and SR 54	Manga, 2015
Panicle length (cm)	IP 1763, IP 1745, IP 5447, IP 10273, IP 12848, IP 10456	Khairwal *et al*., 2007; Manga, 2015
Panicle thickness (mm)	NSS 7776, NSS 7799, IP 4394, IP 7042, IP 7935, IP 5396, IP 18797,IP 15917	Khairwal *et al*., 2007; Manga, 2015
Panicle density (score)	IP 14100,IP 8350, IP 14160	Manga, 2015

Character	Germplasm accession	References
1000-grain weight (g)	IP 399, IP 11893, IP 19160, IP 10705 and IP 14160	Khairwal *et al*., 2007; Manga, 2015
Grain yield per plant (g)	IP 128, IP 3416, IP 33, NSS 7911, IC-296718 HMS 1B	Khairwal *et al*., 2007
Grain yield potential (score)	IP 17350, IP 3150, IP 17945, IP 7095	Manga, 2015
Green fodder yield per plant (g)	IP 3416, IP 17880, IP 104, IP 15304, IP 3616, IP 6125, IP 13885 and IP 6146, IP 6897	Khairwal *et al*., 2007; Manga, 2015
Overall plant aspect (score)	IP 16131, IP 22281, IP 15817, IP 17945, IP 7095	Khairwal *et al*., 2007
Heat tolerance	IP 19799, IP 19877, IP 19743	Yadav *et al*., 2012

The utilisation of wild germplasm has received the least attention. However, a modest attempt at Tifton, Georgia to use wild pearl millet germplasm has produced interesting results, as revealed in the utilisation of rust and leaf spot resistance and cytoplasmic male sterility from *P. glaucum* ssp. *monodii* accessions, greater stalk strength and male fertility restorer genes from *P. purpureum* and apomictic genes from *P. squamulatum* (Hanna, 1992). It has been shown that wild sorghum germplasm can contribute useful variability to highly adapted grain hybrid parents and that introgression through populations is a more effective way of moving this variability than through elite inbred lines (Bramel-Cox and Cox, 1989; Menkir *et al*., 1994).

2.4 Genetics of Important Traits

2.4.1 Quantitative Traits

Pearl millet is an out-breeding crop and is endowed with enormous variability for agronomically important traits in populations adapted to diverse agro-ecological conditions. The assessment of genetic variability is done in terms of variance, genotypic coefficient of variation (GCV) and heritability. Virk (1988) found that the GCV along the African populations was high for grain and green fodder yield, days to flower, leaf number and stem thickness. Similarly, the GCV among Indian varieties was also high for days to flower, panicle length and weight and grain size.

Of several methods used to assess genetic diversity, D^2 analysis among the multivariate procedures has been extensively used in pearl millet (Upadhyay and Murty, 1971; Shukla and Dua, 1983; Andre Savery and Prasad, 1995; Suthamathi and Stephen Dorairaj, 1995b). Most of these studies indicated no correspondence between geographical diversity and genetic diversity. The genetic stocks from Africa and America were closer compared to Asia and Australia. Ouendeba *et al*. (1992) applied Ward's cluster and principal component analysis to pearl millet populations grown in several African countries. The results indicated similarities between landrace populations from Niger and Senegal, and between those from Niger and Nigeria. Days to flower, plant height, stem diameter, primary panicle length and grain yield were the major traits contributing to diversity. Heritability (h^2) and genetic advance (GA) are of interest

to a plant breeder. By and large, h^2 estimates for component traits of grain yield were higher than yield itself. However, h^2 estimates for a given trait also varied depending on the genetic materials and mating designs used (Virk, 1988). Suthamathi and Stephen Dorairaj (1995a) observed high h^2 coupled with high GA for plant height, stem weight, green fodder yield, leaf weight and leaf/stem ratio. Among the grain yield related traits, maximum GA was observed for productive tillers. GA for grain yield was also high (>58%) and GA for days to flower, plant height, panicle length, panicle width and grain weight varied between 16 and 24%. This low GA for grain yield may be due to low genetic variability in the material studied.

In trait association studies in pearl millet, several yield components such as number of effective tillers, panicle length, grain weight, grains per unit area and panicle weight are positively correlated with grain yield. In a number of studies, the values of genotypic correlations were higher than those of phenotypic correlations. Panicle weight had the highest positive correlation with grain yield. Tiller number, harvest index, yield of primary panicle and flag leaf area were next in order. Days to flower and days to maturity were negatively correlated with grain yield, which could be due to poor adaptation of late maturing materials (Khairwal and Singh, 1999). Virk (1988) summarised correlation studies for four groups of materials: Indian varieties, Indian inbreds, African varieties and American inbreds and found that phenotypic correlation between plant height and grain yield was low in Indian varieties but high in Indian inbreds and still higher in African varieties and American inbreds. The number of days to flower was negatively correlated with grain yield in African varieties and American inbreds, but there is a weak or no correlation between these two traits in Indian varieties and Indian inbreds. Gupta *et al*. (1976) found that tiller number was the most important yield component as it had the highest positive direct effect on grain yield in two seasons while grain size had the highest positive direct effect in one season only. On the contrary, days to flower had a negative direct effect in both the seasons. However, Dhillon *et al*. (1977) found that grain yield had highest correlation with grain size followed by tiller number and plant height. Virk (1988) found that panicle weight, productive tiller number, flag leaf area, harvest index and grain weight had high direct positive effects. Patil and Jadhav (1992) observed consistent direct positive effects of plant height, tiller number and seedling emergence rate on green fodder yield in saline soil.

In order to combine several desirable traits into a single genotype, it is desirable to use selection index proposed by Smith (1936). The selection index studies in pearl millet (Shankar *et al*., 1963; Gupta and Athwal, 1966) showed that the index value changed according to the genetic and geographic diversity of the material. Virk (1988) found that grain size, tiller number and plant height were the important traits for selection for grain yield while the leaf number was the important trait for green fodder yield, next in order being leaf size, tiller number, days to flower and plant height.

2.4.1.1 Gene Effects

The efficiency of selection in a breeding programme depends on the type of gene effects for the trait under consideration. In a highly cross-pollinated crop such as pearl millet, where development of hybrids has become commercially viable, the emphasis is on capitalising three types (additive, dominance, epistasis) of gene effects. In pearl millet, several biometrical methods (generation mean analysis, line×tester, diallel, triple test cross, etc.) have been used to determine the genetic architecture of populations for a large number of quantitative traits including grain and fodder yield. Several studies

revealed that grain yield is mainly governed by non-additive or by both additive and non-additive gene effects. Hence it is imperative to increase additive genetic variation in pearl millet populations by using some appropriate mating design such as biparental matings for rapid improvement of the crop.

2.4.2 Qualitative Traits

Information on gene symbols and genetic control of morphological mutant phenotypes has been excellently summarised by Anand Kumar and Andrews (1993). Early flowering in pearl millet is controlled by two genes e_1 and e_2. Plants having e_1e_1 flowered in 49 days and plants having e_2e_2 flowered in 38 days, as against Tift 23, which flowered in 76 days, and it did not have either of these genes (Hanna and Burton, 1984). IP 4021 (Bhilodi) from Gujarat, India, is an excellent source for early flowering (33 days). Dwarfing genes in pearl millet provide lodging resistance, and increase response to fertiliser application. Burton and Fortson (1966) identified two stocks in which dwarfing was conditioned by one or more recessive genes, designated as d_1 and d_2. Appa Rao, Mengesha *et al.* (1986a) reported d_3 dwarf (IP 10401 with poor spike exertion) and d_4 dwarf (IP 10402 with tilted growth habit and good spike exertion). Of these dwarf sources, d2 dwarfing gene has been exploited in the development of different male-sterile lines (Rai, 1990). Brachytic dwarf type was reported by Gupta *et al.* (1985) and designated with a different gene symbol (d_b). For seed colour, yellow and pearly amber are dominant over slate (bluish green) and are controlled by a single dominant gene. Inheritance of other colours was reported by Al-Fakhry *et al.* (1965), Phul *et al.* (1969) and Krishnaswamy (1962). Light pigmented pearl millet grains which vary from white to yellow were identified by Appa Rao *et al.* (1985). These are sweeter and contain more protein (>15%) and have good scope in improving appearance and nutritional quality of bakery products. Cytoplasmic nuclear male-sterility system had made hybrid development commercially viable in pearl millet. Burton and Athwal (1967) classified sterile cytoplasms into A1, A2 and A3, corresponding to the recessive genes ms1ms1, ms2ms2 and ms3ms3. Other sources of sterile cytoplasms, A4 (Hanna, 1989) and A5 (Rai, 1995) have been identified. Among the important diseases of pearl millet, resistance to downy mildew is governed by one or two dominant genes (Appadurai *et al.*, 1975; Gill *et al.*, 1978; Mehta and Dang, 1987). Resistance to smut ranged from monogenic incomplete dominance to monogenic complete dominance and duplicate action of two genes (Yadav, 1974). Single dominant genes for rust resistance have been identified by Andrews *et al.* (1985), Hanna *et al.* (1985) and Sokhi *et al.* (1987).

Among the other useful traits, chlorophyll-deficient mutants exist in pearl millet and they can be maintained in homozygous state (Krishnaswamy, 1962; Burton and Powell, 1968). In most cases, mutant condition is governed by a single recessive gene while Kadam *et al.* (1940) reported both mono- and di-genic ratios for yellow, virescent yellow, golden yellow and zebra characters. In pearl millet, lines with golden, green, red and purple pigmentation on most plants are available (Burton and Powell, 1968). Green pigmentation is dominant over golden and recessive to red and purple. Purple node (pn1pn2) and purple auricle (par1par2) are governed by a pair of complementary genes. Purple midrib, leaf margin and leaf sheath are inherited together and are under the control of a single dominant gene. Koduru and Krishna Rao (1979) reported two dominant complementary genes responsible for purple-stem trait as has been reported by Athwal and Gill (1966) and Gill and Athwal (1970) for purple foliage. Glabrous leaf is

dominant over hairy leaf and is controlled by a single gene (Singh *et al*., 1967; Khan and Bakshi, 1976). Hairy node is dominant over non-hairy node and controlled by a single gene. Hairy ligules are controlled by two dominant genes (Al-Fakhry *et al*., 1965) and hairless sheath dominant over hairy sheath (Krishna Rao and Koduru, 1979). Bristling (Br) in panicles is governed by a single dominant gene (Ahluwalia and Shanker, 1964). Glossiness in leaves is controlled by a single recessive gene and three different non-allelic genes govern this trait (Appa Rao *et al*., 1987a).

2.5 Morphology and Reproductive Biology

Pearl millet seeds germinate in 3–5 days when sown at a depth of 3–5 cm in the soil with sufficient moisture and at optimum temperature. The rate of germination and emergence, seedling survival, leaf-area expansion, and dry-matter accumulation were highest at 33/28°C. The root system of pearl millet consists of primary, secondary and brace roots. The radicle roots *or* seminal roots after germination develop into the primary roots. Secondary roots develop from the nodes of the primary roots. Crown or brace roots develop from the lower nodes of the stem at or above the ground level and provide anchorage to the plant. The maximum root spread in pearl millet is confined to 25–30 cm of the soil area around the plant. The pearl millet shoot consists of stem, tillers and leaves during the vegetative stage. The development of tillers starts from the lower nodes of the stem 3–5 weeks after emergence. These are called primary tillers. The secondary (axillary) tillers develop from the axillary buds at the upper nodes, usually after completion of flowering on the main stem. The leaves are arranged alternately in two vertical rows on the culm. They are linear in shape comprising of a leaf sheath and a blade. The leaf blade is lanceolate, 90–100 cm long and 5–8 cm wide, with a pointed tip. The midrib is dull green. Auricles are present at the base of the leaf blade. The upper leaf surface is scarbid and hairy, while the lower one is smooth and glabrous. The leaf area of pearl millet is calculated by measuring the length and the width (at the broadest point) as suggested by Singh *et al*. (1970).

$$\text{Leaf area} = \text{leaf length}\,(\text{cm}) \times \text{leaf width}\,(\text{cm}) \times 0.7236$$

The pearl millet inflorescence is a false spike, ranging from 5 to 150 cm in length and 1–5 cm in diameter. The panicle is terminal varying in shape from cylindrical to candle-shaped. The spike consists of a central rachis which is closely packed with fascicles. Each fascicle consists of one or more spikelets and a whorl of 70–80 bristles. The tip of the spike has only a single spikelet. The bristles may be free or united to form an involucre. An inflorescence may contain 870–3000 spikelets with an average of 1600 (Khairwal *et al*., 1990). The spikelets are small, lanceolate and acute. Each spikelet consists of two glumes, one outer and one inner. The outer glume is broad, short, membranous and truncate. The inner glume is broad and half the size of the spikelet. Between the two glumes, there are (two) florets. The lower floret is staminate and the upper floret is hermaphrodite. Spikelets are generally bifloret but can sometimes be trifloret or tetrafloret; in rare instances, more than four florets are present (Maiti and Bisen, 1979). The pearl millet androecium consists of three anthers, each attached to a long filament. There is a two-layered epidermis, a tapetum and pollen grains. The anthers are yellow or purple with a tuft of fine hairs at the apex. The gynoecium consists of a

monocarpellary and superior ovary with two styles and a feathery stigma. The mature ovary has an anatropous ovule. The embryo has a scutellum, plumule, coleoptile, primary axis, coleorhiza and radical (Rachie and Majumdar, 1980).

The emergence of the panicle from the sheath takes about 4–6 days (Bhatnagar and Kumar, 1960). Flowering starts after the emergence of the panicle out of the boot, but in some genotypes style exertion commences before completion of panicle emergence. Stylar exertion begins first in the florets in the central upper portion of the panicle and then progresses upward as well as downward. The maximum exertion of styles is on the third day of flowering. The flowering of pearl millet is protogynous, that is, the stigma emerges earlier than the anthers. The stigma remains receptive for 12–16 h. Protogyny is expressed in varying degrees in pearl millet, depending on the genotype and the environment (Rachie and Majumdar, 1980).

Anther emergence begins one day after the emergence of the stigmas is completed on the panicle. It first starts in the hermaphrodite florets followed by the staminate florets. Anther emergence is facilitated by the protogynous styles and the tufts of hair on the tips of the anthers. Anthesis continues throughout the day. The maximum anthesis is between 2000 and 0200 hours (Sundararaj and Thulasidas, 1980). Exertion and emergence of anthers takes about 60 min if it happens during the day; during the night it may take twice as much time or more. Anther emergence starts in the upper portion (at about the two-thirds point) of the panicle and proceeds in both direct ions. The first flush of anthesis is completed in a week's time under irrigated conditions. Panicles emerging from the tillers start flowering later and the process may continue up to three weeks. In rainfed conditions, first-flush anthesis of a plant may take place over 12 days, and it may continue on the tillers till seed formation (Chalam and Venkateswarlu, 1965). After pollination, the stigmas dry up in 24 h. Seed-set can be seen in the panicle about a week after fertilisation (Burton and Powell, 1968) There is a gradual increase in the dry mass of grains from the milk to dough stage, reaching maximum at maturity. Physiological maturity of the grain is indicated by the appearance of a black layer just above the hylar region on the abgerminal side of the grain opposite the embryo (Fussel and Pearson, 1978).

2.6 Selfing and Crossing

The protogynous flowering behaviour of pearl millet makes it a highly cross-pollinated crop. Emergence of stigmas about 2–3 days before anther emergence makes crossing possible without having to resort to emasculation. At the same time, the presence of hermaphrodite flowers and stigma receptivity lasting 3–4 days make selfing also easy. However, if a pearl millet panicle is not protected from outside pollen, more than 90% of its seed are likely to be the products of cross-pollination. Selfing is done for producing the seed of F_2 populations, S_1/S_2 progenies and inbred lines. Crossing is done for producing the seed of F_1 hybrids, full-sib/half-sib progenies and open-pollinated varieties in a breeding nursery. Although both selfing and crossing in pearl millet require ordinary skills, careful planning is essential to ensure that the intended quantity of seed is produced and quality is maintained.

The best plant stage for selfing (bagging) is before stigma emergence. This is generally when about one-third of the panicle has emerged out of the boot. In some genotypes, by this stage of panicle emergence, stigma emergence can already have occurred. Care

should be taken to bag such genotypes as soon as the tip of the panicle is visible out of the boot. The bagged panicles are stapled or clipped in the peduncle region. Selection for good selfed seed-set is one of the selection criteria in the inbred line development of pearl millet. Thus, considering that the selfed seed-set is good, selfing of one panicle per plant will usually provide enough seed for use in pedigree breeding, provided that the panicle is >10 cm long. Selfing of 6–8 panicles of an F1 hybrid can be expected to provide enough seed to grow an F2 population of 1000–2000 plants and still leave enough seed for replanting, if required.

For crossing purposes, white parchment paper bags are most convenient. These bags allow easy detection of panicles that are ready to be used as males and females without having to remove the bags. The bagging procedure is the same as in selfing, except that the bags should be clipped, not stapled. It is essential to choose the full-stigma-emergence stage of a bagged panicle to be used as a female. This ensures that once such panicles are crossed, no new stigmas will emerge later that may get self-pollinated. Forenoon is the best time for crossing, for two reasons: (i) the dew-soaked bags become more transparent and hence allow easy detect ion of the right panicle stage for use as females (whitish stigmas) and males (yellowish pollen accumulated at the base of the panicles) and (ii) the pollen viability is high at this time of the day, especially before 1100 hours. However, experience shows that if the maximum day temperature does not exceed 38°C, crossing can be done in the afternoon as well, although it results in a small reduction in seed-set. First, the bag is held tightly above the point of pollen accumulation, and the clip is removed to release the accumulated pollen at the base. Then, by still holding the bag tightly, the panicle is tapped with the other hand, causing the shedding and accumulation of fresh pollen at the base. This pollen is made to slip towards the glued end of the bag by bending the panicle and peduncle downwards. Thereafter, the panicle is rebagged with the same or another selfing bag if more pollen needs to be collected from it on the following day or if the selfed seed needs to be harvested from it to maintain the line. Where selfed seed is not required from the bagged panicles, these can be bagged at the beginning of anthesis, a day prior to pollen collection. These bags should not be clipped, to distinguish them from those that have been clipped for product ion of selfed seed. Pollen from several bagged panicles of an entry may be collected in one bag, which shall bear the plot or entry number. The pollen collected is dusted onto the female panicles after quickly removing the selfing bags from the latter. Once crossing is completed, the bags are marked with (x) plot or entry number of the pollen parent (Table 2.1), and placed back over the crossed panicle and stapled. This completes the crossing procedure.

2.7 Breeding Methods

Pearl millet is a highly cross-pollinated crop. The hermaphrodite flowers are protogynous with the stigmas remaining receptive for 3–4 days. This facilitates both selfing as well as crossing easily. The other characteristics include tillering response to spacing and input management, high seed number (2000) per panicle, low seed rate (3–4 kg ha^{-1}), short life cycle (75–85 days) and excellent regenerating ability.

Pearl millet breeding involves recurrent selection (within populations formed with incorporation of various desirable characters) and pedigree selection aimed at developing fixed lines. Combinations of fixed lines can be used to form synthetic varieties and

composite varieties can be developed by maintaining mixture of genotypes in bulk. This has influenced the extent of germplasm utilisation, the breeding methods used, prioritisation of target traits and a consideration of alternative cultivar options. Recurrent selection and pedigree breeding are the two most common methods used in the genetic improvement of pearl millet. The basic requirement of random mating for the application of recurrent selection in pearl millet is met through its natural out-breeding behaviour, which is caused by protogynous flowering. Pearl millet is amenable to all forms of recurrent-selection schemes. The wide range of population improvement methods applicable to pearl millet include those based on the phenotype of individual plants (mass selection and phenotypic recurrent selection), on the genotypic worth as reflected in the performance of their progenies (genotypic recurrent selection), improvement of an individual population (intra-population improvement), pair of populations for the improvement of population cross performance (inter-population improvement) or for improving general combining ability or specific combining ability (Allard, 1960). However, a comparative study in pearl millet found no significant difference among various recurrent selection procedures and concluded that the choice of a recurrent-selection scheme should be determined largely by the objective of the programme and the availability of resources (Singh *et al*., 1988).

Pedigree breeding from populations that have mostly been derived from single crosses is the most common method in breeding hybrid parents (Andrews *et al*., 1997). This approach continues to be quite successful, although it has obvious effects in that it narrows the genetic base of hybrid cultivars. Pedigree breeding using composites as base populations has the potential to (i) accelerate the genetic gains for yield in hybrids and (ii) broaden the genetic base of hybrid cultivars that would contribute to yield stability. However, composites will be used for pedigree breeding of hybrid parents only when they fulfil the basic traits required of hybrid parents. The development of composites specifically targeted for breeding hybrid parents is a relatively recent development in pearl millet. However, a diverse range of existing composites, developed primarily for breeding OPVs, can serve as base material for deriving partial inbreds, some of which can be used directly as hybrid parents, but most of which will find use in crosses to further diversify hybrid-parent breeding programmes. In pedigree-breeding method, selection is exercised both among the progenies and among plants within the progenies. Since selection among the progenies is based on the plot performance, progeny selection is more effective than individual plant selection within the progenies. Generally, six to eight selected plants are selfed in the early generation progenies (F3–F4 in variety cross-populations and S1–S2 in composites) to permit final selection of two to three plants at harvest for head to row sowing in the subsequent generation. In later generations (F5/S3 and onwards) when progenies become more uniform, selfing two to four selected plants in each progeny and finally selecting one to two at harvest will be appropriate. Increase in number of plants within progenies would call for higher selection intensity between progenies.

Pedigree bulk method is followed for breeding maintainer lines at ICRISAT. The F3 progenies are bulk advanced to F4 progeny rows and onwards with mild selection within progenies for uniformity of heritable traits. From F3 generation onwards, 8–10 selected plants are selfed in each progeny and 5–6 superior plants are harvested at maturity. Seeds of these plants are bulked to sow each selected progeny the following generation. Only a highly variable F3 or F4 progeny is sown head to row and advanced following standard pedigree procedure. This method helps to conserve the genetic

potential by minimising genetic drift and maintains cryptic variation. The bulk pedigree selected F5 and F6 progenies from elite×elite crosses become reasonably uniform for all the practical purposes and yet retain sufficient cryptic variability for their further fine tuning as parents of hybrids.

Studies in pearl millet indicate that biparental matings in F_2 populations also lead to increased genetic variation (Singh, 1974). Partial inbreds derived from biparental matings in F_2 populations were superior in grain yield and desirable traits than those derived from selfing of individual F_2 plants. To deal with such crosses, a large F_2 population in the range of 5000–10000 plants should be raised. Also, progeny selection in F_3 and F_4 generations may be more effective than single plant selection in the F_2 generation for low heritability traits such as grain yield. Thus, selected F_3 or F_4 progenies from a given population or from a group of populations can be intercrossed to provide further opportunities for the sub-optimal genetic combinations to come together for recombination and develop into optimal genetic combinations. In the maintainer (B)×restorer (R) crosses, simultaneous to evaluation of F_4 progenies for yield and adaptation, their evaluation for sterility maintenance (in hybrids developed by crossing their corresponding F_3 progenies on a male-sterile line) should be done simultaneously. Where off-season facilities exist, evaluation of sterility reaction in hybrids should precede the replicated multi-locational evaluation of F_4 progenies. Those F_4 progenies whose corresponding hybrids are uniformly sterile can be further advanced by either pedigree or pedigree bulk methods. If progenies are derived from B×B crosses or from composites having a high frequency of maintainers (>0.8), then evaluation for sterility maintenance ability may be delayed until the F_5 or F_6 generation. While breeding restorer lines, those producing average pollen shed are also selected whereas in breeding the maintainer lines, only those producing completely sterile hybrids are of value. Studies in pearl millet indicate lack of correlation between grain yields of lines per se and their general combining ability while few studies show significant positive relationship. Hence, it would be appropriate to select for performance per se and then later impose additional for combining ability.

Back-cross breeding is an effective tool for improving hybrid parents and OPVs that excel in a large number of characters but are deficient in a few others (Allard, 1960). When homozygous parental lines of hybrid are used as recurrent parents in a backcross breeding programme, the procedure is the same as that used in self-pollinated crops. However, when an open-pollinated variety or a composite is used as a recurrent parent, pollen from nearly 100 random plants has been used at each backcross stage (Rai, 1990). By the sixth backcross, more than 99% of the genes from the recurrent parent are expected to be recovered.

2.8 Cultivar Development

Both OPVs and hybrids are commercially grown in pearl millet. The highest-yielding hybrids have about 15–30% grain-yield advantage over the best varieties of comparable maturity.

2.8.1 Open Pollinated Varieties

An OPV in pearl millet is a highly heterozygous and heterogeneous population, open to significant genetic changes. Pearl millet OPVs, bred from single progenies (full-sib or

S1–S2), do not perform well and, hence, are not under cultivation. Wider genetic variability is needed to maintain vigour over generations. Thus, pearl millet varieties are often developed by balanced random mating of 5–10 full-sib or S1–S2 progenies. Several OPVs developed on the basis of this procedure have been released (e.g. WC-C75, ICTP 8203 and Raj 171) and are widely grown. Provided that some characters of greatest visual appeal, such as flowering, plant height, panicle size and shape, and grain size, shape and colour, can be kept sufficiently uniform for varietal identification purposes, even larger number of progenies (>50) can be used in breeding productive OPVs of pearl millet (e.g. ICMV 155, ICMV 221, and ICMV 88908 (= Okashana 1). Within a pearl millet variety there is continual reorganisation of variability generating a narrow range of phenotypes within a recognisable norm. Mild mass selection during the seed increase of a variety is a useful exercise to maintain this norm. Genetic shift is likely to occur when a pearl millet variety is grown in a different environment. A corollary of this is that a pearl millet variety can be fine-tuned for its adaptation and productivity to a range of related environments, but seed stocks for each of these environments would then have to be maintained separately. Pearl millet varieties have seed yields two–three times higher than the inbred seed parents. Intra-population variability in pearl millet helps in the genetic management of several diseases. For instance, genetic heterogeneity confers durable resistance to downy mildew, and a variation in flowering confers pollen-based escape from ergot and smut infection; this contrasts well with frequent downy mildew epidemics on single-cross hybrids of pearl millet and their greater vulnerability to ergot and smut. In consequence, improved pearl millet OPVs are readily acceptable to farmers and are easier to multiply and, hence, have carved a niche for themselves even in India, where hybrids are the preferred cultivars. In part, this may have to do with the memory of downy mildew-epidemics on hybrids in India.

2.8.2 Hybrids

All the commercial grain hybrids of pearl millet are single-cross hybrids based on A_1 cytoplasmic-nuclear male sterility (CMS) system. Two other types of hybrids can also be produced. The first one is a top-cross hybrid, which is produced by crossing an OPV with an inbred-seed parent. This type of hybrid achieves a compromise between the positive attributes of both OPVs (yield stability and durable disease resistance) and single-cross hybrids (phenotypic uniformity and higher grain yield). The second type is an inter-population hybrid, also called an inter-varietal hybrid. This type of hybrid can be produced commercially by crossing an OPV with a male-sterile population. Inter-population hybrids would be phenotypically as variable as OPVs but could produce 32–45% greater yields (Ouendeba *et al*., 1993). The higher seed yields and greater durability in downy mildew-resistance of population seed parents would make them economically more attractive proposition for commercial utilisation of inter-population hybrids than inbred seed parents. One top-cross hybrid, ICMH 88088, based on a CMS inbred line is under commercial production in Maharashtra in India (Talukdar *et al*., 1996) and another one, JBH 1 (= GICH 501), has been released by the Madhya Pradesh Variety Release Committee (Hash *et al*., 1997). The protogynous flowering of pearl millet essentially makes its panicle equivalent to a male-sterile until it sheds its own pollen, by which time it would be pollinated by pollen from other plants. This trait can be effectively used to breed top-cross hybrids that might be more desirable in ergot- and smut-prone areas than top-cross hybrids developed on CMS-based inbred seed parents

(Andrews *et al*., 1993). Inter-population hybrids have not been commercialised so far, but this now appears possible, as the feasibility of breeding male-sterile populations using the A_4 CMS system has been demonstrated (Rai and Rao, 1995).

The first commercial hybrid HB-I (Tift 23A×BIL-3B) by Athwal (1965), developed at Punjab Agricultural University (PAU), Ludhiana, and released in India in 1965, had twice the yield of OPVs (Athwal, 1965). Since then, private seed companies in India emerged as the most dominant and reliable force in the commercialisation of hybrid breeding products. Hybrid programmes in India accorded highest priority to grain yield and downy mildew resistance combined with maturity duration mostly in the range of 75–85 days, as per agro-ecological requirements. Apart from the evident quality traits both in the grain (size, shape, colour) and stover (less rust, thinner stem, lodging resistance) that receive some attention, consideration of any other quality traits has been negligible.

2.9 CMS Systems in Pearl Millet

Burton (1958) first reported the CMS system in pearl millet and designated it as A_1. Different sources of MS cytoplasm such as A_2, A_3 from genetic stocks and their derivatives (Athwal, 1961; 1966), Av and A_4 CMS sources from *Pennisetum glaucum* ssp *monodii* (=*violaceum*) accessions (Marchais and Pernes, 1985; Hanna, 1989), Ghana and Botswana sources (Appa Rao *et al*., 1989), A_{egp} and A_5 CMS sources from gene pools (Sujata *et al*., 1994; Rai, 1995), Gero, Maiwa (Aken'ova, 1982) have been discovered. Based on differential male-fertility restoration patterns, it has been established that the A_1, A_2, A_3, A_v, A_4 and A_5 were distinctly different CMS systems.

Although all the commercial hybrids are based on A_1 CMS system, it has been observed that all the A-lines involved in these hybrids produce low frequency of pollen shedders. About 40 years of research with the A_2 and A_3 CMS systems, mostly at PAU, Ludhiana, failed to produce an A-line with stable male-sterility comparable to A_1-system A-lines. In the iso-nuclear background of 81, male sterility of A1 and Av had similar low frequency of pollen shedders, while A4 and A5 had no pollen shedders. These two new CMS systems also appear to have more stable male sterility than the A_1 CMS system. Also for these two CMS systems, much more of the germplasm is in the maintainer class than in the A_1 system, offers the opportunity to accelerate the diversification of the genetic base of pearl millet seed parents (Hanna, 1989; Rai and Rao, 1996; Rai *et al*., 1996). Recently Kumar and Sagar (2009) compared five systems of male sterility in pearl millet and did not find the cytoplasm to be associated with downy mildew susceptibility.

Breeding for seed yield in pearl millet parental lines, especially seed parents, is a higher priority and a greater challenge due to existence of inbreeding depression. The hybrid parents should have good fertility restoration ability of R lines, complete male-sterility maintenance ability in B lines, and acceptable levels of resistance to downy mildew. On top of the above features, there should also be adequate diversity for morpho-physiological and grain traits among the lines to satisfy the diverse needs of farmers. It is only after this has been achieved that evaluation for general combining ability starts, mostly at the F5–F6 or S4–S5 stage. Performance of lines per se and their general combining ability for seed yield in pearl millet, have been found to be either uncorrelated or positively correlated.

Selection criteria in B-lines: At maturity plants with desirable traits such as DM resistance, good tillering, dwarf to medium dwarf plant height, lodging resistance, medium to long panicles, compact panicles, having complete panicle exertion, acceptable seed size, shape and colour were selected for further pedigree breeding of B lines. The complete and stable male-sterility of a-lines, high levels of male fertility restoration of R-lines, good pollen shedding in B-lines and r-lines, flowering synchrony between A-lines and R-lines are also considered. The d_2 dwarf plant height has emerged as the most dominant plant type in seed parents breeding as it reduces danger of lodging, allows for rapid detection and rouging of pollen shedders and off types in A-lines, provides option of breeding hybrids with varying heights.

Selection criteria in R-lines: Restorers must produce profuse pollen that should remain viable at temperatures as high as 42–44°C. Also they should produce highly fertile hybrids that also reduce losses due to ergot and smut. They should be productive, 150–180 cm height but no taller than the A-line and resistant to lodging and downy mildew.

Maharashtra, with a large number of private seed companies and an aggressive State Seed Corporation, had about 18 improved pearl millet cultivars under various scales of cultivation during the mid-1990s as against the 'not more than three' during the mid-1980s. Similar changes in pearl millet cultivar diversity have occurred in Gujarat. These two leading states now have 85–90% of the pearl millet hectarage under high yielding varieties (HYV) cultivation; in Gujarat, this consists mostly of hybrids but, in Maharashtra, a substantial proportion is still an OPV (ICTP 8203). In contrast, Rajasthan, which has about 40% of the total pearl millet area in India, much of it in unfavourable (dry and low soil fertility) environments, grows HYVs on <25% of the area, because there is limited cultivar-development and seed-production efforts directed toward this area.

Development of hybrids of pearl millet in the last 40 years has led to its increased productivity and stability, largely in the regions with relatively better environments, while regions such as western Rajasthan with poor environments still suffer from low productivity of about 470 kg ha^{-1}. This is because most of the hybrids recommended for this region were developed elsewhere and lacked the desired adaptability and characteristics required for this region (Kelley *et al*., 1996).

2.10 Production Constraints

Poor productivity of unimproved cultivars is related to their low harvest index, numerous biotic and abiotic stress factors. Pearl millet is usually grown in areas receiving less than 500 mm of rainfall annually. Pearl millet is one of those cereal grasses which has strong development of underground organs and tends to have efficient adaptive mechanisms to cope with drought (Winkel and Do, 1992; Winkel *et al*., 1997). Because of its tolerance to high temperature and better ability to withstand drought and to grow even in low soil fertility conditions, pearl millet is best suited for arid and semi-arid regions of the country (Khairwal, 2007).

2.10.1 Breeding for Abiotic Stresses

2.10.1.1 Drought

Pearl millet is usually planted at the start of the rains in the arid semi-desert areas of north- east India (Rajasthan) (Bidinger *et al*., 1987a; 1987b). Because the duration of the

rains is normally shorter than the duration of the crop, the crop commonly experiences terminal drought, where by seed filling occurs is affected due to insufficient moisture in the soil. Drought is the most devastating production constraint that can occur at any crop-growth stage. The phenotyping of terminal drought tolerance uses three water regimes: full irrigation, early stress imposed by stopping irrigation at booting and late stress imposed by stopping irrigation at flowering (Serraj *et al*., 2005). Post-flowering (terminal or end of season) drought stress is of greater significance causing a reduction in grain yield by about 45–49% with large variation among the genotypes (Fussell *et al*., 1991). Even under favourable conditions, pearl millet tends to have a shorter crop cycle than other cereals because it has a 'built-in' drought-escape mechanism (early flowering) inherited from its wild progenitors, having evolved in semi-desert environments with adapted short life cycles. Therefore, pearl millet is short-cycled, has a short grain-filling period and has small seed sizes. Its growth potential is no match for other longer-duration cereals growing in favourable environments. Yet, it enjoys a high crop-growth rate that confers a fairly high growth potential under optimal conditions (Begg, 1965), relating in particular to its being a C4 plant, with a large leaf area index (LAI) due to its erect type (Craufurd and Bidinger, 1989) and high radiation-use efficiency (RUE; Squire *et al*., 1986).

The study of the influence of the drought using osmotic solutions is one of the methods in the study of resistance during the germinal phase. Several literatures have indicated the superiority of the germination capacity of pearl millet compared to that of sorghum as well as its remarkable resistance to drought (Van Den Abeele and Vandenput, 1956; Gaudy, 1957; White and Cooper, 1959; Martin and Leonard, 1967). Radhouane (2007) studied seeds of pearl millet from six provenances of Tunisia that were subjected to germination and shoot and root length traits were measured on a filter paper treated with polyethylene glycol 6000 (PEG 6000) solutions. Early and rapid elongation of roots is an important indication of drought resistance. Ability of continued elongation of root under situation of water stress was a remarkable character of most crop species and root length is more affected by drought condition than shoot length (Kulkarni and Deshpande, 2007).

Several physiological parameters such as dehydration tolerance, dehydration avoidance, growth maintenance through stability of cellular membrane, osmotic adjustment, desiccation and heat tolerance, leaf gas exchange rate and radiation reflectance have been identified for screening for drought tolerance though most of these have not found any application in breeding programmes (Yadav and Rai, 2013). The early vigour of the crop as measured by time taken for wilting initiation and permanent wilting is one of the selection criteria followed by breeders (Manga and Yadav, 1995). Early flowering is an important factor determining yield under terminal moisture stress (Fussell *et al*., 1991). Large variability exists for this trait and simple selection has been successful. The most widely used sources are the Iniadi-type landraces from Western Africa (Andrews and Anand Kumar, 1996). Panicle threshing percentage under stress conditions is a good indicator of terminal drought tolerance in pearl millet. In conjunction with grain-yield potential and earliness, it accounts for >80% of the genotypic variation in grain yield under terminal drought stress (Bidinger and Mahalakshmi, 1993).

However, published information confirming the existence of adequate variability for drought-tolerance parameters and adequate repeatable heritability of the trait(s) associated with drought resistance is still lacking. Also, the effectiveness of the screening

techniques available for selecting for drought tolerance has not been demonstrated convincingly in terms of how material selected for superior performance in a drought nursery at one location will perform under drought stress at another location.

2.10.1.1.1 Breeding Strategies for Drought Tolerance

The overall goal of a breeding programme for drought stress is, ultimately, an improved genetic yield, or a more stable yield, under drought conditions. These two objectives are not necessarily related. The latter, the stabilisation of yield across environments in drought-prone areas, is very important because of the large differences in the coefficient of variation of pearl millet production. There are different ways to assess what is commonly called 'drought tolerance', and this depends mostly on how close the assessed trait/parameter is from the final target – an increased genetic yield. Therefore, the approaches to drought tolerance vary.

Three categories can broadly be defined, with advantages and drawbacks as highlighted below:

- Drought tolerance is seen purely as a higher and more stable yield under drought conditions, which is fully in line with the ultimate goal. However, in almost all cases, this is related to a large GEI because yield is the integration of many different processes, each of them having a close interaction with the environment.
- Drought tolerance is considered as the maintenance of different development and growth processes, such as leaf expansion, at levels that are close to control well-watered plants. Here, we assume that these would remain well-linked to yield performance. This approach is straightforward and may be easier to capture than yield itself. However, some of these traits can be cumbersome to measure, which may not allow time to assess large numbers of accessions and progenies.
- Drought tolerance can be seen as more upstream, at the organ or cell level, and can be seen as the capacity to sustain certain biological mechanisms, such as maintaining leaf turgor, close to the level of well-watered plants. Measuring such traits requires screening under controlled environment conditions where better management and reproducibility of environmental variation can help reach low levels of GEI. However, the main drawback of this approach is that the traits may be loosely related to the final yield under stress.
- Abscisic acid (ABA) levels under well-watered conditions were higher in tolerant genotypes, including near isogenic lines (NIL)- Quantitative trait loci (QTL), than in sensitive genotypes, and ABA did not increase under water stress. Well-watered Tr was lower in tolerant than in sensitive genotypes at all vapour pressure deficit (VPD) levels. Except for one line, Tr slowed down in tolerant lines above a breakpoint at 1.40–1.90 kPa, with the slope decreasing >50%, whereas sensitive lines showed no change in that Tr response across the whole VPD range. It is concluded that two water-saving (avoidance) mechanisms may operate under well-watered conditions in tolerant pearl millet: (i) a low Tr even at low VPD conditions, which may relate to leaf ABA; and (ii) a sensitivity to higher VPD that further restricts Tr, which suggests the involvement of hydraulic signals. Both traits, which did not lead to TE differences, could contribute to absolute water saving seen in part due to dry weight increase differences. This water saved would become critical for grain filling and deserves consideration in the breeding of terminal drought-tolerant lines (Kholova *et al.*, 2010).

Over the past decade, ICRISAT and its partners have made substantial investments in developing mapping populations (Hash and Witcombe, 1994) and in DNA-based molecular marker systems including restriction fragment length polymorphism (RFLP; Liu *et al*., 1994), sequence-tagged sites (STS; Devos *et al*., 1995), amplified fragment length polymorphism (AFLP), and simple sequence repeat (SSR) markers (Qi *et al*., 2000; Allouis *et al*., 2001), and a bacterial artificial chromosome (BAC) library (Allouis *et al*., 2001) for pearl millet. These genetic tools have been used to develop a DNA-marker-based linkage map for pearl millet (Liu *et al*., 1994), and to map quantitative trait loci (QTL) conferring resistance to biotic stresses (Jones *et al*., 1995; Morgan *et al*., 1998; Jones *et al*., 2002) and tolerance to terminal drought stress (Yadav *et al*., 2002b). Levels of DNA marker polymorphism in pearl millet are very high, even between elite inbred parental lines of hybrids. The current pearl millet DNA marker based genetic linkage map covers about 700cM (Haldane function) distributed across the expected seven linkage groups for this diploid ($2n = 2x = 14$) species, and at least one free-floating pair of linked RFLP markers. These DNA marker-based linkage groups have not been definitively linked with the chromosome map of this species (Minocha and Sidhu, 1981; Kaul and Sidhu, 1997), which has been developed over the past 35 years using morphological markers (Anand Kumar and Andrews, 1993) and conventional cytogenetic methods (Jauhar and Hanna, 1998). Compared to most other grasses, the pearl millet genome appears to have undergone a large number of structural rearrangements (Devos and Gale, 2000).

Tillering and Developmental Plasticity This trait is derived from the wild parents. Pearl millet develops primary tillers and then the secondary tillers from the primary ones. The secondary tillers will compensate yield in case of mid-season drought (Mahalakshmi and Bidinger, 1986). As the period between floral initiation and flowering is similar, the plant has tillers in all stages of apical development at all times (Craufurd and Bidinger, 1988a; 1988b). It is often considered that pearl millet is not affected very much by mid-season drought, provided that moisture is available for the end of the season (Mahalakshmi and Bidinger, 1985a; 1985b).

Early flowering is important as a drought-escape mechanism. However, it appears that the prospect of breeding for earliness is limited because of the often poor predictability of rainfall events in the semi-arid tropics. Therefore, there seems to be an optimal time for flowering, suited to the average season length. It is within that particular range of flowering times for any particular environment that other traits likely to improve performance under water-limited conditions must be found. Low tillering and large panicles are commonly being used as a selection criterion in pearl millet breeding. Selecting for these traits results in higher grain yield per panicle (Bidinger *et al*., 1987b; Yadav, 1994a). Breeding lines with stay-green trait have also been identified in pearl millet (Yadav and Rai, 2013). Pearl millet is known to be deep and profusely rooted, with the ability to match its rooting to water availability in a very plastic manner, leading to a highly varying root-growth to shoot-growth ratio, depending on the intensity of water limitation (Squire *et al*., 1987). Roots appear to play an important role in pearl millet genotypes that differ in the presence or absence of a major terminal drought tolerance QTL (Vadez *et al*., 2005). Further efforts are needed to clarify the extent of the role of the root in the drought tolerance of pearl millet.

Drought Resistance Index It has been found that about 50% of yield variation under drought-stress conditions could be explained by differences in the yield potential of genotypes and their flowering time (Bidinger *et al.*, 1982; 1987a). This led to develop an index, the 'drought resistance index' (DRI), in which the effect of yield potential and drought escape (flowering time) are removed by assuming that yield under stress is a function of yield potential (control yield in the test environment), drought escape (proxied by time to flowering), and a residual that accounts for drought tolerance/susceptibility. So that:

$$\hat{}Ys = aYc + bFl + Residual$$

where $\hat{}Ys$ is the predicted yield under stress based on the yield under control conditions, respectively, the flowering time (Fl) and a residual. This residual variation in grain yield under stress that is not explained by either the potential yield (Yc) or by the flowering time (Fl) represents the DRI. The value of the residual (= DRI) is obtained as follows: $DRI = Ys - \hat{}Ys$, where Ys is the actual grain yield under stress conditions. Therefore, the DRI represent the deviation in grain yield under stress from a baseline yield that depends on the yield potential and flowering time and it therefore allows comparing genotype's performance regardless of their yield potential and flowering time. The DRI approach has been used in a selection programme for improved drought tolerance, using the panicle harvest index (PNHI), that is, the ratio of grain yield to panicle yield on a plot basis, as a proxy to assess the DRI.

DRI in both midseason and terminal stress treatments was unrelated to yield component structure in the irrigated control treatment, indicating that selection for plant type under non-stressed conditions will not influence drought response. The correlation of DRI and individual panicle yield was of sufficient magnitude for the latter to serve as a selection index in terminal stress. (Bidinger *et al.*, 1987a).

Water Use Efficiency Being a C4 plant, pearl millet already has high transpiration efficiency (TE). However, it seems that the major strategy of pearl millet is to maximise carbon fixation as long as water is available. Therefore, stomatal movements adapt in such a way that the transpiration rate is kept as high as possible (Squire, 1979; Henson and Mahalakshmi, 1985). It also appears that stomata are sensitive to the vapour pressure deficit (VPD), particularly during the pre-flowering stage, this being related to differences in the ABA content of the leaves (Henson and Mahalakshmi, 1985). In any case, there have been no studies to assess the range of variation in TE across a diverse range of pearl millet cultivars and lines, nor on the sensitivity of stomata to VPD.

Number of grains per panicle and the 100-grain weight were the yield components most affected under terminal drought conditions, leading to a decrease in the panicle harvest index (PNHI). DRI represents the share of the variation in yield across a set of genotypes that cannot be explained either by differences in yield potential or time to flowering, and is closely related to yield under stress conditions. Bidinger *et al.* (1987a; 1987b) have also shown DRI was closely related to the PNHI and therefore, a high DRI was closely related to a higher percentage grain set and better grain filling, which are the major components of the PNHI. In subsequent works, the PNHI has then been used as an indirect proxy for DRI, and is readily and cost-effectively measured.

2.10.1.1.2 Trait-based Conventional Approach

This approach was initially used to select genotypes achieving a high PNHI under terminal drought conditions. PNHI was initially tested in hybrid-parent breeding, where it was used as a selection criterion by the following procedure:

1) Conduct bidirectional selection for combining ability for high and low PNHI in replicated potential maintainer (B) and restorer (R) line test cross-nurseries (three testers each) grown in managed terminal drought-stress environments.
2) Cross parents selected for high and low PNHI under stress conditions on three different A- or R-line testers from those used in the original test-cross nurseries in which selection was carried out.
3) Evaluate these test crosses for general combining ability (GCA) for PNHI, grain yield and yield components, in both fully irrigated control environments and in managed stress environments.

2.10.1.1.3 Trait-based Molecular Breeding Approach in Current Use

This is the current approach to pearl millet breeding for drought tolerance. It is based on the fact that PNHI remains a highly complex trait for which a molecular approach can increase precision during the selection process. We have shown earlier that the yield under terminal drought was a function of the yield potential under no stress, a drought escape mechanism, and DRI per se. Therefore, it is not advisable to cross parents with large variations in yield potential or flowering time if the intention is to develop a recombinant inbred line (RIL) population to map terminal drought tolerance. This approach has been used successfully for the identification of terminal drought tolerance QTL (Yadav *et al*., 2000; 2002b; 2003), and the introgression of a terminal drought tolerance QTL into the background of the popular pearl millet hybrid HHB67 to create the new hybrid HHB67-improved. This terminal drought tolerance QTL has a major effect, explaining over 30% of the yield variation under terminal drought. It is located on linkage group 2 (LG2). Further efforts are still needed to reduce the size of that QTL to improve the precision of its introgression.

2.10.1.2 Heat Tolerance

Pearl millet, *Pennisetum glaucum* (L.) R. Br., is the staple cereal grain and fodder crop grown by subsistence farmers in the hottest and driest regions of the Sahelian zone of sub-Saharan Africa and the Indian subcontinent where rainfed crop production is possible. High temperatures have relevance at both seedling and reproductive stages of pearl millet. Failure of seedling establishment due to extreme high soil temperatures at the start of the growing season results in the need to re-sow and an increased likelihood that the crop will be exposed to the damaging effects of post-flowering drought. Some of the pearl millet populations were shown to have good seedling emergence and survival at soil surface temperatures exceeding 62°C. Rapid screening procedures for seedling survival under these high temperatures have been shown and genotypes with tolerance to high temperature levels are identified (Soman and Peacock, 1985; Peacock *et al*., 1993). Pearl millet is cultivated as an irrigated summer season (February–June) crop in parts of Gujarat, Rajasthan and Uttar Pradesh in India where high temperatures (>42°C) is of common occurrence during flowering. Such high temperatures coinciding with flowering can cause spikelet sterility, leading to drastic reduction in grain yield. Large genetic variation for tolerance to heat at reproductive stage has been

observed and heat tolerant lines have been identified such as ICMB 92777, ICMB 05666, ICMB 00333, ICMB 01888, ICMB 02333 and ICMB 03555 among the maintainer lines and ICMV 82132, MC 94, ICTP 8202 and MC-bulk among the populations (Yadav *et al*., 2012).

2.10.2 Breeding for Biotic Stress Resistance

2.10.2.1 Downy Mildew (DM)

About 111 diseases have been reported on pearl millet in India and Africa. Pearl millet downy mildew, caused by *Sclerospora graminicola* (Sacc.) J. Schroet is an important constraint, especially on those hybrids having DM-susceptible lines in their parentage (Yadav and Rai, 2013). Its impact on pearl millet production, in a global context, is secondary to that of drought, even though downy mildew epidemics on single-cross hybrids have occurred repeatedly in India and can be expected to occur on such cultivars in Africa as well. Breeding for resistance to downy mildew, however, has been accorded the highest priority among the biotic stress factors (Hash *et al*., 1997), and it is an integral part of a majority of the breeding programmes in India (especially at ICRISAT, Patancheru) and Africa, because (i) a large number of resistance sources (including elite breeding lines) have been identified in diverse genetic backgrounds and effective screening techniques have been developed (Singh *et al*., 1997) and (ii) inheritance of resistance is better understood, with most of the evidence in favour of resistance being dominant and displaying continuous variation in segregating populations (Singh, 1995).

Since the introduction of hybrids in India, downy mildew has been a major production constraint and major focus of pearl millet improvement research. The symptoms of downy mildew can appear at any stage of crop growth. Leaf symptoms begin as chlorosis at the base of first infected leaf, and subsequent leaves show progressively greater chlorotic symptoms. Severely infected plants remain stunted and do not produce panicles. The most typical symptom is the transformation of infected floral parts into leafy structures. Following good understanding of epidemiology of the pathogen, highly effective field (Williams *et al*., 1981) and green house (Singh and Gopinath, 1985) techniques are developed and widely utilised.

Progenies are periodically evaluated for downy mildew resistance during the course of inbreeding and selection for DM resistance runs concurrent to agronomic evaluation finally producing B-lines and R-lines resistant to this disease. It has been found that selection for resistance to one pathotype is effective, to some extent, in selecting for resistance to another diverse pathotype. Several putative QTL have been identified that determine a significant proportion of DM resistance in pearl millet (Jones *et al*., 1995; Hash *et al*., 1997; Hash and Witcombe, 2001; Breese *et al*., 2002; Jones *et al*., 2002). Integrated conventional and marker-assisted back-crossing was taken up to introgress DM resistance QTL from sources IP 18293 and P 1449-2 into the genetic backgrounds of maintainer lines 81B, 843B and PT 732B advanced by a generation following screens against highly virulent pathogen isolates from Patancheru and New Delhi. Resistance alleles at two DM QTL, one each on linkage groups 1 (LG1) and 4 (LG4) were added to the male parent (H77/833-2) of widely grown hybrid HHB 67 through marker assisted back crossing from the resistance donor ICMP 451 and a DM resistant version was released as 'HHB 67 improved' (Yadav and Rai, 2013).

There is clear evidence that the A_1 cytoplasm is not associated with susceptibility or resistance (Yadav, 1994b; 1996). There is ample evidence for nuclear genes controlling resistance to this disease. Except in one case, where resistance was reported to be recessive (Singh *et al*., 1978), reports generally confirm that resistance is inherited as a dominant trait and variation in segregating populations is continuous (Singh, 1995). In a few cases where clear Mendelian segregations has been observed, the number of dominant genes governing resistance has been one or two (Deswal and Govila, 1994). Quantitative inheritance studies have been more successful and non-additive gene action is responsible for much of the heritable variability (Tyagi and Singh, 1989; Deswal and Govila, 1994; Kataria *et al*., 1994). Such non-additive gene action can contribute substantially to general combining ability (GCA), since parents having dominant resistance can be expected to have high GCA for this trait when compared to more susceptible parents.

2.10.2.2 Other Biotic Constraints

Other biotic constraints have received relatively low priority in breeding programmes targeted to the semi-arid tropical regions of Asia and Africa. These can be grouped into two categories. The first category includes ergot (*Claviceps fusiformis* Lovelesse) and smut (*Moesziomyces penicillariae* (Bref.) Vánky), diseases of pearl millet; for these, good resistance sources and effective screening techniques have been developed (Sharma *et al*., 1991; Thakur *et al*., 1992; Sharma *et al*., 1993; Thakur *et al*., 1993; Pande *et al*., 1994; Ejeta *et al*., 1997). However, these have been shown not to have as large an impact on yield, on as large a geographical scale. Also, some of these can, to some extent, be managed by other means, for instance, by breeding for improved male fertility restoration in hybrids and by resorting to alternative cultivar options (e.g. OPVs, top-cross hybrids, and protogyny-based single-cross hybrids where in seed is produced using protogynous flowering rather than by male-sterile seed parents) can be effective in reducing ergot and smut severity in pearl millet). Simply inherited recessive 'tr' allele, which conditions trichomelessness to most above ground parts, including stigmas, confers a useful degree of smut resistance. Rust of pearl millet is of minor importance as it generally occurs after grain filling stage. Rust resistance has been demonstrated to be under the control of a single dominant gene (Andrews *et al*., 1985). Two QTL have been identified for rust resistance but their deployment in the parental lines is yet to begin (Yadav and Rai, 2013). Blast incidence has increased considerably in the recent years (Lukose *et al*., 2007). Field and greenhouse screening techniques have been developed, and sources of resistance have been identified (Thakur *et al*., 2009; Sharma *et al*., 2013). Inheritance studies have indicated single-dominant gene control of blast (Wilson *et al*., 1989; Gupta *et al*., 2012). However, three independent dominant genes have also been reported (Hanna and Wells, 1989).

The second category includes stem borers of pearl millet (*Coniesta ignefusalis* Hampson); and head miner (*Heliocheilus albipunctella* de Joannis) for which confirmed sources of good resistance are not available and (or) the trait inheritance is too complex to permit its effective utilisation in breeding. This category has received little attention in breeding programmes in Asia and Africa.

Pearl millet is also cultivated for forage mostly in North India. Varieties and hybrids are available exclusively for forage purpose. Green forage yield, dry forage yield and crude protein of pearl millet are more compared to sorghum and maize. Yield of green and dry forage and crude protein contents of sorghum, pearl millet, maize and pigeon pea are given in Table 2.2.

Table 2.2 Yield of green and dry forage and crude protein contents of sorghum, pearl millet, maize and pigeon pea.

Crop	Green forage yield (t/ha)	Dry forage yield (t/ha)	Crude protein (%)
Sorghum	32.7	77	6
Pearl millet	37.6	8.5	8.7
Maize	30.9	6.5	5.5
Pigeon pea	40.6	12.6	23.7

Source: Adapted from NRAA (2012).

2.11 Grain Quality

Pearl millet is a highly nutritious cereal with higher levels of proteins reaching up to 24.3% in the germplasm (Jambunathan and Subramanian, 1988) and 19.8% in the breeding lines (Singh *et al*., 1987). Breeding lines and germplasm exceeding 100 ppm Fe and 60 ppm Zn density have been identified (Rai *et al*., 2012). It has been observed that Fe and Zn densities in pearl millet are largely under additive genetic control (Velu *et al*., 2011; Govindaraj *et al*., 2013) and high positive correlation ($r = 0.84^{**}$) exists between Fe and Zn density implying that population improvement and OPV development for these two micronutrients is highly effective. Golden millet with about 1.37 ppm of beta-carotene, which is comparable to beta-carotene in golden rice and three–five times more than traditional pearl millet, was identified in a photosensitive background. The yellow endosperm acts as a proxy to beta-carotene.

2.12 Alternate Uses of Pearl Millet

There is a huge demand for pearl millet for the extraction of alcohol, provided the starch content in pearl millet is increased from the present level of 55–65%. Presently, most of the distilleries are using broken rice, as rice has high starch content and the unit cost of starch from rice is cheaper than starch from the pearl millet. Hence, the demand for pearl millet from the distilleries depends on the relative prices of broken rice and pearl millet (Nagaraj *et al*., 2011).

The simplest and the most common traditional food made from pearl millet are thin porridge (gruel); thick porridge (fermented and unfermented) and flat and unfermented bread such as chapatti. Various types of snacks are also made from pearl millet flour in India. Pearl millet flour is not a good raw material for the baking industry, since it does not contain gluten and this forms dough of poor consistency. However, pearl millet flour hydrated with water, dried, and supplemented with 0.6% unrefined soy lectin can produce cookies with spread characteristics equal to those made from soft wheat flour. Various types of biscuits developed by incorporating different levels of blanched as well as malted pearl millet flour have been found to be acceptable and store well up to 3 months (Singh, 2003).

Extrusion is being used increasingly for making ready-to-eat foods. In extrusion processes, cereals are cooked at high temperature for a short time. Starch is gelatinised

and protein is denatured, which improves their digestibility. Anti-nutritional factors that are present may be inactivated. Pearl millet grit and flour can be used to prepare ready-to-eat (RTE) products. The acid-treated pearl millet yields products of better acceptability as compared to that from just decorticated pearl millet. Pearl millet, blended with soy or protein-rich ingredients, such as legumes or groundnut (peanut) cake, on extrusion gives nutritionally balanced supplementary foods (Malleshi *et al*., 1996). Pearl millet flaking would be a new avenue for its widespread utilisation. Since stabilisation of the oil occurs during flaking, pearl millet flakes will have longer shelf life. Popping of pearl millet is not very popular, but the popped pearl millet is a good source of energy, fibre and carbohydrates. Pearl millet can be malted and utilised for the development of weaning foods, as it can satisfy the nutritional requirement of Infants. Pearl millet can find uses in preparing various types of health foods and food ingredients as it contains a relatively higher proportion of insoluble dietary fibre. This causes slow release of sugar, thus making the food products based on them especially suitable for those suffering from or prone to diabetes. For instance, various pearl millet-based food products were found to have a lower glycemic index (GI) than those based on wheat. Pearl millet is rich in oil and linoleic acid accounts for 4% of the total fatty acids in this oil, giving it a higher percentage of n-3 fatty acids as compared to maize in which linoleic acid accounts for only 0.9% of the total fatty acids. The n-3 fatty acids play an important role in many physiological functions, including platelet aggregation, cholesterol accumulation and the immune system. Apart from these, pearl millet flour is used in making different types of drinks.

2.13 Future Research Thrust Areas

a) *Utilisation of alternate CMS systems*: The A_1, A_4 and A_5 CMS resources are well characterised for their commercial potential. The utilisation of A_4 and A_5 as the more stable and useful CMS systems compared to the widely used A_1 CMS system should be enhanced. The pace of shift to these two new CMS sources depend on the pace of their restorer development, for which various approaches (pedigree breeding, backcross breeding and population approaches) have been shown to be effective.
b) *Hybrid options*: The continuing genetic gains of over 24 kg ha^{-1} $year^{-1}$ for grain yield realised in India indicates the impressive use of hybrid1 technology. Considering the increasingly dominant role of the private sector in hybrid development and seed production, single-cross hybrids will remain the only commercial option. Hence, inbred seed-parent development with high yield potential, DM resistance and adaptation to the regions concerned should be focused. Hybrid development should focus on better-endowed environments and strategic research should be taken up for marginal environments.
c) *Trait focus*: Grain yield and DM resistance should be given top priority. Emphasis should be given for dual-purpose hybrids for northern India, and medium maturing hybrids for central and southern India. Breeding for earliness and forage hybrids should also be taken up. Farmer-preferred traits such as panicle compactness, panicle size, lodging resistance, grain size and colour should be considered while selection.
d) *Exploitation of germplasm and breeding lines*: Past-breeding efforts have introgressed large seed size, panicle length and girth and tillering ability. Apart from these, new germplasm sources for high biomass yield, panicle compactness combined with good

panicle size should be utilised. Breeding lines with complementary traits for generating productive lines should be used.

e) *Marker-assisted breeding*: Marker-assisted back-cross breeding should be followed for DM resistance gene deployment. Based on funding, other traits such as drought tolerance, stover quality, drought tolerance, soil-salinity tolerance and heat stress at flowering, heterotic grouping of elite breeding lines and germplasm should be taken up.

References

Acheampong, E., Anisetty, N.M. and Williams, J.T. (1984) *A World Survey of Sorghum and Millets Germplasm*, IBPGR, Rome, Italy.

Ahluwalia, M. and Shankar, K. (1964) Inheritance of bristling in pearl millet. *Science and Culture*, **30**, 340–341.

Aken'ova, M.E. (1982) Male-sterility in Nigerian bulrush millets [*Pennisetum americanum* (L.) K. Schum.]. *Euphytica*, **31**, 161–165.

Al-Fakhry, A.K., Grogan, C.O. and Sarvella, P. (1965) Some genetic studies on babala. *Pennisetum typhoideum (L.) Rich. Zeitschrift fur Pflanzenzuchtung*, **54**, 182–187.

Allard, R.W. (1960) *Principles of Plant Breeding*, John Wiley and Sons, New York, USA.

Allouis, A., Qi, X., Lineup, S. *et al.* (2001) Construction of a BAC library of pearl millet, *Pennisetum glaucum*. *Theoretical and Applied Genetics*, **102**, 1200–1205.

Anand Kumar, K. and Andrews, D.J. (1993) Genetics of qualitative traits in pearl millet: a review. *Crop Science*, **33**, 1–20.

Anand Kumar, K. and Appa Rao, S. (1987) Diversity and utilisation of pearl millet germplasm. In *Proceedings of the International Pearl Millet Workshop* (eds J.R. Witcombe and S.R. Beckerman), held at ICRISAT, Patancheru, India, April 7–11, 1986. International Crops Research Institute for the Semi-Arid Tropics, Patancheru, India, pp. 69–82.

Andre Savery, M. and Prasad, M.N. (1995) Genetic diversity in pearl millet, Pennisetum typhoides. *Madras Agricultural Journal*, **82**, 8–11.

Andrews, D.J. and Anand Kumar, K. (1996) Use of the West African pearl millet landrace *Iniadi* in cultivar development. *Plant Genetics Resources Newsletter*, **105**, 15–22.

Andrews, D.J., Ejeta, G., Gilbert, M. *et al.* (1997) Breeding hybrid parents. Proceedings of an International Conference on the Genetic Improvement of Sorghum and Pearl Millet, held at Lubbock, Texas, September 22–27, 1996. International Sorghum and Millet Research (INTSORMIL) – International Crops Research Institute for the Semi-arid Tropics (ICRISAT), pp. 173–187.

Andrews, D.J., Kiula, B. and Rajewski, J.F. (1993) The use of protogyny to make hybrids in pearl millet, in *New Crops* (eds J. Janick and J. Simpson), John Wiley & Sons, Inc., New York, pp. 208–210.

Andrews, D.J., Rai, K.N. and Singh, S.D. (1985) A single dominant gene for rust resistance in pearl millet. *Crop Science*, **25**, 565–566.

Appa Rao, S., Mazhani, L.M. and Attere, A.F. (1986) Collecting in Botswana. *Plant Genetic Resources Newsletter*, **68**, 27–28.

Appa Rao, S., Mengesha, M.H. and Rajagopal Reddy, C. (1984) Characteristics and inheritance of viable chlorophyll mutants in *Pennisetum americanum* (L.) Leeke. *Indian Journal of Botany*, **7**, 1–5.

Appa Rao, S., Mengesha, M.H. and Rajagopal Reddy, C. (1986a) New sources of dwarfing genes in pearl millet (*Pennisetum americanum*). *Theoretical and applied genetics*, **73**, 170–174.

Appa Rao, S., Mengesha, M.H. and Rajagopal Reddy, C. (1986b) New sources of dwarfing genes in pearl millet (*Pennisetum americanum*). *Theoretical and Applied Genetics*, **73**, 170–174.

Appa Rao, S., Mengesha, M.H. and Rajagopal Reddy, C. (1986c) Variation and adaptation of pearl millet germplasm in Tamil Nadu. *Indian Journal of Genetics and Plant Breeding*, **46**, 449–455.

Appa Rao, S., Mengesha, M.H. and Rajagopal Reddy, C. (1986d) Pearl millet (*Pennisetum americanum*) germplasm from Senegal. *Indian Journal of Genetics and Plant Breeding*, **46**, 413–422.

Appa Rao, S., Mengesha, M.H. and Rajagopal Reddy, C. (1987a) Glossy genes in pearl millet. *Journal of Heredity*, **78**, 333–335.

Appa Rao, S., Mengesha, M.H. and Rajagopal Reddy, C. (1987b) Glossy genes in pearl millet. *Journal of Heredity*, **78**, 333–335.

Appa Rao, S., Mengesha, M.H. and Rajagopal Reddy, C. (1988a) Characteristics, inheritance and allelic relationships of midribless mutants in pearl millet. *Journal of Heredity*, **79**, 18–20.

Appa Rao, S., Mengesha, M.H. and Rajagopal Reddy, C. (1988b) New sources of early-maturing germplasm in pearl millet (*Pennisetum glaucum*). *Indian Journal of Agricultural Sciences*, **58**, 743–746.

Appa Rao, S., Mengesha, M.H. and Rajagopal Reddy, C. (1989) Development of cytoplasmic male-sterile lines of pearl millet from Ghana and Botswana germplasm, in *Perspectives in Cytology and Genetics* (eds G.K. Manna and U. Sinha), Kalyani, India, pp. 817–823.

Appa Rao, S., Mengesha, M.H. and Sharma, D. (1985) Collection and evaluation od pearl millet (Pennisetum americanum) germplasm from Ghana. *Economic Botany*, **39**, 25–38.

Appa Rao, S., Mengesha, M.H. and Subramanian, V. (1982) Collection and evaluation of sweet stalk pearl millet (*Pennisetum*). *Economic Botany*, **36**, 286–290.

Appa Rao, S., Mengesha, M.H., Sibale, P.K. and Rajagopal Reddy, C. (1986) Collection and evaluation of pearl millet (*Pennisetum*) germplasm from Malawi. *Economic Botany*, **40**, 27–37.

Appadurai, R., Parambaramani, C. and Natarajan, U.S. (1975) Note on the inheritance of susceptibility of pearl millet to downy mildew. *Indian Journal of Agricultural Sciences*, **45**, 179–180.

Athwal, D.S. (1961) Recent developments in the breeding and improvement of bajra (pearl millet) in the Punjab. *Madras Agricultural Journal*, **48**, 18–19. (Abstract.)

Athwal, D.S. (1965) Hybrid bajra-1 marks a new era. *Indian Farming*, **15**, 6–7.

Athwal, D.S. (1966) Current plant breeding research with special reference to *Pennisetum*. *Indian Journal of Genetics and Plant Breeding*, **26A**, 73–85.

Athwal, D.S. and Gill, G.S. (1966) Inheritance of bristling and purple pigmentation in *Pennisetum typhoides* (Burm.) Stapf and Hubb. *Punjab Agricultural University Journal of Research*, **3**, 253–259.

Baker, H.G. (1962) Comments on a thesis that there was a major centre of plant domestication near the headwaters of river Niger. *Journal of African History*, **3**, 229–233.

Basavaraju, R., Safeeulla, K.M. and Murty, B.R. (1981) Genetic variance and heritability for resistance to downy mildew in pearl millet. *Indian Journal of Genetics and Plant Breeding*, **41**, 137–143.

Begg, J.E. (1965) The growth and development of a crop of bulrush millet (*Pennisetum typhoides* S and H). *Journal of Agricultural Sciences*, **65**, 341–349.

Bhatnagar, M.P. and Kumar, K. (1960) Anthesis studies in Rajasthan bajra (*Pennisetum typhoides*). *Indian Journal of Agricultural Sciences*, **30**, 185–195.

Bidinger, F.R. and Mahalakshmi, V. (1993) Selection for drought tolerance, in *The 1992 Annual Report on the Cereals Program of the International Crops Research Institute for the Semi-arid Tropics (ICRISAT)*, Annual Report. ICRISAT, Patancheru, India, pp. 57–59.

Bidinger, F.R., Mahalakshmi, V. and Rao, G.D.P. (1987a) Assessment of drought resistance in pearl millet (*Pennisetum americanum* (L.) Leeke). I Factors affecting yields under stress. *Australian Journal of Agricultural Research*, **38**, 37–48.

Bidinger, F.R., Mahalakshmi, V. and Rao, G.D.P. (1987b) Assessment of drought resistance in pearl millet (*Pennisetum americanum* (L.) Leeke). II Estimation of genotype response to stress. *Australian Journal of Agricultural Research*, **38**, 49–59.

Bidinger, F.R., Mahalakshmi, V., Talukdar, B.S. and Alagarswamy, G. (1982) Improvement in drought resistance in pearl millet, in *Drought Resistance in Crops with Emphasis on Rice*, International Rice Research Institute, Manila, Philippines, pp. 357–376.

Blum, A. and Sullivan, C.Y. (1986) The comparative drought resistance of landraces of sorghum and millet from dry and humid regions. *Annals of Botany*, **57**, 835–846.

Bono, M. (1973) Contribution a la morpho-systematique des *Pennisetum* annuels cultives pour leur grain en afrique occidentale francophone. *L Agronomie Tropicale*, **28**, 229–355.

Bramel-Cox, P.J. and Cox, T.S. (1989) Use of wild germplasm in sorghum improvement, in *Proceedings of the 43rd Annual Corn and Sorghum Industry Research Conference*, held at Chicago, IL. American Seed Trade Association, Washington, DC, pp. 13–26.

Breese, W.A., Hash, C.T., Devos, K.M. and Howarth, C.J. (2002) Pearl millet genomics - an overview with respect to breeding for resistance to downy mildew, in *Sorghum and Millets Pathology* (ed. J.F. Leslie), Ames, Iowa State Press, pp. 243–246.

Brunken, J.N. (1977) A systematic study of *Pennistum* Sect. *Pennisetum* (Gramineae). *American Journal of Botany*, **64**, 161–176.

Burton, G.W. (1958) Cytoplasmic male-sterility in pearl millet [*Pennisetum glaucum* (L.) R. Br.]. *Agronomy Journal*, **50**, 230–231.

Burton, G.W. and Athwal, D.S. (1967) Two additional sources of cytoplasmic male-sterility in pearl millet and their relationship to Tift 23A. *Crop Science*, **7**, 209–211.

Burton, G.W. and Fortson, J.C. (1966) Inheritance and utilization of five dwarfs in pearl millet (*Pennisetum typhoides*) breeding. *Crop Science*, **6**, 69–72.

Burton, G.W. and Powell, J.B. (1968) Pearl millet breeding and cytogenetics. *Advances in Agronomy*, **20**, 49–89.

Chalam, G.V. and Venkateswarlu, J. (1965) *Introduction to Agricultural Botany in India*, vol. **I**, Asia Publishing house, Bombay, India.

Chowdhury, M.K.U. and Smith, R.L. (1988) Mitochondrial DNA variation in pearl millet and related species. *Theoretical and Applied Genetics*, **76**, 25–32.

Clement, J.C. (1985) *Les mils Penicillaires de L Afrique de L Quest: Prospections et Collectes*, IBPGR, Rome, Italy.

Craufurd, P.Q. and Bidinger, F.R. (1988a) Effect of the duration of the vegetative phase on crop growth, development and yield in two contrasting pearl millet hybrids. *Journal of Agricultural Sciences*, **110**, 71–79.

Craufurd, P.Q. and Bidinger, F.R. (1988b) Effect of the duration of the vegetative phase on shoot growth, development and yield in pearl millet (*Pennisetum americanum* (L.) Leeke). *Journal of Experimental Botany*, **39**, 124–139.

Craufurd, P.Q. and Bidinger, F.R. (1989) Potential and realized yield in pearl millet (*Pennisetum americanum*) as influenced by plant population density and life-cycle duration. *Field Crops Research*, **22**, 211–225.

de Wet, J.M.J. (1987) Pearl millet (*Pennisetum glaucum*) in Africa and India, in *Proceedings International Pearl Millet Workshop* (eds J.R. Witcombe and S.R. Beckerman), ICRISAT, Patancheru, India, pp. 3–4.

Deshmukh, H.G., More, B.B. and Utikar, P.G. (1978) Screening germplasm of pearl millet against downy mildew. *Sclerospora graminicola (Sacc.) Schroet. Indian Journal of Agricultural Research*, **12**, 85–88.

Deswal, D.P. and Govila, O.P. (1994) Genetics of resistance to downy mildew (*Sclerospora graminicola*) in pearl millet (*Pennisetum glaucum*). *Indian Journal of Agricultural Sciences*, **64**, 661–663.

Devos, K.M. and Gale, M.D. (2000) Genomic relationships: the grass model in current research. *Plant Cell*, **12**, 637–646.

Devos, K.M., Pittaway, T.S., Busso, C.S. *et al*. (1995) Molecular tools for the pearl millet nuclear genome. *International Sorghum and Millets Newsletter*, **36**, 64–66.

Dhillon, B.S., Gupta, V.P. and Sethi, A.S. (1977) Path coefficient analysis of grain yield in pearl millet. *Genetica Agraria*, **31**, 411–415.

Ejeta, G., Butler, L.G., Hess, D.E. et al. (1997) Breeding for *Striga* resistance in sorghum. *In Proceedings of an International Conference on the Genetic Improvement of Sorghum and Pearl Millet*, held at Lubbock, Texas, 22–27 September (1996. International Sorghum and Millet Research (INTSORMIL) – International Crops Research Institute for the Semi-arid Tropics (ICRISAT), pp. 504–516.

FAOSTAT (2006) *FAOSTAT – Agriculture*, FAO, Rome.

Fussell, L.K., Bidinger, F.R. and Bieler, P. (1991) Crop physiology and breeding for drought tolerance: research and development. *Field Crops Research*, **27**, 183–199.

Fussell, L.K. and Pearson, C.J. (1978) Course of grain development and its relation to black region appearance in *Pennisetum americanum*. *Field crops Research*, **1**, 21–31.

Gaudy, M. (1957) *Manuel d'Agriculture tropicale*, La maison Rustique, Paris, pp. 139–140.

Gaut, B.S. and Clegg, M.T. (1993) Nucleotide polymorphism in the adh 1 locus of pearl millet (*Pennisetum glaucum*) (Poaceae). *Genetics*, **135**, 1091–1097.

Gill, G.S. and Athwal, D.S. (1970) Genetics of some ear characters and plant pigmentation in pearl millet. *Indian Journal of Genetics and Plant Breeding*, **30**, 519–525.

Gill, K.S., Phul, P.S., Chahal, S.S. and Singh, N.B. (1978) Inheritance of resistance to downy mildew in pearl millet. *Cereal Research Communications*, **6**, 71–74.

Godawat, S.L. and Kaul, B.K. (1981) Genetic variability and path analysis of protein contributing characters in pearl millet. *Indian Journal of Agricultural Sciences*, **51**, 147–149.

Govindaraj, M., Rai, K.N., Shanmugasundaram, P. *et al*. (2013) Combining ability and heterosis for grain iron and zinc densities in pearl millet. *Crop Science*, **53**, 507–517.

Gupta, S.C., Monyo, E.S. and Appa Rao, S. (1983) Registration of SDML 89107 brown midrib pearl millet germplasm. *Crop Science*, **33**, 882.

Gupta, S.K., Premachandran, M.N. and Choubey, R.N. (1985) Inheritance of dwarfing source in pearl millet. *Zeitschrift fur Pflanzenzuchtung*, **94**, 255–258.

Gupta, S.K., Sharma, R., Rai, K.N. and Thakur, R.P. (2012) Inheritance of foliar blast resistance in pearl millet (*Pennisetum glaucum*). *Plant Breeding*, **13**, 217–219.

Gupta, V.P. and Athwal, D.S. (1966) Genetic variability, correlation and selection indices for green fodder characteristics in pearl millet. *Punjab Agricultural University Journal of Research*, **3**, 111–117.

Gupta, V.P., Dhillon, B.S. and Sethi, A.S. (1976) The path analysis of protein, mineral content and grain yield of pearl millet. *Crop Improvement*, **3**, 80–85.

Hanna, W.W. (1987) Utilization of wild relatives of pearl millet, in *Proceedings International Pearl millet Workshop* (eds J.R. Witcombe and S.R. Beckerman), ICRISAT, Patancheru, India, pp. 33–42.

Hanna, W.W. (1989) Characteristics and stability of a new cytoplasmic-nuclear male-sterile source in pearl millet. *Crop Science*, **29**, 1457–1459.

Hanna, W.W. (1992) Utilization of germplasm from wild species, in *Desertified Grasslands: Their Biology and Management* (ed. G.P. Chapman), Academic Press, London, pp. 251–257.

Hanna, W.W. and Burton, G.W. (1984) Morphological characteristics and genetics of two mutations for early maturity in pearl millet. *Crop Science*, **24**, 79–81.

Hanna, W.W. and Wells, H.D. (1989) Inheritance of pyricularia leaf spot resistance in pearl millet. *Journal of Heredity*, **80**, 145–147.

Hanna, W.W., Wells, H.D. and Burton, G.W. (1985) Dominant gene of rust resistance in pearl millet. *Journal of Heredity*, **76**, 134.

Harlan, J.R. (1971) Agricultural origins: centers and non-centers. *Science*, **14**, 468–474.

Harlan, J.R. and de Wet, J.M.J. (1971) Toward a rational classification of cultivated plants. *Taxonomy*, **20**, 509–517.

Harlan, J.R., de Wet, J.M.J. and Stemler, A.B.L. (1975) Plant domestication and indigenous African Agriculture, in *Origins of African Domestication* (eds J.R. Harlan, J.M.J. de Wet and A.B.L. Stemler), Mouton Publishers, The Hague, The Netherlands, pp. 1–9.

Hash, C.T., Bhasker Raj, A.G., Lineup, S. *et al.* (2003) Opportunities for marker-assisted selection (MAS) to improve the feed quality of crop residues in pearl millet and sorghum. *Field Crops Research*, **84**, 79–88.

Hash, C.T. and Witcombe, J.R. (1994) Pearl millet mapping populations at ICRISAT, in *Use of Molecular Markers in Sorghum and Pearl Millet Breeding for Developing Countries* (eds J.R. Witcombe and R.R. Duncan), Overseas Development Administration, London, pp. 69–75.

Hash, C.T. and Witcombe, J.R. (2001) Pearl millet molecular marker research. *International Sorghum and Millets Newsletter*, **42**, 8–15.

Hash, C.T., Witcombe, J.R., Thakur, R.P. *et al.* (1997) Breeding for pearl millet disease resistance, in *Proceedings of an International Conference on the Genetic Improvement of Sorghum and Pearl Millet*, held at Lubbock, Texas, September 22–27, 1996. International Sorghum and Millet Research (INTSORMIL) – International Crops Research Institute for the Semi-arid Tropics (ICRISAT), pp. 337–372.

Henson, I.E. and Mahalakshmi, V. (1985) Evidence for panicle control of stomatal behavior in water-stressed plants of pearl millet. *Field Crops Research*, **11**, 281–290.

ICRISAT (1989) *Collaboration on Genetic Resources: summary proceedings of a Joint ICRISAT/NBPGR (ICAR) Workshop on Germplasm Exploration and Evaluation in India, November 14–15, 1988*, ICRISAT Center, Patancheru, AP, ICRISAT, India.

Jambunathan, R. and Subramanian, V. (1988) Grain quality and utilisation in sorghum and pearl millet, in *Workshop on Biotechnology for Tropical Crop Improvement*, ICRISAT, Patancheru, pp. 1330–1339.

Jauhar, P.P. and Hanna, W.W. (1998) Cytogenetics and genetics of pearl millet. *Advances in Agronomy*, **64**, 1–26.

Jones, E.S., Breese, W.A., Liu, C.J. *et al.* (2002) Mapping quantitative trait loci for downy mildew resistance in pearl millet: field and glass house screens detect the same QTL. *Crop Science*, **42**, 1316–1323.

Jones, E.S., Liu, C.J., Gale, M.D. *et al.* (1995) Mapping quantitative trait loci for downy mildew resistance in pearl millet. *Theoretical and Applied Genetics*, **91**, 448–456.

Kadam, B.S., Patel, S.M. and Kulkarni, R.K. (1940) Consequences of inbreeding in bajra. *Journal of Heredity*, **31**, 201–207.

Kataria, R.P., Yadan, H.P., Beniwal, C.R. and Narwal, M.S. (1994) Genetics of incidence of downy mildew (*Sclerospora graminicola*) in pearl millet (*Pennisetum glaucum*). *Indian Journal of Agricultural Sciences*, **64**, 664–666.

Kaul, J. and Sidhu, J.S. (1997) Establishment of chromosome map of pearl millet through the use of interchanges. *Journal of Cytology and Genetics*, **32**, 113–123.

Kelley, T.G., Rao, P.P., Weltzien, R.E. and Purohit, M.L. (1996) Adoption of improved cultivars of pearl millet in an arid environment: Straw yield and quality considerations in western Rajasthan. *Experimental Agriculture*, **32**, 161–171.

Khairwal, I.S. (2007) Coordinator's review, in *Annual Report 2006–2007*, All India Coordinated Pearl Millet Improvement Project (Indian Council of Agricultural Research), Mandor, Jodhpur, Rajasthan, India, pp. 1–11.

Khairwal, I.S., Ram, C. and Chhabra, A.K. (1990) *Pearl Millet Seed Production and Technology*, Manohar Publications, New Delhi, India.

Khairwal, I.S. and Singh, S. (1999) Quantitative and qualitative traits, in *Pearl Millet Breeding* (eds I.S. Khairwal, K.N. Rai, D.J. Andrews and G. Harinarayana), Oxford and IBH Co. Pvt. Ltd., New Delhi, pp. 119–155.

Khairwal, I.S., Yadav, S.K., Rai, K.N. *et al.* (2007) Evaluation and identification of promising pearl millet germplasm for grain and fodder traits. *Journal of SAT Agricultural Research*, **5** (1), 1–6.

Khan, A.Q. and Bakshi, J.S. (1976) Inheritance of four qualitative characters in pearl millet. *SABRAO Journal*, **8**, 135–139.

Kholova, J., Hash, C.T., Kumar, P.L. *et al.* (2010) Terminal drought-tolerant pearl millet [*Pennisetum glaucum* (L.) R. Br.] have high leaf ABA and limit transpiration at high vapour pressure deficit. *Journal of Experimental Botany*, **61** (5), 1431–1440.

Koduru, P.R.K. and Krishna Rao, M. (1979) Inheritance of anthocyanin and wavy stem in Pennisetum. *Journal of Cytology and Genetics*, **14**, 18–20.

Krishna Rao, M. and Koduru, P.R.K. (1979) Genetics of five hairy phenotypes and a linkage group of *Pennisetum americanum*. *Euphytica*, **28**, 445–451.

Krishnaswamy, N. (1962) *Bajra*, *Pennisetum typhoides (Burm.) S&H*. Indian Council of Agricultural Research, New Delhi, India.

Kulkarni, M. and Deshpande, U. (2007) In vitro screening of tomato genotypes for drought resistance using polyethylene glycol. *African Journal of Biotechnology*, **6**, 691–696.

Kumar, R. and Sagar, P. (2009) Effect of cytoplasm on downy mildew vulnerability in pearl millet (*Pennisetum glaucum* (L.) R. Br.). *Indian Journal of Genetics*, **69**, 115–121.

Lagudah, E.S. and Hanna, W.W. (1990) Patterns of variation for seed proteins in the Pennisetum gene pool. *Journal of Heredity*, **81**, 25–29.

Leeke, P. (1907) Untersuchung uber Abstammung and Heimat der Negerhirse (*Pennisetum americanum* (L.) L schum.). *Zeitschrift fiir Naturwissenchaften*, **79**, 1–108.

Liu, C.J., Witcombe, J.R., Pittaway, T.S. *et al.* (1994) An RFLP-based genetic map of pearl millet (*Pennisetum glaucum*). *Theoretical and Applied Genetics*, **89**, 481–487.

Lukose, C.M., Kadvani, D.L. and Dangaria, C.J. (2007) Efficacy of fungicides in controlling blast disease of pearl millet. *Indian Phytopathology*, **60**, 68–71.
Mahalakshmi, V. and Bidinger, F.R. (1985a) Flowering response of pearl millet to water stress during panicle development. *Annals of Applied Biology*, **106**, 571–578.
Mahalakshmi, V. and Bidinger, F.R. (1985b) Water deficit during panicle development in pearl millet: yield compensation by tillers. *Journal of Agricultural Science*, **106**, 113–119.
Mahalakshmi, V. and Bidinger, F.R. (1986) Water deficit during panicle development in pearl millet (*Pennisetum americanum*): yield compensation by tillers. *Journal of Agricultural Science*, **106**, 113–120.
Maiti, R.K. and Bisen, S.S. (1979) *Pearl Millet Anatomy*. Information Bulletin No. 6. ICRISAT, Patancheru, India.
Malleshi, N.G., Hadimani, N.A., Chinnaswamy, R. and Klopfenstein, C.F. (1996) Physical and nutritional qualities of extruded weaning foods containing sorghum, pearl millet, or finger millet blended with mung beans and non-fat dried milk. *Plant Foods for Human Nutrition*, **49**, 181–189.
Manga, V.K. (2015) Diversity in pearl millet [*Pennisetum glaucum* (l.) R. Br.] and its management. *Indian Journal of Plant Sciences*, **4** (1), 38–51.
Manga, V.K. and Yadav, O.P. (1995) Effect of seed size on development traits and ability to tolerate drought in pearl millet. *Journal of Arid Environments*, **29**, 169–172.
Marchais, L. and Pernes, J. (1985) Genetic divergence between wild and cultivated pearl millets (*Pennisetum typhoides*). I. Male sterility. *Zeitschrift für Pflanzenzüchtung* **95**, 103–112.
Martin, J.H. and Leonard, W.H. (1967) Principles of Field Crop Production, 2nd ed. The MacMillan Co. New York, pp. 526–528.
McDonough, C.M. and Rooney, L.W. (1987) Variation in the physical and structural characteristics of pearl millet varieties from the world collection. *Cereal Foods World*, **32**, 665.
Mehta, N. and Dang, J.K. (1987) Studies on the inheritance of downy mildew, ergot and smut of pearl millet. *Indian Journal of Mycology and Plant Pathology*, **17**, 200–203.
Mengesha, M.H., Khanna, P.P., Chandel, K.P.S. and Kameswara Rao, N. (1989) Conservation of world germplasm collection of ICRISAT mandate crops, in *Collaboration on Genetic Resources*, Summary proceedings of a workshop on germplasm exploration and evaluation in India. ICRISAT, Patancheru, India, pp. 65–69.
Menkir, A., Bramel-Cox, P.J. and Witt, M.D. (1994) Comparisons of methods for introgressing exotic germplasm into adapted sorghum. *Theoretical and Applied Genetics*, **89**, 233–239.
Merkle, O.G., Starks, K.J. and Casady, A.J. (1983) Registration of pearl millet germplasm lines with chinch bug resistance. *Crop Science*, **23**, 601.
Minocha, J.L. and Sidhu, J.S. (1981) Establishment of Trisomic Stocks and Linkage Groups in *Pennisetum typhoides*. Final Research Report of PL480 Project, Punjab Agricultural University, Ludhiana, India.
Morgan, R.N., Wilson, J.P., Hanna, W.W. and Ozias-Akins, P. (1998) Molecular markers for rust and pyricularia leaf spot disease resistance in pearl millet. *Theoretical and Applied Genetics*, **96**, 413–420.
Murdock, G.P. (1959) *Africa: Its People and Their Cultural History*, McGraw Hill, New York, USA.
Murty, B.R., Upadhyay, M.K. and Manchanda (1967) Classification and cataloguing of a world collection of genetic stocks of Pennisetum. *Indian Journal of Genetics and Plant Breeding*, **27**, 313–394.

Nagaraj, N., Basavaraj, G. and Rao, P.P. (2011) *Policy Brief on Future Outlook and Options for Target Crops: The Sorghum and Pearl millet economy of India*, ICRISAT.

NRAA (2012) Products, Diversification, Marketing and Price Discovery of Pearl Millet in India. Policy Paper No. 2 National Rainfed Area Authority, NASC Complex, DPS Marg, New Delhi, India, 48p.

Ouendeba, B., Ejeta, G., Hanna, W.W. and Anand Kumar, K. (1992) Genetic variation among African pearl millet populations, in *Proceedings of the International Sorghum and Millets CRSP Conference*, Corpus Christi, Texas: INTSORMIL Lincoln, Nebraska, U.S.A., p. 263.

Ouendeba, B., Ejeta, G., Nyquist, W.E. *et al.* (1993) Heterosis and combining ability among African pearl millet landraces. *Crop Science*, **33**, 735–739.

Pande, S., Thakur, R.P., Karunakar, R.I. *et al.* (1994) Development of screening methods and identification of stable resistance to anthracnose in sorghum. *Field Crops Research*, **38**, 157–166.

Patil, F.B. and Jadhav, S.D. (1992) Correlation and path analysis in pearl millet times Napier hybrids. *Journal of Maharashtra Agricultural Universities*, **17** (2), 199.

Peacock, J.M., Soman, P., Jayachandran, R. *et al.* (1993) Effect of high surface soil temperature on survival in pearl millet. *Experimental Agriculture*, **29**, 215–225.

Phul, P.S., Athwal, D.S. and Gill, B.S. (1969) Genetics of grain colour in pearl millet. *Indian Journal of Genetics and Plant Breeding*, **29**, 438–445.

Pray, C.E. and Ribeiro, S. (1990) Government seed policy, the development of private seed industry, and the impact of private R&D in India. The Final Report of the Indian Seed Industry Project. New Brunswick, N.J.: Department of Agricultural Economics, Rutgers University.

Qi, X., Pittaway, T., Allouis, S. *et al.* (2000) Development of simple sequence repeats (SSRs) markers from small and large insert libraries in pearl millet, in *Abstracts, Plant and Animal Genome VIII Conference*, (San Diego, CA). Available online at: http://www.intl-pag.org/8/abstracts/ pag8875.html

Rachie, K.O. and Majmudar, J.V. (1980) *Pearl Millet*, Pennsylvania State University Press, University Park, Pennsylvania, USA.

Radhouane, L. (2007) Response of Tunisian autochthonous pearl millet (*Pennisetum glaucum* (L.) R. Br.) to drought stress induced by polyethylene glycol (PEG) 6000. *African Journal of Biotechnology*, **6**, 1102–110.

Rai, K.N. (1990) Development of high yielding dwarf composites of pearl millet. *Crop Improvement*, **17**, 96–103.

Rai, K.N. (1995) A new cytoplasmic-nuclear male sterility system in pearl millet. *Plant Breeding*, **114**, 445–447.

Rai, K.N. and Anand Kumar, K. (1994) Pearl millet improvement at ICRISAT – an update. *International Sorghum and Millets Newsletter*, **35**, 1–29.

Rai, K.N., Govindaraj, M. and Rao, A.S. (2012) Genetic enhancement of grain iron and zinc content in pearl millet. *Quality Assurance and Safety of Crops and Foods*, **4**, 119–125.

Rai, K.N., Murty, D.S., Andrews, D.J. and Bramel-Cox, P.J. (1999) Genetic enhancement of pearl millet and sorghum for the semi-arid tropics of asia and Africa. *Genome*, **42**, 617–628.

Rai, K.N. and Rao, A.S. (1995) Commercial feasibility of growing interpopulation hybrids in pearl millet. *International Sorghum and Millets Newsletter*, **36**, 49–50.

Rai, K.N. and Rao, A.S. (1996) A new CMS system and its restorers in pearl millet. In Proceedings of an International Crop Science Congress, held at New Delhi, India, November 17–24, 1996. Abstract P5-0018.

Rai, K.N., Virk, D.S., Harinarayana, G. and Rao, A.S. (1996) Stability of male-sterile sources and fertility restoration of their hybrids in pearl millet. *Plant Breeding*, **115**, 494–500.

Rooney, L.W. and McDonough, C.M. (1987). Food quality and consumer acceptance in pearl millet, in *Proceedings of the International Pearl Millet Workshop* (eds J.R. Witcombe and S.R. Beckerman), April 7–11, 1986, ICRISAT, Patancheru, pp. 43–61.

Serraj, R., Hash, C.T., Rivzi, S.M.H. *et al.* (2005) Recent advances in marker-assisted selection for drought tolerance in pearl millet. *Plant Production Science*, **8**, 334–337.

Shankar, K.M., Ahluwalia, M. and Jain, S.K. (1963) The use of selection indices in the improvement of pearl millet population. *Indian Journal of Genetics and Plant Breeding*, **23**, 30–33.

Sharma, R., Upadhyaya, H.D., Manjunatha, S.V. *et al.* (2013) Pathogenic variation in the pearl millet blast pathogen *Magnaporthe grisea* and identification of resistance to diverse pathotypes. *Plant Disease*, **97**, 189–195.

Sharma, H.C., Agrawal, B.L., Abraham, C.V. *et al.* (1993) Identification and utilisation of resistance to sorghum midge, *Contarinia sorghicola*. Coq. *Crop Protection*, **12**, 343–350.

Sharma, H.C., Taneja, S.L., Leuschner, K. and Nwanze, K.F. (1991) Techniques to screen sorghum for resistance to insects. International Crops Research Institute for the Semi-arid Tropics (ICRISAT) Information Bulletin No. 32. ICRISAT, Patancheru, India.

Shukla, D. and Dua, R.P. (1983) Genetic divergence in pearl millet for fodder attributes. *Indian Journal of Agricultural Sciences*, **53**, 12–14.

Singh, B.B. (1974) Expected and realised response to selection in biparental and selfed populations of pearl millet. *Indian Journal of Genetics and Plant Breeding*, **34**, 405–410.

Singh, D., Singh, V. and Chandei, S.R.S. (1970) Determination of leaf area in bajra (*Pennisetum typhoides* Burm S & H). *Science and Culture*, **36**, 46–47.

Singh, D.P., Mishra, S.N., Singh, A.B. and Singh, S.P. (1967) Inheritance in pearl millet. *Indian Journal of Genetics and Plant Breeding*, **27**, 426–428.

Singh, F., Singh, R.K., Singh, R.M. and Singh, R.B. (1978) Genetic analysis of downy mildew (*Sclerospora graminicola*) resistance in pearl millet (*Pennisetum typhoides* (Burm) S&H). *Zeitschrift für Pflanzenzüchtung*, **81**, 54–59.

Singh, G. (2003) Development and nutritional evaluation of value added products from pearl millet (*Pennisetum glaucum*) [PhD thesis]. Hisar, Haryana, India: CCS Haryana Agricultural University.

Singh, P., Singh, U., Eggum, B.O. *et al.* (1987) Nutritional evaluation of high protein genotypes of pearl millet (*Pennisetum americanum* (L.) Leeke). *Journal of the Science of Food and Agriculture*, **38**, 41–48.

Singh, S.D. (1995) Downy mildew of pearl millet. *Plant Disease*, **79**, 545–550.

Singh, S.D. and Gopinath, R. (1985) A seedling inoculation technique for detecting downy mildew resistance in pearl millet. *Plant Disease*, **69**, 582–584.

Singh, S.D., King, S.B. and Werder, J. (1993) Downy mildew disease of pearl millet. Information Bulletin No. 37, ICRISAT, Patancheru, India.

Singh, S.D., Wilson, J.P., Navi, S.S. *et al.* (1997) Screening techniques and sources of resistance to downy mildew and rust in pearl millet. International Crops Research Institute for the Semi-arid Tropics (ICRISAT) Information Bulletin No. 48. ICRISAT, Patancheru, India.

Singh, P., Rai, K.N., Witcombe, J.R. and Andrews, D.J. (1988) Population breeding methods in pearl millet improvement (*Pennisetum americanum*). *Agronomia Tropical*, **43**, 185–193.

Singh, P., Singh, U., Eggum, B.O. *et al.* (1987) Nutritional evaluation of high protein genotypes of pearl millet (*Pennisetum americanum* (L.) Leeke). *Journal of the Science of Food and Agriculture*, **38**, 41–48.

Smith, H.F. (1936) A discriminant function for plant selection. *Annals of Eugenics*, **7**, 240–250.

Sokhi, S.S., Barrana, H.S. and Pannu, P.P.S. (1987) A note on the genetics of resistance in pearl millet against rust. *Indian Phytopathology*, **40**, 423–424.

Soman, P. and Peacock, J.M. (1985) A laboratory technique to screen seedling emergence of sorghum and pearl millet at high soil temperature. *Experimental Agriculture*, **21**, 335–341.

Squire, G.R. (1979) The response of the stomata of pearl millet (*Pennisetum typhoides* S and H) to atmospheric humidity. *Journal of Experimental Botany*, **30**, 925–933.

Squire, G.R., Marshall, B. and Ong, C.K. (1986) Development and growth of pearl millet (*Pennisetum typhoides*) in response to water supply and demand. *Experimental Agriculture*, **22**, 289–299.

Squire, G.R., Ong, C.K. and Montecito, J.L. (1987) Crop growth in semi-arid environments, in *Proceedings of the International Pearl Millet Workshop* (eds J.R. Witcombe and S.R. Beckerman), April 7–11, 1986, ICRISAT, Patancheru, pp. 219–231.

Subba Rao, M.V., Sujatha, D.M., Saideswara Rao, Y. and Manga, V. (1988) Chemotoxonomic characters in twelve species of the genus Pennisetum (poaceae) Proceedings Indian Academy of Sciences. *Plant science*, **98**, 11–112.

Sujata, V., Sivaramakrishnan, S., Rai, K.N. and Seetha, K. (1994) A new source of cytoplasmic male sterility in pearl millet: RFLP analysis of mitochondrial DNA. *Genome*, **37**, 482–486.

Sundararaj, D.D. and Thulasidas, G. (1980) *Botany of Field Crops*, The MacMillan Company India Ltd., New Delhi, India, p. 508.

Suthamathi, P. and Stephen Dorairaj, M. (1995a) Variability, heritability and genetic advance in fodder pearl millet. *Madras Agricultural Journal*, **82**, 238–240.

Suthamathi, P. and Stephen Dorairaj, M. (1995b) Analysis of genetic divergence in fodder pearl millet. *Madras Agricultural Journal*, **82**, 241–243.

Talukdar, B.S., Singh, S.D. and Prakash Babu, P.P. (1996) Prospects of topcross hybrids in increasing and stabilizing grain yield in pearl millet. *Crop Improvement*, **23**, 147–150.

Thakur, R.P., Sharma, R., Rai, K.N. *et al.* (2009) Screening techniques and resistant sources for foliar blast in pearl millet. *Journal of SAT Agricultural Research*, **7**, 1–5.

Thakur, R.P., Singh, S.D. and King, S.B. (1988) Registration of four populations of pearl millet germplasm with multiple disease resistance. *Crop Science*, **28**, 381–382.

Thakur, R.P., King, S.B., Rai, K.N. and Rao, V.P. (1992) Identification and utilization of smut resistance in pearl millet. International Crops Research Institute for the Semi-arid Tropics (ICRISAT) Research Bulletin No. 16. ICRISAT, Patancheru, India.

Thakur, R.P., Rai, K.N., King, S.B. and Rao, V.P. (1993) Identification and utilization of ergot resistance in pearl millet. International Crops Research Institute for the Semi-arid Tropics (ICRISAT) Research Bulletin No. 17. ICRISAT, Patancheru, India.

Thakur, R.P., Rao, V.P., Amruthesh, K.N. *et al.* (2003) Field surveys of pearl millet downy mildew: Effects of hybrids, fungicide, and cropping sequence. *Journal of Mycology and Plant Pathology*, **33**, 387–394.

Tostain, S. (1992) Enzyme diversity in pearl millet (*Pennisetum glaucum* L.) 3. Wild millet. *Theoretical and Applied Genetics*, **83**, 733–742.

Tyagi, C.S. and Singh, I. (1989) Genetics of downy mildew resistance in pearl millet. *Bhartiya Krishi Anusandhan Patrika*, **4**, 24–30.

Upadhyay, M.K. and Murty, B.R. (1970) Genetic divergence in relation to geographical distribution in pearl millet. *Indian Journal of Genetics and Plant Breeding*, **30**, 704–715.

Upadhyay, M.K. and Murty, B.R. (1971) Genetic diversity and combining ability in pearl millet. *Indian Journal of Genetics and Plant Breeding*, **31**, 63–71.

Upadhyaya, H.D., Reddy, K.N. and Gowda, C.L.L. (2007) Pearl millet germplasm at ICRISAT genebank – status and impact. *SAT eJournal*, **3**, 1–5.

Upadhyaya, H.D., Reddy, K.N., Sube, S. *et al.* (2014) Diversity and Gaps in *Pennisetum glaucum* subsp. *monodii* (Maire) Br. Germplasm Conserved at the ICRISAT Genebank. *Plant Genetic Resources: Characterization and Utilization*, **12** (2), 226–235.

Vadez, V., Kashiwagi, J., Krishnamurthy, L. *et al.* (2005) Recent advances in drought research at ICRISAT: using root trait sandrd29a: DREB1A to increase water use and water use efficiency in drought-prone areas, in *Abstract P5.88 in: Abstracts of Lectures and Posters, Inter drought II: The 2nd International Conference on Integrated Approaches to Sustain and Improve Plant Production Under Drought Stress*, (Rome, Italy), September 24–28, 2005. Available online at: http://www.plantstress.com/ID2/Abstract%20book%20updated.pdf

Van den Abeele, M. and Vandenput, R. (1956) *Les principales cultures du Congo Belge*, Ministère des colonies, Bruxelles, pp. 179–183.

Vavilov, N.I. (1949/1950) The origin, variation, immunity and breeding of cultivated plants. *Chronica Botanica*, **13**, 113–120.

Velu, G., Rai, K.N., Muralidharan, V. *et al.* (2011) Gene effects and heterosis for grain iron and zinc density in pearl millet (*Pennisetum glaucum* (L.) R. Br.). *Euphytica*, **180**, 251–259.

Virk, D.S. (1988) Biometrical analysis in pearl millet – a review. *Crop Improvement*, **15**, 1–29.

White, R.O. and Cooper, J.P. (1959) *Les Graminées en Agriculture*, FAO, Rome, pp. 418–419.

Williams, R.J., Singh, S.D. and Pawar, M.N. (1981) An improved field screening technique for downy mildew resistance in pearl millet. *Plant Disease*, **65**, 239–241.

Wilson, J.P., Wells, H.D. and Burton, G.W. (1989) Inheritance of resistance to *Pyricularia grisea* in pearl millet accessions from Burkina Faso and inbred Tift 85DB. *Journal of Heredity*, **80**, 499–501.

Winkel, T. and Do, F. (1992) Caracteres morphologiques et physiologiques de resistance du mil. [*Pennisetum glaucum* (L.) R. Br.] a la secheresse. *Agronomia Tropical*, **46**, 330–351.

Winkel, T., Renno, J.N. and Payne, W. (1997) Effect of timing of water deficit on growth, phenology and yield of pearl millet. [*Pennisetum glaucum* (L.) R. Br.] growth in Sahelian conditions. *Journal of Experimental Botany*, **48**, 1001–1009.

Yadav, R.P. (1974) Inheritance for smut resistance in pearl millet. *Agra University Journal of Research Science*, **23**, 37–40.

Yadav, O.P. (1994a) Genetic divergence in pearl millet accessions of Indian and exotic origin. *Indian Journal of Genetics and Plant Breeding*, **54**, 89–93.

Yadav, O.P. (1994b) Influence of A1 cytoplasm in pearl millet. *Plant Breeding (Abstracts)*, **64**, 1375–1379.

Yadav, O.P. (1996) Downy mildew incidence of pearl millet hybrids with different male-sterility inducing cytoplasms. *Theoretical and Applied Genetics*, **92**, 278–280.

Yadav, O.P. and Rai, K.N. (2013) Genetic improvement of pearl millet in India. *Agricultural Research*, **2(4)**: 275–292. doi: 10.1007/s40003-013-0089-z

Yadav, O.P., Rai, K.N. and Gupta, S.K. (2013) Chapter 12: Pearl millet: Genetic improvement for tolerance to abiotic stresses, in *Improving Crop Productivity in Sustainable Agriculture* (eds N. Tuteja, S.S. Gill and R. Tuteja), Wiley-Blackwell.

Yadav, O.P., Rajpurohit, B.S., Kherwa, G.R. and Kumar, A. (2012) Prospects of enhancing pearl millet (*Pennisetum glaucum*) productivity under drought environments of north-western India through hybrids. *Indian Journal of Genetics and Plant Breeding*, **72**, 25–30.

Yadav, O.P., Weltzien-Rattunde, E., Bidinger, F.R. and Mahalakshmi, V. (2000) Heterosis in landrace-based topcross hybrids of pearl millet across arid environments. *Euphytica*, **112**, 285–295.

Yadav, R.S., Bidinger, F.R., Hash, C.T. *et al*. (2003) Mapping and characterization of QTL × E interactions for traits determining grain and stover yield in pearl millet. *Theoretical and Applied Genetics*, **106**, 512–520.

Yadav, R.S., Hash, C.T., Cavan, G.P. *et al*. (2002b) Quantitative trait loci associated with traits determining grain and stover yield in pearl millet under terminal drought stress conditions. *Theoretical and Applied Genetics*, **104**, 67–83.

3

Improvement in Finger Millet: Status and Future Prospects

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3.1 Introduction

Finger millet, *Eleusine coracana* (L.) Gaertn., is the fourth most important millet across the world, next to sorghum, pearl millet and foxtail millet. In Asia, the crop is grown in India, Myanmar, Sri Lanka, Nepal, China and Japan; in Africa, it is grown in Uganda, Kenya, Tanzania, Ethiopia, Eritrea, Rwanda, Zaire and Somalia (Upadhyaya *et al.*, 2010). The grains of finger millet are rich in quality protein, having high amounts of tryptophan, cystine and methionine, fibre (10–15% dietary fibre), phytochemicals, calcium and other minerals (Upadhyaya *et al.*, 2010; Chandrashekhar *et al.*, 2012). Finger millet is comparatively resistant to storage insect pests, which makes the crop an important source of food during famine, as the grains can be stored as long as 50 years without much loss due to deterioration (Ayyangar, 1932). Traditionally, the grains are consumed in the form of unleavened bread (*rotis*), thin porridge (*ambali*) and thick porridge/pudding (dumpling). However, recently, upscaled value-added products such as biscuits, *vermicelli*, *pasta* and multigrain flour have become available, especially in the urban market. In addition to grain, the straw after the harvest of grains is a source of nutritional fodder for animals. Considering other small millets such as foxtail millet, little millet, proso millet, kodo millet and barnyard millet, progress is more pronounced in finger millet, resulting in the highest productivity across millet crops. A number of cultivars are developed and released especially in India that are suited for cultivation across a range of environmental conditions. The chapter discusses the various aspects of crop improvement and future prospects in detail.

3.2 Area Production and Productivity

The important finger-millet-growing countries in Eastern and Southern Africa are the sub-humid regions of Ethiopia, Kenya, Tanzania, Zambia, Malawi, Zaire, Uganda and Zimbabwe. Similarly, in South Asia, the crop is widely cultivated in India and extended to certain regions in Nepal, Bhutan and Sri Lanka. It is also reported to be grown in some regions of China and Japan. In India, the major proportion of the crop is in Karnataka (60%), followed by Uttarakhand, Orissa, Maharashtra, Andhra Pradesh and Tamil Nadu.

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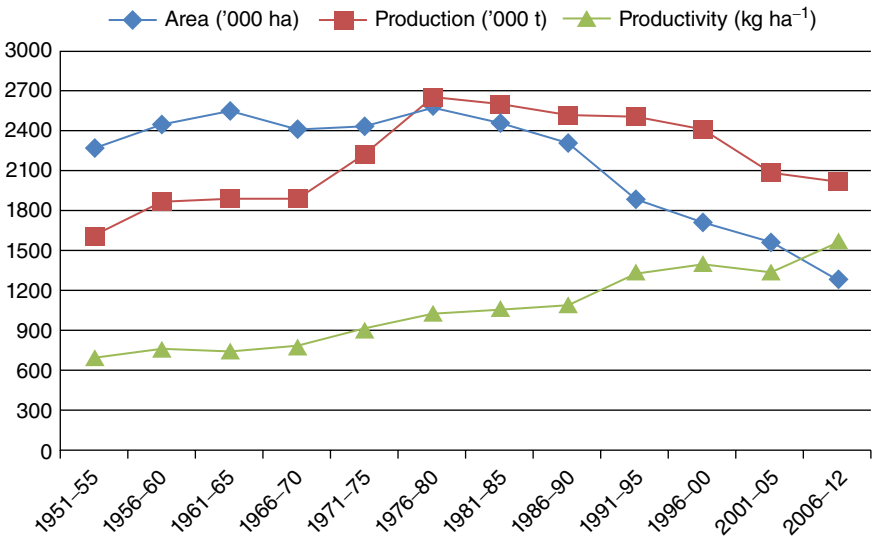

Figure 3.1 Quinquennial area, production and productivity of finger millet in India.
Source: Krishnegowda *et al.*, 2015. (*See color plate section for the color representation of this figure.*)

Globally, finger millet is estimated to be cultivated on an area of 4–4.5 million hectares, with a production of about 4.5 million tonnes (Guarino, 2012). India and Africa together constitute 70–80% of the global finger millet production. In India, the crop is grown under a wide range of environmental conditions – from sea level to the hilly regions of the Himalayas, but it thrives best on well-drained, loamy type of soils. In India, the production was about 1.6 million t during 1951–1955 (Figure 3.1). The production gradually increased and reached about 2.2 million t during 1971–1975. During 1976–1980, the highest production of 2.6 million t was recorded, and this was due to the increase in area during this period. The production gradually declined after 1980 and reached around 2 million t during 2011–2012 (Krishnegowda *et al.*, 2015). Among the finger-millet-growing states in India, the highest production is obtained from Karnataka (1.2 million t), followed by Tamil Nadu (0.224 million t), Uttarakhand (0.174 million t), Maharashtra (0.138 t) and Andhra Pradesh (0.040 million t) during 2011–2012.

Improvement of productivity in African countries is not widely reported. However in India, it showed continuous improvement. The productivity in India was 704 kg ha^{-1} during 1951–1955 which improved gradually and reached 1021 kg ha^{-1} during 1976–1980. The productivity further increased to 1641 kg ha^{-1} during 2011–2012. Over the years, the yield has increased more than two-folds from 704 kg ha^{-1} (1951–1955) to 1641 kg ha^{-1} (2011–2012) at the national level (Krishnegowda *et al.*, 2015). This increase in productivity is contributed by cultivation of the improved varieties, especially those developed by crossing the Indian types with the exotic types mainly from the African genepool, which was otherwise isolated in Indian breeding programme. GPU 28, a high-yielding and blast-resistant variety has made a major contribution to the yield improvement in Karnataka.

3.3 Origin and Domestication

Finger millet is an annual crop that grows to a height of 30–150 cms and generally matures in 75–140 days. Domestication of the crop started around 5000 years ago in

Western Uganda and Ethiopian highlands and the crop reached the Western Ghats of India around 3000 BC (Hilu *et al.*, 1979). The cultivated *E. coracana* is a tetraploid ($2n = 4x = 36$) and it is believed that *E. coracana* originated from its related species *E. indica*. Cytological studies show that *E. indica* has contributed one of the genome (AA) to the cultivated genome (AABB). *E. africana* ($2n = 36$) which is also a tetraploid, resembles *E. coracana* in morphological characteristics. Both *E. coracana* and *E. africana* are genetically related and the hybridisation occurs between them naturally suggesting that *E. coracana* possibly originated from *E. africana* through selection and further mutation which resulted in larger grains (Channaveeraiah and Hiremath, 1974; Hilu and de Wet, 1976). The place of origin of *E. coracana* has remained controversial due to its high diversity both in Africa and India and also its morphological similarity to both *E. indica* and *E. africana*. However, Africa is the most widely accepted as the primary centre and India as the secondary centre of origin of the crop (Hilu and de Wet, 1976). Together from the morphological and cytogenetical observations and distribution it is revealed that *E. coracana subsp. africana* is wild finger millet and is distributed widely in East African highlands. It was believed that finger millet originated from the East African highlands and was subsequently introduced into India (Hilu and de Wet, 1976). The primary wild relatives of this crop are *E. africana*, *E. indica* and *E. kigeziensis*. The secondary wild relatives are *E. tristachya*, *E. floccifolia* and *E. intermedia* and tertiary wild relatives are *E. jaegeri*, *E. multiflora* and *E. compressa*. The species *coracana* has four races (*elongata*, *plana*, *compacta* and *vulgaris*). Race *elongata* has three subraces (*laxa*, *reclusa* and *sparsa*), plana race has three subraces (*seriata*, *confundere* and *grandigluma*) and race *vulgaris* has four sub-races *liliaceae*, *stellata*, *incurvata* and *digitata*). Race *compacta* does not have any sub-race (Guarino, 2012).

3.4 Botanical Features and Breeding Behaviour

3.4.1 Botanical Classification

Kingdom	: *Plantae*
Subkingdom	: *Tracheobionta*
Superdivision	: *Spermatophyta*
Division	: *Magnoliophyta*
Class	: *Liliopsida*
Subclass	: *Commelinidae*
Order	: *Cyperales*
Family	: *Poaceae*
Genus	: *Eleusine* Gaertn
Species	: *Eleusine coracana* (L.) Gaertn.

3.4.2 Botanical Description

Finger millet has an annual or perennial growth habit. The culms are compressed and green in colour. The nodes of the culms are glabrous and the internodes are solid or

hollow. The leaf sheaths are notably flattened and keeled. The leaf blades are narrow, linear, flat or folded and with no cross-veination, persistent, rolled in bud or once-folded in bud. The ligule is a fringed membrane. The inflorescence comprises of digitally arranged spikes in a terminal umbel form, open, digitate, terminal whorl bears around 2–12 spikes. Spikelets are at adaxial, strongly compressed laterally, curved into two rows on the outer sides of the spike. Each spikelet has around 4–6 flowers and consists of approximately 1500–3000 flowers per earhead. Lemma is pointed, without awns and hairs and are three-nerved. Palea is also awnless and two-nerved. The lodicules are two in number, joined or free and fleshy. There are two glumes and both are of almost equal in size. Lower glume is single-nerved while the upper glume is three- to five-nerved. The fully matured flower consists of three stamens, short anthers and a longer filament. Ovary is glabrous and styles are free to their bases. Stigmas are branched and are brown or white in colour. The grains are globose in shape and the plant possesses adventitious root system.

3.4.3 Floral Biology and Breeding Behaviour

Finger millet is a highly self-pollinated crop. Its inflorescence has been described by Coleman (1920) and Ayyangar (1932) as terminal whorl having 2–10, with an average of five or six fingers arranged giving the appearance of birds foot. Subsequently the floral biology has been described in detail by Rachie and Peters (1977) are as discussed. The inflorescence consists of a whorl with 2–11 digitate, slightly curved or straight spikes or fingers (Gupta *et al*., 2011). The inflorescence rests on a peduncle from which 4–10 spikes spread out in a form of a whorl resembling fingers, with an odd one little lower known as thumb. Each spikelet consists of 3–13 florets. Florets are hermaphrodite having boat-shaped lemma, a small palea with two lodicules, three stamens with long filaments and short oblong anthers and an ovary with which two styles with plumose stigma. The terminal floret is sterile. Anthesis and pollination in finger millet were analysed by Ayyangar (1932), Ayyangar and Wariar (1934), Chavan *et al*. (1955) and Chavan and Shendge (1957). Ayyangar and his group observed that the complete emergence of the inflorescence requires about 10 days. Anthesis commences from top spikelets and proceeds downwards in the spikes and occurs between 0100 and 0500 hours. (Gupta *et al*., 2011). The opening of the florets starts from bottom to top within the spikelets. Maximum number of flowers open on the third day. Flower opening varies from place to place depending on the temperature and humidity. Flowering takes place simultaneously in all fingers. Pollen viability is very short, 10–15 min and stigma receptivity is up to 5 h (Dodake and Dhonukshe, 1998). Complete emergence of the inflorescence takes 7–8 days (Gupta *et al.*, 2011). Self-pollination is the rule because of the short period of the anthesis. Cross-fertilisation by wind or insects is reported to contribute less than 1% (Seetharam, 1998).

3.5 Emasculation and Pollination Techniques

3.5.1 Hand Emasculation

In millet crops such as sorghum, hand emasculation is practised by the forceful removal of the immature anthers using forceps or needles from the florets, which are likely to open the next day morning. However, such methods are difficult in finger millet and other small millets due to the tiny nature of the florets. Temperature- and humidity-induced flower opening is reported to have been used where the fingers are covered

with a polythene bag after spraying the fingers with cold water and then fixing them airtight. The glumes slowly open and the premature anthers get exposed and thereafter the three immature anthers are removed carefully without injuring the stigma (Personal communication with Sathish, R.G., All India Coordinated Small Millets Improvement Project (AICSMIP), Bangalore. The emasculated fingers are once again sprinkled with cold water to prevent drying of the pistil. For pollination of the desired male parent, the finger of male parents is tied loosely to the emasculated seed parent and covered using a butter paper bag. For successful crossing, genotypes with pigmentation in the nodes are to be used as male parent (Gupta, 2006) for identification of true F_1s.

3.5.2 Hot-water Treatment

Numerous investigators have used the hot-water treatment for emasculation in order to overcome the problem of manually removing the anthers from the florets. The florets which are likely to flower in the next few (2–3) days are selected, and the fingers are immersed in hot water of desired temperature. The treatments of 52 °C for 2 min (Raj *et al.*, 1964), 48 °C for 5 minutes and 47 °C for 10 min were reported to be effective in inducing maximum amount of pollen sterility and without affecting the seed set per cent. However, this procedure requires standardisation depending on temperature and climatic conditions of a particular environment.

3.5.3 Gametocide-induced Male Sterility

Male sterility can also be induced through the use of chemicals, which are commonly known as male gametocide. Chemicals such as maleic hydrazide, giberellic acid and ethrel with various concentrations are reported to cause male sterility in different cereal crops. In finger millet, the application of GA3 at 1600 ppm at fifth leaf stage, in which, the juncture of top five leaf is invisible is applied through capillary tube for creation of male sterility (personal communication with Sathish, R.G., AICSMIP, Bangalore). However this technique requires standardisation for effectively inducing male sterility.

3.5.4 Use of Genetic Male Sterility

This has been used as one of the techniques for enhancing hybridisation and creation of variability at AICSMIP, University of Agricultural Sciences, Bangalore. A GMS line was developed, INFM 95001, which was jointly developed by ICRISAT at Matapos, Zimbabwe; Kano, Nigeria; and the Department of Agronomy, University of Nebraska, USA (Gupta *et al.*, 1997). Subsequently, a new partial sterile line was isolated from GPU 28 through EMS mutagenesis at AICSMIP Bangalore to circumvent the difficulties in the maintenance of genetic male sterility. Further, the investigations on breeding behaviour revealed partial nature of sterility and are reportedly controlled by a single recessive gene. The results of the controlled out-crossing were reported to produce high per cent of the F_1 hybrids.

3.6 Genetics of Traits

Genetics for various plant and grain characters was initiated by Ayyangar and his coworkers in as early as the 1930s. They observed two basic kinds of plant pigmentation (green and purple) of pericarp with different shades and intensities. Ayyangar

et al. (1931) reported light green and normal green in pericarp colour. The light green has less number of chloroplasts (9) while the normal green pericarp had higher number of chloroplasts (14). Inheritance studies revealed that normal-green to be governed by a single dominant factor/gene and associated with pale orange yellow dry anther mass while the light-green pericarp is associated with ivory yellow anther mass. Purple pigmentation gave a characteristic purple colour to the earhead during flowering stage. Purple pigmentation was considered to be dominant over unpigmented green conditions (Ayyangar and Krishnaswami, 1931; Shanthappa, 1980) Similar results were also obtained by Ravikumar and Seetharam (1990) and a pleiotropic effect of the pigmentation gene (pigmentation of the leaf junction, seedling and panicle during flowering was observed. Shanthakumar and Gowda (1997) reported that the pigmentation was controlled by two duplicate dominant genes. Presence of either one or both the genes in dominant state results in purple pigmentation. Segregation of grain colour showed similar inheritance pattern as that of plant pigmentation. Brown grain colour is predominant in finger millet and is restricted to the seed coat. Brown colour of grain colour was dominant over white. Joint segregation study revealed presence of pleiotropy or tight linkage between the genes for pigmentation and grain colour.

Ayyangar and coworkers recognised two broad panicle shapes, (i) the spikes of the inflorescence curved and (ii) the spikes of the inflorescence open. A factor 'Q' is governing the close packing of fingers/spikelets of the rachis and is present in the curved and not in open panicles. The curved types are sub-classified into in-curved and top-curved. In in-curved, the whole fingers curve in while in the latter the fingers are longer and only the tip portion curves-in. Another factor designated as 'E', determines the elongation of the rachis. The factor E is also present in the open-panicle types and is sub-grouped into two groups as long-opens and the short-opens based on its presence of absence. The fingers/spikes of the in-curved types are short, curve in and do not possess a central hollow giving the earhead an obovate appearance. In the top-curved, the fingers are longer and as the result they possess a hollow shape in the centre of the panicle. In the open-panicle types, the fingers are longer and give a funnel-shape appearance. When dry, they curve out slightly and, therefore, these characters can be best studied in the milky stage. The length of the fingers range from 7 to 12 cm in short-opens while in long-opens it ranges between 10 and 19 cm. The factors Q and E are independent of the factors for plant pigmentation (Ayyangar 1932; Ayyangar *et al.*, 1932). A new head type called 'fist-like', with fingers in-curved very compactly was described by Ayyangar (1932), Ayyangar and Rao (1932) and Ayyangar *et al.* (1933). Two E factors act in the presence the Q factor, resulting in the curving of the fingers through increased density of the spikelets. When none of the E factors is present, the finger length is very short, and in the presence of Q, they form fist-like structure. An E factor alone gives the short fingers as previously described, while both together give long fingers with the corresponding top-curved and in-curved forms when factor Q is present. All the three factors were found independent of the various factors associated with plant, grain and unripe pericarp colour. For yield and related traits, Krishnappa *et al.* (2009) reported that both additive and dominant genetic variation with preponderance of the dominant gene action in the expression of the day's 50% flowering, plant height and dry-fodder weight per plant while only dominant genetic variation was responsible for the expression of tiller per plant, fingers per ear and green weight/plant.

3.7. Gene Pool of *Eleusine coracana*

Eleusine coracana is highly variable in their centres of origin in Africa and the Indian sub-continent. The species *E. coracana* consists of sub-species *africana* and *coracana*. The sub-species *africana* is a wild type and consists of *africana* and *spontanea* races. The sub-species *coracana* is a cultivated type and is further classified into four races namely *elongata*, *plana*, *compacta* and *vulgaris* based on inflorescence morphology (Prasada Rao *et al.*, 1993). The classification of the races and sub-races of *E. coracana* is represented in Figure 3.2.

3.7.1 Sub-species *Africana*

This is found along the highlands of East Africa and the grasslands of the Southern Africa. It is a tufted annual having geniculately ascending culms and branching emerges at the lower nodes. Leaf blades are about 36 cm in length and have a width of nearly 10 mm. The flowering culms are about 135 cm tall, inflorescence branch is long and range between 8 and 17 cm with a width of about 5 mm. The spikelets are arranged in two rows on one side of the rachis. Each spikelet has four to nine flowers and about 5–8 mm long. Glumes are shorter than spikelet, lanceolate–oblong, rarely more than 5 mm and narrow-winged along the keel (Bharathi, 2011).

3.7.2 Subspecies *Coracana*

The sub-species *coracana* includes all the cultivated finger millet types. Plants are annual, tufted, erect or with geniculately ascending culms with a height of about 165 cm. The subspecies coracana includes four races and sub-races. The morphological characteristics of the each of the sub-races are discussed below (Bharathi, 2011).

3.7.2.1 Race *Elongata*

This race is morphologically the most distinct of the four races (Prasada Rao *et al.*, 1993). It is characterised by long and slender inflorescence, 10–24-cm long branches, arranged digitately, spikes spreading and curved outward during maturity. The sub-race *laxa* has long and open fingers and the spikelets are arranged in narrow rows on the inflorescence branches, resembling the wild race *africana*. The sub-race *reclusa* has short, open fingers, and the spikelets are arranged in clusters on the inflorescence branch with naked space between them.

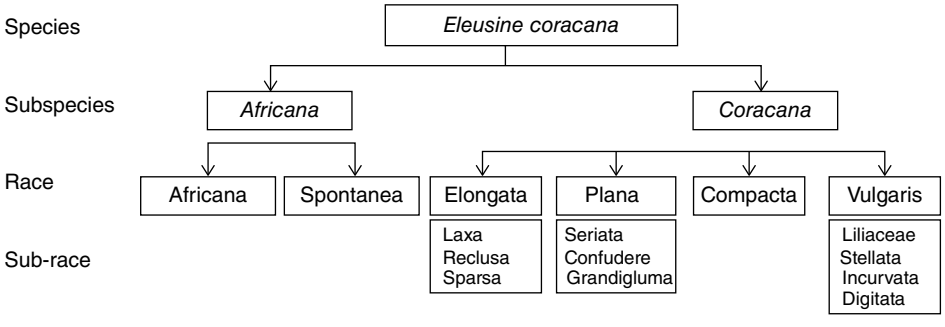

Figure 3.2 Race and sub-races of *Eluesine coracana.*

3.7.2.2 Race *Plana*

This is characterised by 8–15-cm large spikelets arranged in two or more rows along the rachis giving the inflorescence branch a flat ribbon-like appearance. In the sub-race *seriata*, the spikelets are arranged serially, giving a ribbon-like inflorescence, and in sub-race *confundere*, the fertile florets are numerous and surround the rachis at maturity, giving a compact look to the panicle. The *grandigluma* sub-race is characterised by long, pointed glumes, which are longer than the spikelets.

3.7.2.3 Race *Vulgaris*

This is commonly found in Africa and Asia. It is characterised by four to eight florets in a spikelet, giving a semi-compact appearance and generally with the tip in-curved at maturity (Guarino, 2012). The inflorescence fingers are reflexed in sub-race *liliaceae*, twisted in the sub-race *stellata*, in-curved in the sub-race *incurvata* giving the appearance of fist structure and top-curved in sub-race *digitata.*

3.7.2.4 Race *Compacta*

The members of this race are generally referred to as *cockscomb finger millet* in both Africa and Asia. Spikelets are composed of nine or more number of florets and the inflorescence axis is divided at the base ascending and in-curved at the top to give large fist-like appearance.

Both the wild (sub-species *africana*) and the cultivated finger millets (sub-species *coracana*) are important from the point of germplasm collection, conservation and utilisation since they form the primary gene pool. The sub-species *africana* occasionally crosses with the sub-species *coracana* to produce fully fertile hybrids. Derivatives of such crosses are aggressive colonisers and are grouped under the race *spontanea* (De Wet *et al*., 1984). Wild finger millet is native to Africa and is believed to have migrated to warmer parts of Asia and America. The diploid wild species *E. indica*, *E. floccifolia* and *E. tristachya* are believed to have formed the secondary gene pool while the species *E. intermedia*, *E. gaegeri*, *E. kigeziensis*, *E. multiflora* and *E. semisterlis* (*E. compressa*) form the tertiary gene pool (Guarino, 2012).

3.8. Germplasm and Genetic Diversity

Gene bank assumes a greater role and serves as reservoir of diversity and source of alleles for the genetic enhancement of crop plants. The details of the germplasm conservation in various countries have been described by Guarino (2012). In India, the National Active Germplasm Collection Site (NAGS) located at All India Coordinated Small Millets Improvement Project (AICSMIP), Bangalore, made efforts to assemble a large collection of germplasm at the global level, with a total of 7070 germplasm. Similarly, the National Bureau of Plant Genetic Resources (NBPGR) based at New Delhi, India, maintains about 10507 accessions of finger millet under long-term conservation. Most of these collections are of native origin with about 117 accessions of exotic origin. These Indian collections also include six wild relatives, 154 improved varieties and 64 breeding/research materials. The global-in-trust collections managed by ICRISAT, Patancheru, India, maintains a total of 5957 accessions, of which 4585 accessions are of non-Indian or exotic origin, comprising of 105 wild species, 5665 landraces, 137 improved cultivars and 50 breeding/research materials. The Agricultural Research

Station of the USDA in Griffin, Georgia, maintains 766 finger millet accessions, of which 17 are wild relatives (*E. floccifolia*, *E. indica*, *E. jaegeri*, *E. multiflora* and *E.tristachya*). These collections are from 11 countries which include Ethiopia, India, Kenya, Nepal, Pakistan, South Africa, Tanzania, Uganda, Zaire, Zambia and Zimbabwe. The other South Asian countries holding major collections include Nepal (877), Sri Lanka (393) and Bhutan (84). Among the African regions, the collections were reported from Kenya (1902), Zimbabwe (1158), Uganda (1155), Zambia (497), Tanzania (293), Malawi (145), Eritrea (120), Burundi (113), Ethiopia (71), Nigeria (20) and South Africa (17). China (300), the Russian Federation (110) and Vietnam (52) are also reported to conserve finger millet collections.

For genetic conservation and subsequently for its utilisation of the germplasm, it is imperative that we know the diversity existing among the germplasm collections. Compared to other coarse cereals, finger millet has not been extensively investigated for understanding the diversity in germplasm collections. Indian and African germplasm are highly diverse, and very few systematic studies have been conducted to compare the diversity among the accessions available in the gene banks. In general, the Indian germplasm are reported to be diverse for grain and dry-stover yield. Early-maturing varieties combining high grain yield, quality and stover yield are ideally preferred by farmers. The African germplasm exhibited larger variation for tallness, stout plant stature, long narrow finger, higher number of spikelets, poor threshability, late maturity and poor harvest index. The African germplasm are said to possess higher level of resistance to blast, the most devastating disease in finger millet (Kiran Babu *et al.*, 2013).

For the effective utilisation of the germplasm for genetic improvement programme, Upadhyaya *et al.* (2006) established a core collection of 622 genotypes representing geographical regions and biological races from the total set of collection. The African (58.7%) and Asian (35.8%) collections were predominant while those from America and Europe were represented by 0.8 and 1.1%, respectively. The cultivated sub-species *coracana* occupied 97.4% of the core while African accessions represented only 2.6%. Among the *coracana* sub-species, race *vulgaris* was predominant (62.5%), followed by *plana* (16.8%), *compacta* (12.4%) and *elongata* (8.3%). The core collections were evaluated for 15 quantitative and five qualitative traits, and a mini-core set of 80 accessions was constituted. Wide variability was reported among the mini-core collections for economically important traits such as days to flowering (51.24–93.73), plant height (72.66–113.31 cm), length of longest finger (49.79–139.73 mm), fingers per ear (6.13–9.41) and grain yield (691–2430 kg ha^{-1}). Chandrashekhar *et al.* (2012) reported a core collection of 77 germplasm constituted from a set of 1000 accessions of finger millet belonging to both India and Africa using morpho-agronomic data on 11 quantitative and 12 qualitative characters. The same study indicated that the characters plant height, finger length, number of productive tillers per plant, days to 50% flowering, days to maturity and ear weight per plant could be used as indirect selection for high grain yield in finger millet. The phenotypic variability of finger millet was reported by several researchers (Prabhakar and Prasad, 1983; Goswami and Asthana, 1984; Abraham *et al.*, 1989; Verma, 1989; Naik *et al.*, 1993; Mahto *et al.*, 2000; Anantharaju, 2001; Upadhyaya *et al.*, 2011). The range and pattern of variations in leaf sheath, plant height, maturity and ear morphology in 541 Indian collections was reported by Kempanna and Govindu (1969). Hussaini (1973) reported the diversity of 640 germplasm lines from the world collection and found highly significant differences among the germplasm lines for the 18 vegetative characters. The variability pattern of 1064

accessions from diverse geographic origins and reported wide variability among the accessions was reported by Mallana *et al.* (1978). Bedis *et al.* (2006) reported a large variability among the germplasm studied for flowering, maturity, ear length, finger number, fodder and grain yield. The diversity in 909 accessions introduced from the southern and eastern African regions from ICRISAT gene bank was reported by Upadhyaya *et al*. (2007) who observed large variability for plant pigmentation, growth characters, flowering, plant height and inflorescence length and width and grain colour. Their study also characterised the variability among different finger millet races. Daba and Keneni (2010) reported little or low effect of geographical origin on the pattern of diversity of native and exotic collections in Ethiopia. Their study revealed that biomass, earweight and grain weight contributed more towards the observed diversity. Mnyenyembe and Gupta (1998) reported high variability for flowering, plant height, finger length, finger width, number of fingers, productive tillers, panicle yield, grain yield and finger blast resistance based on their studies from 196 germplasm. Reddy *et al*. (2009) characterised 5949 germplasm for various qualitative and quantitative traits accessions, of which about 2000 were from Eastern Africa. Wide variability for flowering ranging from 50 to 120 days was observed and early flowering accessions were mostly from Burundi while late accessions were from Ethiopia. Among the eastern African accessions, green plant types were dominant over pigmented with dominance of erect growth habit. Majority of lodging-resistant accessions were from Uganda. The east African germplasm were dominated by race *vulgaris*. Efforts were made by different research centres to identify location-specific genotypes for different economic traits such as days to flowering, plant height, number of ears, ear length, productive tillers, days to maturity, grain yield, grain quality and 1000 grain weight. The promising accessions for various economic traits are given in Table 3.1. Efforts were also made to study the correlation among grain yield and quality parameters. Krishnasastry *et al*. (1982) reported that high dry matter production and higher ear weight were desirable plant characteristics for selection of high-yielding genotypes for rain-fed conditions.

3.9. Varietal Improvement in India

Various breeding methods such as mass selection, pure-line selection, recombination breeding and mutation breeding are widely approached for the genetic improvement in finger millet. Mass selection has been extensively used for purification of the cultivars (landraces) and multiplication of varieties bred by pure-line or pedigree breeding. Mass selection resulted in a marginal increase in the performance of the farmer's varieties such as *Gidda Ragi*, *Hullubele* of Karnataka, *Saluchodi* of Andhra Pradesh, *Udumalpet ragi* and *Guddapah Rajampet Ragi* of Tamil Nadu and *Murky* and *Nangkatna* of Sikkim. Pure-line selection has also been widely practised in finger millet improvement. Single plants were selected from landraces (germplasm) and improved farmer's varieties and the superior progenies mostly for earliness, pest and disease resistance and grain yield were tested under multi-locational trials and released as varieties. Pure-line selection resulted in the development and release of 41 varieties of finger millet. The varietal developments have been discussed in detail by Harinarayana (1986).

Progress through hybridisation has received greater attention in finger millet. Until the 1950s, the finger millet genetic improvement revolved around the locally adapted

Table 3.1 Promising genotypes for economic traits in finger millet.

Target trait	Details of the accessions	Source
Early maturity	lE 2828, lE 2830, IE 2984, IE 2957, 1E 2832 and IE 2838	NBPGR Report, 1986
Drought tolerance	GE 208, GE 496, GE 596, GE 1855, GE 4434, GE 4730, GE 4976	AICSMIP, UAS, Bangalore
High temperature tolerance (>35 °C)	GE 4, GE 99, GE 128, GE 145, GE 909, GE 1013, GE1028, GE 1274, GE 1815, GE 2370, GE 2911, GE 3303, GE 3265,GE 3266, GE 3885 GPU 26, L-5, PES 110, Chilika, KMR 301, Poorna	AICSMIP, UAS, Bangalore
Grain calcium content (>450 mg kg^{-1})	IE 4476, IE 2030, IE 6546, IE 4708, IE 2568	Upadhyaya *et al.*, 2011
Grain iron content (>40 mg kg^{-1})	IE 4708, IE 2921, IE 4709, IE 588, IE 5736, IE 4476	Upadhyaya *et al.*, 2011
Grain zinc content (>24 mg kg^{-1})	IE 3120, IE 7508	Upadhyaya *et al.*, 2011
Grain protein content (10%)	IE 6537, IE 0009, IE 4709	Upadhyaya *et al.*, 2011
Blast resistance	GE 1559 (IE 990), GE 569 (IE 339), GE 1330 (P228), GE 4440, GE 4449, GE 669 (IE 1012), GE 1356 (P282), GE 1026 (HR 23-8-9), GE 5192 (IE 3655), GE 132 (IE 329), GE 145 (IE 293)	AICSMIP, UAS, Bangalore
Popping (>70%)	Co-10, Indaf 3, Kari kaddi ragi, PR 202, GPU 66, GN 4	AICSMIP, UAS, Bangalore
White seeded	GPU 71, VR 936, GE 728	AICSMIP, UAS, Bangalore
Diverse germplasm	IE 501, IE 741, IE 1335, IE2336, IE 2640, IE2790, IE2684, IE 2467, IE 2581, IE 2791, IE 2871, IE2860, IE 2933, IE3158, IE 3428	ICRISAT

lines by centres located in the states. Subsequent improvement was carried forward after the establishment of Project for Implementation of Regional Research on Cotton, Oilseeds and Millets (PIRRCOM) during late 1950s followed by the initiation of the All India Coordinated Millets Improvement Project during 1965. Germplasm of finger millet and other millets were assembled during 1960s. The exotic germplasm mainly from Africa was introduced to India during 1970s. The African germplasm had high vigour, large ears, more grain density and thick robust stems with broad dark green leaves (Seetharam, 1982). Hybridisation was performed among indigenous, exotic and indigenous with exotic accessions. Pedigree selections were followed and selections were made from Indian × Indian, Indian × exotic or exotic × Indian and exotic × exotic crosses for early (<100 days), mid-late (100–110 days) and late (>110 days) entries. The varieties HR 374 (early) and Co-6 (late) were developed from the exotic × exotic crosses and had productivity of less than 2000 kg ha^{-1}. Large number of varieties was developed from Indian × exotic crosses. Among them, Indaf 9 was early, Co-9 and Indaf 5 were mid-late and Indaf 1, Indaf 3, K5, Indaf 7, Indaf 8, Indaf 6, HR 911 and Indaf 11 were late-maturing varieties. The Indian × exotic cross has productivity of more than

2500 kg ha^{-1}. Varieties from Indian × Indian crosses such as Udaya, K 7 (early), Purna and Annapurna (mid-late) and Cauvery, Shaktii and HPB 7-6 (late) with intermediate productivity were developed and released. Hybridisation among the Indian × exotic crosses provided the real breakthrough in breaking yield barriers and improving productivity of finger millet. This aided in achieving more than 50% increase in productivity in Karnataka (Seetharam, 1982) and by 60% increase in Tamil Nadu (Nagarajan and Raveendran, 1985). Subsequently large-scale efforts were made by major finger-millet-growing states to develop location-specific varieties by combining high productivity, blast resistance and drought tolerance. GPU 28 is a medium duration variety released during 1996, which mature in 110–115 days. This variety is suited for delayed sowing under terminal drought conditions. It is also resistant to neck and finger blast, which is a major pest in finger millet production. The potential yield of this variety is 3500–4000 kg ha^{-1}. However, under farmers' field condition, the productivity increased from 1000 kg ha^{-1} to 2000 kg ha^{-1} by the introduction of this variety. Presently this variety is grown on a larger area (about 70% area) in Karnataka. Joint efforts were made by the Department of Agriculture in each of the finger-millet-growing states, State Seed Corporation, State Agricultural Universities and private seed sectors for augmenting the availability of quality seed of GPU 28. GPU 28 was released during 1996. During the initial stages, about 1100 kg certified seed was produced during 1998–1999 and about 15548 of the total certified seeds were produced during 2008–2009, out of which 93% was GPU 28, and it has become the most popular variety of finger millet in Karnataka state. Farmer's participatory varietal selection was carried out at UAS, Bangalore, under the MC Knight Foundation–funded project on the development of high-yielding, disease-resistant and drought-tolerant finger millet genotypes suited for southern part of Karnataka. Twenty-eight superior recombinant inbred lines derived from IE 6012 × Indaf 5 were evaluated through farmer's participatory varietal selection. The study identified ML 31, ML 322 and ML 365 as the better preferred genotypes based on grain yield, fodder yield and quality, cooking quality and nutritional parameters. For drought response, ML 181 was identified, which is superior for grain and straw yield and generated up to 4.5 t ha^{-1} grain yield. For widening the genetic base of the breeding materials, crosses were attempted involving germplasm lines with related/wild species such as *E. multiflora*, *E. trystachyda*, *E. jagari*, *E. indica* and *E. africana* (Annual Report 2013–2014). Efforts were also made to cross the cultivated *E. coracana* with *E. africana*. Inter-specific hybrid *Eleusine coracana* × *E. africana* were intermediate for productive tillers, finger length, finger number, days to 50% flowering and exhibited reduced pollen fertility.

3.10 Varietal Development in Africa

Finger millet is an important millet grown in Eastern and Southern Africa, particularly in Kenya, west of Rift Valley and Lake Victoria regions, the second largest growing region in the world next to Karnataka, India (National Research Council, 1996). The productivity of finger millet in this region is low due to lack of improved cultivars and poor agronomic management (Odouri, 1998). ICRISAT-HOPE project in collaboration with DRD, Tanzania, released cultivars such as P 224 and U 15 in Tanzania and the same cultivars were also released in Kenya and Uganda due to higher yield, better blast resistance and higher tolerance to drought than the existing varieties (www.icrisat.org).

Systematic improvement on finger millet is not reported. In 1965, finger millet research was initiated at Serere region under East African Agriculture and Forestry Research Organization with a major objective of developing high-yielding varieties resistant to blast disease. Several short-duration cultivars with white seed and high protein, targeting agri-food industry, were developed. The varieties namely Gulu E, Engeny, Serere 1, Pese 1, Seremi 1, Seremi 2 and Seremi 3 were released. Tenywa *et al*. (1999) reported that the farmer got the grain yield of 400–800 $kgha^{-1}$ in Uganda which is very low compared to potential yield of 2500 $kgha^{-1}$ under research conditions. The low yields are a manifestation of the low attention and research input accorded to the crop (Bedis *et al.*, 2006). Use of unimproved landraces susceptible to blast disease and drought are the other major reasons for low yields in Uganda. Wanyera *et al*. (2007) reported blast as one of the major constraints to finger millet production in Uganda affecting all stages of crop growth. The study also reported that the damage by blast in finger millet resulted in major yield losses.

In Uganda, finger millet is continuously cultivated for more than 3000 years. Selection and preservation of superior panicles from local landraces or varieties formed major basis of seed for the ensuing season, and this has been a major step towards genetic improvement (Jameson, 1970; Khizzah, 1985). The white-seeded varieties were developed at Serere Research Station, and these include WC 65 × Serere 1/1/78 and WC 65 × Engeny 1/1 but their yield levels were lower compared to the brown-seeded types. Traditional crossing techniques such as hot-water emasculation and subsequent hand pollination were used for the creation of new variability and development of improved genotypes. The centre has also created new male-sterile mutants using fast neutrons in cultivar Gulu E background. The F_1s were reported to be fertile when crossed with male-sterile mutants. The segregation studies indicated a ratio of 3:1 fertile to sterile, and this depended on variety and season (Mukuru *et al.*, 1974); however, other ratios of 5:1, 2:1 and 1:1 fertile to sterile was also obtained. The variation in the expression male sterility was governed by modifier genes and the environment (Zake *et al.*, 1984). The male sterility was also transferred in different genetic backgrounds for generating populations, and this has enhanced out-crossing to a great extent and widening of the gene pool. Early-maturing finger millet varieties were important especially in regions of low and uneven rainfall. Attempts were made to develop varieties with short maturity periods and high basal tillering capacities. The improved lines flowered in 70 days and some entries were on par or produced greater yields than the longer-maturing varieties.

For developing varieties suiting different environments, the Department of Agriculture has divided Uganda into 11 agricultural zones, determined by rain seasons, amount of rainfall per annum, altitude, soils and the basic agricultural and livestock management activities (Zake and Khizzah, 1986). The programme makes use of the multilocational trial sites to identify desirable varieties for farmers. They identified Serere cross 10, P 277 and U 10 to be performing well compared to the varieties such as Engeny, Serere 1 and Gulu E. The mean yield across sites of Serere cross 10 exceeded 50 q ha^{-1}. Most entries showed higher levels of resistance to neck blast and lodging. Over the years, the cereals programme has released several improved finger millet varieties, namely, Engeny, Gulu E, Serere 1, Pese 1, Seremi 1, Seremi 2, and Seremi 3, including three more varieties on restricted release, namely, SX 8, SEC 915 and SEC 934 (Wanyera, 2005).

A systematic research programme for grain yield and quality improvement was initiated in 1985 at Matopos (Zimbabwe) by South African Development Community

(SADC)/ICRISAT Sorghum and Millet Improvement Project. A total of 1285 germplasm accessions have been collected locally or introduced from elsewhere for evaluation at four to five locations in different SADC countries during the rainy season of 1986–1987 (Gupta *et al.*, 1986). The selected lines were used in finger millet improvement programmes. Although the centre of origin of finger millets is in the highlands of the central to eastern African region, the diversity observed for various desirable traits in the landraces were limited. Due to this reason, despite the continuous efforts to identify better varieties from among the Ethiopian landraces, it has never been successful. In 1993, about 57 lines were introduced from East African Regional Sorghum and Millets Network. Two lines (KNE# 1098 & KNE# 409) were identified by the national programme to be better yielding across the Ethiopian millet-growing intermediate–high-altitude areas. These lines were approved for commercial release in 1998 with the names *Tadesse* and *Padet*, respectively. From the same set, another line, KNE# 411, was identified by the Bako Agricultural Research Center and released for production in the western Ethiopian region in 2002 with the name *Boneya* (Adugna, 2007).

Finger millet is also grown in the regions of southern highlands of Tanzania but mainly concentrated in Sumbawanga and Nakani, Mbozi, Ileji and Mbeya, and to a certain extent in Iringa and Ruvuma regions (Mwambene, 1986). The crop is mainly grown for food, for home brewing for making light beer (Pombe), and as a cash crop. Although sorghum and millets were given priority in the semi-arid areas of central and western Tanzania, finger millet gained importance in the southern highlands of Tanzania, especially in the Ufipa and Mbozi plateaus, with the concentration of research work at Ilonga Agricultural Research Institute (TARO, ILONGA). Traditional finger millet farmers and consumers in this region continued to grow local finger millet types for food and beer making than improved varieties.

More effort was directed to make new introductions from Serere, Uganda and to evaluate them in a wide range of environments. Preliminary evaluation of local finger millet collections at Uyole has shown that the southern highlands are rich in finger millet germplasm and the variability existing is large in each locality visited. The high-altitude types of finger millet are quite productive, yielding up to $5\,t\,ha^{-1}$. Having observed a lot of variability among local landraces, a research programme was initiated at Uyole in 1976. From multi-locational trails of southern highlands of Tanzania, Mbeya local, Sumbawanga, Engenyi and Serere local yield better compared to P224, Gulu E, Rombo Local, 1/19 and Eding.

3.11 Genetic Improvement for Blast Resistance

Blast disease caused by *Magnaporthe grisea* is a destructive disease in India and Africa causing substantial losses in the yield. Blast affects the crop at all growth stages, that is, vegetative (leaf blast) and reproductive stages (neck and finger blast). The infection is favoured by cloudy skies, frequent rain and drizzles, which support accumulation of dew in leaves for longer time. The rate of sporulation increases with increase in humidity (90%) and with temperature 25–28 °C. Average loss has been reported to be 28–36% (Vishwanath *et al.*, 1986, Nagaraja *et al.*, 2007) and yield losses in endemic areas is as high as 80–90% (Rao *et al.*, 1990). Although a number of cultural and chemical methods are available for the management of blast disease, it can be effectively managed by host plant resistance and numbers of resistance sources are available in germplasm, especially

the African types. Kiran Babu *et al*. (2012) developed an effective field-screening technique and which involves the use of systematic susceptible checks after every four test rows, artificial spray inoculation at pre-flowering stage with an aqueous conidial suspension (1×10^5 spores ml^{-1}) of *Magnaporthe grisea* fm strain multiplied on oatmeal agar medium at 27 ± 1 °C for 10 days, and maintaining high humidity and leaf wetness through sprinkler irrigation twice a day for 4 weeks following inoculation. The scoring for neck blast was recorded on a 1–5 scale, and the finger blast was measured as severity percentage on all the tillers of 10 selected plants in a row at physiological maturity.

A systematic study of the entire core collection was done by Kiran Babu *et al*. (2012) to identify promising sources of blast resistance for wide utilisation in finger millet improvement programmes. Out of 622 accessions tested for neck and finger blast, about 402 were resistant to neck blast, 436 to finger blast and 372 accessions exhibited a combined resistance to both neck and finger blast. However, the extent of resistance varied among the germplasm types. The resistant accessions belonged to one wild and four cultivated races of finger millet that originated from 19 countries representing the wide geographical diversity. Comparison of accessions of Asian and African origins revealed that accessions of Asian origin were susceptible to neck and finger blast while the African types were mostly resistant. The mini-core collections were screened by Kiran Babu *et al*. (2013), resulting in the identification of 66 accessions resistant to leaf, neck and finger blast. High and significant correlation was observed between neck and finger blast ($r = 0.92$). Greenhouse screening of the same set by artificial inoculation identified 58 accessions exhibiting blast resistance. These accessions represented one wild (Africana) and four cultivated races (plana, vulgaris, elongata and compacta) originating from 13 countries of Africa and Asia which exhibited a considerable diversity for agronomic traits such as maturity, plant height and panicle type.

In India, a systematic breeding programme is in place for the development of improved high-yielding cultivars coupled with blast resistance. Identification of several sources of stable resistance to blast disease and their deployment in breeding programmes has been highly rewarding in the evolution of high-yielding, blast-resistant cultivars in finger millet in the country. Blast resistance was incorporated into a number of improved cultivars/breeding lines and a number of varieties/genotypes – GPU 28, GPU 45, VL 315, GPU 48, OEB 259, VL 34 0, PRM 9809, HR 374 and VL 149 – are reported to be blast resistant. The blast-resistant variety GPU 28 occupied a predominant position in the farmer's field in the major finger-millet-growing regions of the country.

The disease is also highly destructive in the finger-millet-growing regions in Kenya and Uganda, with more than 50% loss in grain yield. Wanyera (2007) reported the blast disease as one of the highest-priority constraints in finger millet production in Uganda, affecting the crop at all growth stages and affecting most of the landraces and other genotypes. The disease progression in different genotypes was studied by Pande *et al*. (1995), and the genotypes were classified as fast- and slow-blasting genotypes. In fast-blasting genotypes, the disease progressed at an exponential rate, and most of the panicles showed maximum disease within 2–3 weeks of the initial disease appearance. The pattern of disease development caused the maximum yield loss. The genotypes identified as fast-blasting are KNE 479, KNE 672, KNE 744, KNE 755, KNE 801, KNE 808, KNF 891, KNE 898, KNE 920, KNE 1124, KNE 1142, and KNE 1012, while KNE 479 and KNE 755 were severely affected. The disease in slow-blasting genotypes progressed at slower rate and did not show severity at maturity. The genotypes identified as slow-blasting are KNE 701, KNE 719, KNI 739, KNE 784, KNE 706, KNE 812, KNE 814,

KNE 842, KNE 904, KNE 1159, P 224 and KNE 812, while KNE 814 and P224 were least affected.

Varietal mixture as an option for controlling blast in finger millet was suggested by Bijendra Kumar and Kumar (2011). Combinations of varieties PRM 1 and VL 149 showed 0.84% neck blast and 10.42 % finger blast as against the individual varieties which showed 96.4 and 94.14% neck and finger blast, respectively. They reported yield increase of 36.56% and 19.51% over both varieties. Increased chlorophyll content, total phenolics, peroxidase activity and polyphenol oxidase activity along with decreased ascorbic acid content and IAA oxidase activity were reported to be associated with resistant genotypes of GPU 26 and GPU 28. Low-molecular-weight protein fractions (14 KD, 29 KD and 43 KD) were well expressed in resistant genotypes. Among the genotypes GPU 26 enhanced the physiological and biochemical parameters (Kalarani *et al.*, 2002). Glume cover and seed-protein content were significantly and positively correlated with neck and finger-blast incidence. Accessions having shorter finger length and low calcium were more prone to blast (Nagaraja *et al.*, 2010). RIL populations of the crosses PR 202 × GPU 48, VR 708 × GPU 48, GPU 28 × KM 252, PR 202 × GPU 28 were developed at AICSMIP, Bangalore, to map the genomic regions associated with blast resistance.

3.12 Development of Genetic Male Sterility

Finger millet is predominantly a self-pollinating crop owing to the facultative cleistogamous nature of flowers. Hybridisation and recombination breeding is difficult in finger millet since emasculation and cross pollination are tedious due to small florets and low success of emasculation techniques. Alternatively male sterility is one of the useful techniques to overcome the hybridisation difficulties. A genetic male-sterile line in finger millet INFM 95001 was developed by Gupta (1999) from the finger millet germplasm line IE 3318 using EMS mutagenesis. Inheritance studies using INFM 95001, its sister male-fertile lines (IE 3318) and three unrelated male-fertile lines (FMV1, FM 2 and SDFM 957) revealed that the male sterility is governed by single-recessive gene. This male-sterile line is reported to produce fully fertile F_1 progeny when pollinated by any parent homozygous (Ms1MS1) for male sterility. The GMS line is easily distinguishable from the male-fertile line at anthesis. INFM 95001 is reported to have an erect growth habit with a mean plant height of 1.29 m and medium duration (94 days to 75% panicle exertion). Seeds are round and white at physiological maturity, and average seed mass 3.5 g. The identified male-sterile source would facilitate crossing for development of finger millet hybrid progenies to generate new recombinants, enhance genetic recombination in recurrent selection programmes and facilitate exploitation of background selection in marker-assisted back-crossing programmes.

Till now cytoplasmic male-sterility systems are not reported in finger millet. More research is required to identify a cytoplasmic-based male-sterility system because of the problem associated with genetic male system in hybrid seed production. However, genetic male-sterility systems can be used as breeding tool to facilitate the production of segregating populations derived from controlled crosses, particularly in small-flowered self-pollinated species in other millets. Where it is otherwise difficult to produce large numbers of seeds from crossed required for efficient recurrent selection or back-crossing programmes. Subsequently back-crossing programmes are carried out

at many research centres. Recently, GMS conversion programme is being reported at the Coimbatore centre where the GMS line was crossed with GPU 28, Co 14 and Paiyur 2. The identified male-sterile lines F_1s were then continuously back-crossed with GPU 28, Co 14 and Paiyur 2, and the material are in different stages of back-crossing. The INFM 95001 GMS line was increasingly used in the finger millet improvement programmes. Due to the recessive allele governing male-sterility, the maintenance of lines needs perpetuation through heterozygotes, which is tedious and requires skilled manpower. To circumvent the difficulties associated with this, a new partial sterile line (PS 1) was isolated from GPU 28 through EMS mutagenesis at AICSMIP, Bangalore. Investigation of breeding behaviour revealed the partial nature of sterility, which was found to be controlled by a single recessive gene. Results of controlled out-crossing revealed a high per cent recovery of the F1 hybrids (up to 76.52%). Easy maintenance of sterile line, with high recovery of hybrids besides its superior genetic background and high level of resistance to finger blast makes it an ideal parent especially in breeding for high-yielding blast-resistant cultivars for different finger-millet-growing regions in the country.

Heterosis is not commercially exploited in finger millet as in the case in sorghum and pearl millet. In recent years, in spite of persistent efforts, the newly evolved varieties are not showing high yield advantage over the varieties bred and released in recent years (Patroti and Jayarame Gowda, 2013). Several earlier studies on heterosis revealed predominance of non-additive gene action for yield and its component traits. The test crosses GE 4596 × L 5, GE 4596 × GE 5095, GPU 28 × L 5, GPU 28 × GE 5095 and GE 4906 × GE 5095 showed significant heterosis for most of the traits (Patroti *et al.*, 2011). Few heterosis studies on grain quality also have been reported. Indaf 11 × DPI 2011 and CO 9 × PES 400 for grain yield, CO 9 × CO (RA) 14 for protein content and CO 9 × GPU 28 and CO 9 × TRY 1 for calcium content were reported (Siva Gurunathan *et al.*, 2006). Further there is also scope for improving sterile line in different genetic backgrounds. For effective utilisation of male sterility in crop breeding programmes, there is a need to search for cytoplasmic genetic male sterility system, which is widely exploited in other millets such as sorghum and pearl millet.

3.13 Mutation Breeding

Mutation breeding was effectively used in finger millet for the development of early-maturing types, generation of polygenic variability and development of complete/partial male-sterile lines. Physical, chemical and combinations of mutagens were used for this purpose. Hamsa an early mutant of finger millet with increased finger number and grain-bearing area was obtained using gamma irradiation (Nayar *et al.*, 1979). Mutation breeding led to release of the early-maturing Dibya Singh (90 days), which originated from the variety Sarada (110 days) from Orissa, and Co-3 (110 days) originating from CO-1 (120 days) in Tamil Nadu. The mutagenic efficiency in TRY 1 variety was investigated by Eswari *et al.* (2014) leading to the identification of desirable mutants for plant height, tillers/plant, productive tillers, finger number, finger length and 1000-grain weight. The study also suggested that a concentration of 0.15% was found to be ideal for increasing the frequency of obtaining desirable segregants. The genetic male-sterile line INFM 95001 was developed using EMS mutagenesis of the germplasm line IE 3318. A partial sterile line (PS 1) was isolated through EMS mutagenesis of GPU 28.

3.14 Strategies to Bridge Research Gaps for Enhancing Productivity and Utilisation of Finger Millet

3.14.1 Germplasm Evaluation

Details of priorities and approaches for genetic improvement are given in Figure 3.3. In finger millet, valuation of genetic diversity collected and conserved in gene banks needs urgent attention in order to identify accessions possessing specific traits. In the context of climate change. water scarcity and high-input agriculture, there is increasing need to identify germplasm and develop cultivars adaptive to climate change. Few studies have been made to screen the core/mini core collection that led to identification of large variation for quantitative traits as well as for nutritional traits (Upadhyaya *et al.,* 2011). However, there is a need for systematic evaluation of a large number of indigenous and exotic germplasm available with the national gene bank under multi-location trials to identify end-use specific germplasm, especially for early maturity, photo insensitivity, drought tolerance, blast and other disease and pest resistance, nutritional quality (protein, calcium, iron, zinc and essential amino acids) and antioxidants of therapeutic value.

3.14.2 Participatory Selection and Varietal Development

Farmers grow finger millet under harsh conditions, and the performance of these varieties largely depend on its ability to adjust fluctuating edaphic and climatic conditions which is least represented in research stations. This warrants participation of the

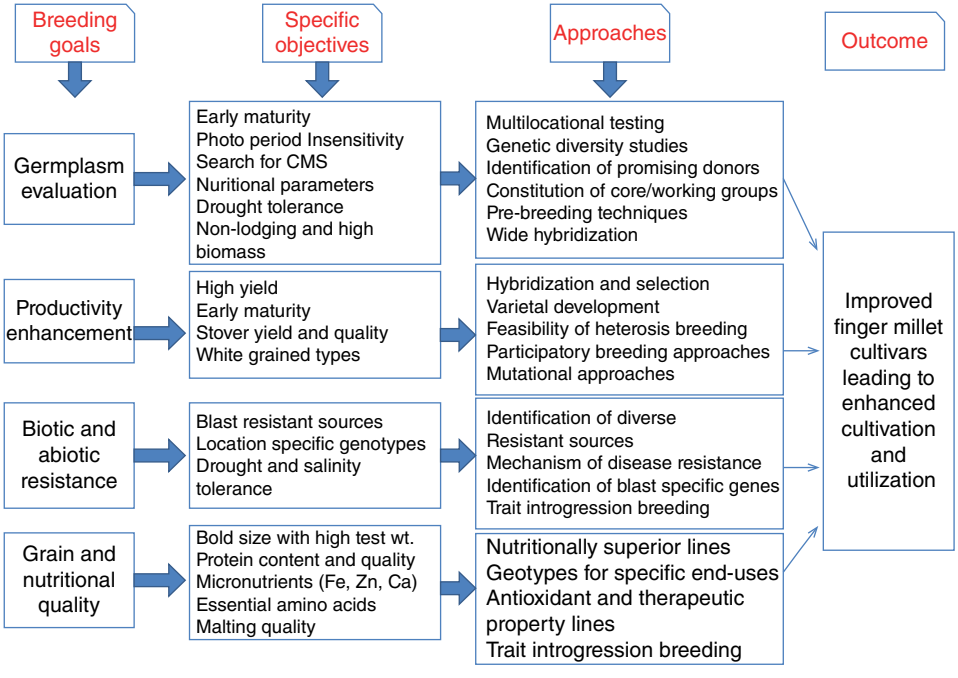

Figure 3.3 Priorities and approaches for genetic improvement in finger millet. (*See color plate section for the color representation of this figure.*)

farmers in selection of desired genotypes/varieties. Appropriate selection and breeding efforts involving farmers' participatory approach is required to be taken up to develop high-yielding finger millet varieties for different production systems under varying environmental conditions.

3.14.3 Interspecific Hybridisation and Search for Novel Traits

Three primary wild relatives (*E. Africana*, *E. indica* and *E. Kigeziensis*), secondary wild relatives (*E. tristachya*, *E. Floccifolia* and *E. intermedia*) and tertiary wild relatives (*E. Jaegeri*, *E. multiflora* and *E. compressa*) are recognised in finger millet. There is need to research novel traits in wild species, especially disease resistance, cytoplasmic genetic male sterility, etc. The search and discovery of genetic or cytoplasmic male sterility would be a substantial breakthrough in the improvement of this crop by opening up the possibilities for effective population improvement according to modern genetic principles and breeding techniques. Moreover, the quantity of pollen shed in finger millet would seem adequate for wind-dispersion if such steriles were available.

3.14.4 Development of Early-maturing, Photoperiod-insensitive Varieties for Different Cropping Systems

Most of the released cultivars mature in 110–115 days, and there are not many superior early-maturing cultivars, except VR 520 and VR 708, which can mature in 90–95 days. From germplasm screening germplasm experiments, early germplasm with 50–52 days flowering are available and there is need to utilise these germplasm for development of early-maturing superior genotypes which can fit in different cropping systems as well as provide substantial yield under water stress. Indian types are generally short fingered, small grains and photoperiod insensitive while the African types have long fingers, bold grains, stiff straw and are photosensitive. There is need to utilise these two types for development of improved early-maturing, high-yielding types.

3.14.5 Genetic Improvement for Drought Tolerance

Finger millet is a relatively hardy crop, survives water deficit and is known to show remarkable recovery on stress alleviation. Few basic studies and with limited set of genotypes indicate large variation among the genotypes for drought and other abiotic stresses. Many studies have used the source IE 1012 for drought tolerance breeding. However, systematic studies have to be made to identify diverse drought-tolerant genotypes, understand mechanisms of drought tolerance from multi-locational screening as well as to identify key surrogate/adaptive traits. The identified lines should be used in introgression breeding for development of improved drought-tolerant finger millet genotypes.

3.14.6 Stover Yield and Quality Improvement

Although finger millet crop is predominantly grown for grain/food purpose, the stover after harvest of crop is an excellent source of nutritive fodder to cattle. The straw of finger millet was compared with that of pearl millet, paspalum millet, wheat, rice and sorghum in feeding tests with 8-year-old bullocks, and found finger millet straw as having the highest proportion of total digestible nutrients (60.8%), compared to 50–57% in other species. Varieties with good grain and fodder yield and blast resistance are highly

desired by farmers. The tall types are known to be susceptible to lodging, and therefore the recently released high-yielding cultivars are dwarf types and medium maturing. There is need to identify non-lodging tall types with superior grain and fodder yield. The African types are known to possess more plant height, and there is need to utilise these types for improvement of fodder yield and quality. Also, very few isolated reports are available on the nutritive value and feeding trials of fodder, and therefore there is need to strengthen these research gaps.

3.14.7 High-yielding White Finger Millet Varieties

Only a fraction of the available germplasm is being used in crop improvement programmes. Therefore, the economic value and usefulness of large amounts of conserved germplasm in almost all gene banks are still to be assessed. This activity needs to be strengthened as a priority and should receive attention. In addition to major consumption of the grains of finger millet in the form of *mudde* (dumplings), the grain is also used for malting purpose, and the white-grained types are preferred for this purpose. The white-grain types are rich in protein (~12%) compared to coloured types (~8%), but are low yielding. Therefore, there is need to develop improved white-grained finger millet genotypes for malting purposes as well as other end-uses such as weaning foods, infant foods, malted milk foods, etc.

3.14.8 Nutritional Improvement

Finger millet is highly nutritious, and thus calls for intensive evaluation of germplasm to assess its nutritional qualities. Finger millet grains, besides providing energy, are also a rich source of calcium and iron, and its proteins are good source of essential amino acids and can greatly contribute to micronutrient and protein malnutrition, also known as 'hidden hunger', affecting women and children in African and Southeast Asian countries. The most cost-effective approach for mitigating micronutrients and protein malnutrition is to introduce varieties bred for Fe, Zn and protein content in grains. Attempts to breed finger millet for enhanced grain nutrients are still in its infancy. Evaluation of finger millet core germplasm for grain nutrients and agronomic traits revealed a substantial genetic variability for grain Fe, Zn, Ca and protein contents. Therefore, the identified accessions may be used for development of nutritionally rich cultivar development in finger millet.

3.14.9 Breeding for Blast Resistance and Other Pests

In addition to yield improvement, progresses have been made to introgress blast resistance in the elite genotypes/varieties such as GPU 28, GPU 45 and GPU 48. Among various pests, blast disease is major problem in finger millet, affecting the crop at all stages of growth, and a number of varieties are susceptible. Large-scale screening techniques are available which led to the identification of blast-resistant sources among the germplasm. Most of the Asian origin was susceptible to neck and finger blasts, while those from Africa origin were resistant. However, it is likely that the resistance may break down owing to development of new pathotypes. Therefore, understanding the pathogen diversity in the geographical area and development of blast resistance genotypes based on knowledge of the strains is desirable for development of durable blast-resistant genotypes.

References

Abraham, M.J., Gupta, A.S. and Sharma, B.K. (1989) Genetic variability and character association of yield and its components in finger millet (*Eleusine coracana* [L.] Gaertn.) in an acidic soil of Meghalaya. *Indian Journal of Agricultural Sciences*, **59**, 579–581.

Adugna, A. (2007) The role of introduced sorghum and millets in Ethiopian agriculture. *SAT eJournal*, **3** (1).

Anantharaju, P. (2001) Studies on genetic variability, association and diversity in finger millet (*Eleusine coracana* [L.] Gaertn.) for yield, yield attributes and salinity tolerance. M.Sc. (Ag.), Thesis submitted to T.N.A.U., Coimbatore, India.

Ayyangar, G.N.R., Rao, P.K. and Krishnaswami, N. (1931) The inheritance of characters in ragi, *Eleusine coracana* Gaertn., Part IV. Depth of green in the pericarp. *Indian Journal of Agricultural Sciences*, **1**, 563–568.

Ayyangar, G.N.R. (1932) The inheritance of characters in ragi. *Eleusine coracana* Gaertn. *Madras Agricultural Journal*, **20**, 1–9.

Ayyangar, G.N.R. and Krishnaswamy, N. (1931) The inheritance of characters in ragi. *Eleusine coracana Gaertn. Part III. Sterility. Indian Journal of Agricultural Sciences*, **1**, 554–562.

Ayyangar, G.N.R. and Rao, P.K. (1931) The inheritance of characters in ragi, *Eleusine coracana* Gaertn., Part V. Albinism. *Indian Journal of Agricultural Sciences*, **1**, 569–576.

Ayyangar, G.N.R. and Rao, U.A. (1932) Inheritance of characters in ragi, *Eleusine coracana* (Gaertn.), Part VI. Earhead shapes. *Indian Journal of Agricultural Sciences*, **2**, 254–265.

Ayyangar, G.N.R. and Wariar, U.A. (1934) Anthesis and pollination in ragi, *Eleusine coracana* Gaertn., the finger millet. *Indian Journal of Agricultural Sciences*, **4**, 386–393.

Ayyangar, G.N.R., Wariar, U.A. and Ramabhadran, G. (1933) Inheritance of characters in ragi, *Eleusine coracana* Gaertn., the finger millet; Part VI 1. Earhead colour factors. *Indian Journal of Agricultural Sciences*, **3**, 1080–1084.

Bedis, M.R., Ganvir, B.N. and Path, P.P. (2006) Genetic variability in finger millet. *Journal of Maharashtra Agricultural University*, **31** (3), 369–370.

Bharathi, A. (2011) Phenotypic and genotypic diversity of global finger millet (*Eleusine coracana* [L.] Gaertn.) composite collection. PhD dissertation submitted to Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, India.

Kumar, B. and Kumar, J. (2011) Management of blast disease of finger millet (*Eleusine coracana*) through fungicides, bioagents and varietal mixture. *Indian Phytopathology*, **64** (3), 272–274.

Chandrashekhar, H., Gowda, J. and Jayashree, U. (2012) Formation of core set in Indian and African finger millet (*Eleusine coracana* [L.] Gaertn.) germplasm accessions. *Indian Journal of Genetics*, **72** (3), 358–363.

Channaveeraiah, M.S. and Hiremath, S.C. (1974) Genome analysis of *Eleusine coracana* (L.) Gaertn. *Euphytica*, **23**, 489–495.

Chavan, V.M. and Shendge, P.Y. (1957) Plant breeding in South Asia with reference to millets. *Indian Journal of Genetics and Plant Breeding*, **17**, 156–175.

Chavan, V.M., Gopalkrishna, N. and Khadilkar, B.T. (1955) Blooming and anthesis in nagli (*Eleusine coracana* (Linn.) Gaertn. *Poona Agricultural College Magazine*, **46**, 175–179.

Coleman, L.C. (1920) The cultivation of ragi in Mysore. *Bulletin, Department of Agriculture, Mysore. General Series*, **11**, 1–152.

Daba, C. and Keneni, G. (2010) Morpho-agronomic classification of some native and exotic finger millet (*Eleusine coracana* L.) germplasm accessions in Ethiopia. *East African Journal of Science*, **4** (1), 20–26.

De Wet, J.M.J., Prasada Rao, K.E., Brink, D.E. and Mengesha, M.H. (1984) Systematic and evolution of *Eleusine coracana* (Gramineae). *American Journal of Botany*, **71**, 550–557.

Dodake, S.S. and Dhonukshe, B.L. (1998) Variability in floral structure and floral biology of finger millet (*Eleusine coracana* [L.] Gaertn.). *Indian Journal of Genetics*, **58**, 107–112.

Eswari, K., Gogulan, G., Hari Prathab, K.A. and Sakila, M. (2014) Development of early maturing mutants in finger millet. *Research Journal of Agriculture and Forestry Sciences*, **2** (6), 1–9.

Goswami, P. and Asthana, A.N. (1984) Genetic variability in indigenous varieties of finger millet in Sikkim. *Indian Journal of Agricultural Sciences*, **54**, 959–961.

Guarino, L. (2012) *Global strategy for the ex situ conservation of finger millet and its wild relatives, Global Crop Diversity Trust, International Crops Research Institute for the Semi Arid Tropics (ICRISAT),* Patancheru, Andhra Pradesh, India.

Gupta, A. (2006) Improvement of millets and pseudo-cereals for rainfed agriculture in hill region, in *Sustainable Production from Agricultural Watersheds in North West Himalaya* (eds H.S. Gupta, A.K. Srivastva and J.C. Bhatt), Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora, Uttaranchal, India, pp. 163–174.

Gupta, A., Sood, S., Agarwal, P.K. and Bhatt, J.C. (2011) Floral biology and pollination system in small millets. *The European Journal of Plant Sciences and Biotechnology*, **6** (2), 81–86.

Gupta, S.C. (1999) Inheritance of genetic male sterility in finger millet. *African Crop Science Journal*, **7** (2), 125–128.

Gupta, S.C., Appa Rao, S. and House, L.R. (1986) Finger millet research in the SADCC (Southern African) region, in *Small Millets in Global Agriculture* (eds A. Seetharam, K.W. Riley and G. Harinarayana), Proceedings of the first International small millets workshop, Bangalore, India, October 29–November 2, 1986, Oxford & IBH Publishing Co. Pvt. Ltd.

Harinarayana, G. (1986) Breeding and varietal improvement of small millets in India, in *Small Millets in Global Agriculture* (eds A. Seetharam, K.W. Riley and G. Harinarayana), Proceedings of the First International Small Millets workshop, Bangalore India, October 29–November 2, 1986, Oxford & IBH publishing Co. Pvt. Ltd.

Hilu, K.W. and de Wet, J.M.J. (1976) Domestication of *Eleusine coracana* (L.) Gaertn. *Economic Botany*, **30**, 199–208.

Hilu, K.W. and de Wet, J.M.J. (1976) Racial evolution in *Eleusine coracana* Subsp. coracana (finger millet). *American Journal of Botany*, **63**, 1311–1318.

Hilu, K.W., De Wet, J.M.J. and Harlan, J.R. (1979) Archeobotany and the origin of finger millet. *American Journal of Botany*, **66**, 330–333.

Hussaini, S.H. (1973) Multivariate analysis and group distribution in the world collection *Eleusine coracana*, Gaertn. PhD thesis submitted to the North Carolina State University at Raleigh, p. 81.

Jameson, J.D. (1970) *Agriculture in Uganda*, Second edn, Oxford University Press, UK, pp. 127–138.

Kalarani, M.K., Thangaraj, M., Ramanathan, A. *et al.* (2002) Physiological and biochemical aspects of blast resistance in finger millet (*Eleusine coracana*. *Gaertn) Crop Research*, **23** (3), 526–531.

Kempanna, C. and Govindu, H.C. (1969) Pattern of phenotypic variability in the Indian collection of *Eleusine coracana*. *The Mysore Journal of Agricultural Science*, **111**, 306–312.

Khizzah, B.W. (1985) Finger millet breeding in Uganda, Proceedings of the Regional Workshop on Sorghum and Millets Improvement in Eastern Africa, Soroti, Uganda, July 22–26, 1985, pp. 23–25.

Kiran Babu, T., Thakur, R.P., Reddy, R.P. *et al.* (2012) Development of a field screening technique and identification of blast resistance in finger millet core collection. *Indian Journal of Plant Protection*, **40** (1), 45–51.

Kiran Babu, T., Thakur, R.P., Upadhyaya, H.D. *et al.* (2013) Resistance to blast (*Magnaporthe grisea*) in a mini-core collection of finger millet germplasm. *European Journal of Plant Pathology*, **135** (2), 299–311.

Krishnappa, M., Ramesh, S., Chandraprakash, J. *et al.* (2009) Genetic analysis of economic traits in finger millet. *SAT e Journal*, **7**.

Krishnasastry, K.S., Udayakumar, M. and Viswanath, H.R. (1982) Desirable plant characteristics in genotypes of finger millet (*Eleusine coracana* Gaertn.) for rainfed conditions. *Proceedings of the Indian National Science Academy B*, **48** (2), 264–270.

Krishnegowda, K.T., Ashok, E.G., Shashidhara, G.C. and Anil Kumar (2015) Sustainable production of small millets under varied ecological conditions. In Paper presented at the Annual Workshop of Small Millets, March 29–31, 2015 at Navsari, Gujarat.

Mahto, R.N., Karmakar, S. and Haider, A.Z. (2000) Genotype x environment interaction study in finger millet. *Environment and Ecology*, **18**, 681–684.

Mallanna, K.N., Mallikarjunardhya, K., Channabyregowda, K. and Umashankar, R. (1978) *A study of variability in a world collection of Eleusine. Paper presented in the National Symposium in Genetic Resources*, IARI, New Delhi, India.

Mnyenyembe, P.H. and Gupta, S.C. (1998) Variability for grain yield and related traits in finger millet germplasm accessions from Malawi. *African Crop Science Journal*, **6** (3), 317–322.

Mukuru, S.Z., Makumbi, V., Khizzah, B.W. *et al*. (1974) *Finger Millet Breeding*. East African Agriculture and Forestry Research Organisation E.A.C. Record of Research.

Mwambene, R.O.F. (1986) Finger millet research in the southern highlands of Tanzania. In *Small Millets in Global Agriculture* (eds A. Seetharam, K.W. Riley, G. Harinarayana), Proceedings of the First International Small Millets Workshop, Bangalore India, October 29–November 2, 1986, Oxford & IBH Publishing Co. Pvt. Ltd.

Nagaraja, A., Jagadish, P.S., Ashok, E.G. and Krishne Gowda, K.T. (2007) Avoidance of finger millet blast by ideal sowing time and assessment of varietal performance under rainfed production situations in Karnataka. *Journal of Mycopathological Research*, **45** (2), 237–240.

Nagaraja, A., Nanja Reddy, Y.A., Jayarame, G. and Anjaneya Reddy, B. (2010) Association of plant characters and weather parameters with finger millet blast. *Crop Research*, **39** (1, 2 & 3), 123–126.

Nagarajan, C. and Raveendran, T.S. (1985) Germplasm mobilization and utilization in finger millet in Tamil Nadu. National Seminar on Finger Millet. Genetics and Breeding, UAS, Bangalore, January 12–13, 1983.

Naik, B.J., Shankare Gowda, B.T. and Seetharam, A. (1993) Pattern of variability in relation to domestication of finger millet in Africa and India, in *Advances in Small Millets* (eds K.W. Piley, S.C. Gupta, A. Seetharam and J.N. Mushonga), Oxford and IBH Publishing Co. Pvt. Ltd., New Delhi, pp. 347–364.

Nayar, K.M.D., Pushpa, G. and Reddy, B.G.S. (1979) Open earhead Hamsa true breeding early mutants of finger millet. *Current Research*, **8**, 212–213.

Oduori, C.O.A. (1998) *Finger Millet Better Varieties – Better Crop Care – More Food*. DFID and GON produced by DEVCOM & AIC.

Pande, S., Mukuru, S.Z., King, S.B. and Karunakar, R.I. (1995) Biology of and resistance to finger millet blast in Kenya and Uganda. In *Proceedings of the Eighth EARSAM Regional Workshop on Sorghum and Millets* (eds S.Z. Mukuru and S.B. King), October 30–November 5, 1992, Sudan, ICRISAT, Andhra Pradesh, pp. 83–92.

Patroti, P.D., Gowda, J., Satish, R.G. and Mallikarjun, N.M. (2011) Heterosis and combining ability studies for yield and yield attributing characters in finger millet (*Eleusine coracana* [L.] Geartn.). *Electronic Journal of Plant Breeding*, **2** (4), 494–500.

Patroti, P.D. and Gowda, J. (2013) Estimation of heterosis for yield and its attributing characters and study of intra-spikelet competition for seed size in finger millet *Eleusine coracana* L. *The Journal of Research ANGRAU*, **41** (2), 33–41.

Prabhakar and Prasad, M.N. (1983) Correlation and path analysis in segregating populations of finger millet (*Eleusine coracana*, Gaertn.). *Madras Agricultural Journal*, **70**, 366–371.

Prasada Rao, K.E., de Wet, J.M.J., Gopal Reddy, V. and Mengesha, M.H. (1993) Diversity in the small millets collection at ICRISAT, in *Advances in Small Millets* (eds K.W. Riley, S.C. Gupta, A. Seetharam and J.N. Mushonga), Oxford and IBH Publishing Co. Pvt. Ltd., New Delhi, India, pp. 331–346.

Rachie, K.O. and Peters, L.V. (1977) *The Eleusines: A Review of the World Literature*, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), p. 187.

Raj, S.M., Mahudeswaran, K. and Shanmugasundaram, A. (1964) Observation on the hot water technique of emasculation of ragi flowers (*Eleusine coracana* Gaertn.). *Madras Agricultural Journal*, **51**, 71–75.

Rao, A.N.S. (1990) Estimates of losses in Finger millet (*Eleusine coracana*) due to blast disease (*Pyricularia grisea*). *Journal of Agricultural Sciences*, **24**, 57–60.

Ravikumar, R.L. and Seetharam, A. (1990) Inheritance of plant pigmentation in finger millet. *Crop Improvement*, **17** (2), 141–143.

Reddy, V., Gopal, U., H.D. *et al.* (2009) Characterization of eastern African finger millet germplasm for qualitative and quantitative characters at ICRISAT. *Journal of SAT Agricultural Research*, **7** (1).

Seetharam, A. (1982) Finger millet improvement. *Indian Farming*, **32** (3), 3–6.

Seetharam, A. (1998) Small millets research: Achievement during 1947–1997. *Indian Journal of Agricultural Sciences*, **68** (8), 431–438.

Shanthakumar, G. and Gowda, B.T.S. (2011) Inheritance of qualitative character in ragi (*Eleusine Coracana* G.) of cross WR9 x U6. *Karnataka Journal of Agricultural Sciences*, **10** (3), 704–707.

Shanthappa, M.B. (1980) Inheritance studies in *Eleusine coracana* Gaertn. crosses. *Mysore Journal of Agricultural Sciences*, **14** (2), 260.

Siva Gurunathan, M., Veerabadhiran, P. and Senthil, N. (2006) Heterosis studies in finger millet (Eleusine coracana [L.] Gaertn) for yield and quality traits. *Crop Research*, **31** (2), 267–270.

Tenywa, J.S., Nyende, P., Kidoido, M. *et al.* (1999) Prospects and constraints of finger millet production in eastern Uganda. *African Crop Science Journal*, **7**, 569–583.

Upadhyaya, H.D., Gowda, C.L.L., Pundir, R.P.S. *et al.* (2006) Development of core subset of finger millet germplasm using geographical origin and data on 14 quantitative traits. *Genetic Resources and Crop Evolution*, **53**, 679–685.

Upadhyaya, H.D., Ramesh, S., Sharma, S. *et al.* (2011) Genetic diversity for grain nutrients contents in a core collection of finger millet (*Eleusine coracana* [L.] Gaertn.) germplasm. *Field Crops Research*, **121**, 42–52.

Upadhyaya, H.D., Sarma, N.D.R.K., Ravishankar, C.R. *et al.* (2010) Developing a mini-core collection in finger millet using multilocation data. *Crop Science*, **50** (5), 1924–1931.

Upadhyaya, H.D., Gowda, C.L.L. and Reddy, V.G. (2007) Morphological diversity in finger millet germplasm introduced from Southern and Eastern Africa. *SAT eJournal*, **3** (1).

Verma, V.S. (1989) Variability patterns in quantitative traits of ragi (*Eleusine coracana* [L.] Gaertn.). *Madras Agricultural Journal*, **76**, 626–629.

Vishwanath, S., Sanne Gowda, S., Seetharam, A. and Shankare Gowda, B.T. (1986) Reaction to blast disease of released and pre-released varieties of finger millet from different states. *Millet Newsletter*, **5**, 31.

Wanyera, N.M.W. (2005) Finger millet (*Eleusine coracana* [L.] Gaertn) in Uganda finger millet blast management in East Africa. Creating opportunities for improving production and utilization of finger millet. In *Proceedings of the First International Finger Millet Stake-holders Workshop* (eds M.A. Mgonja, J.M. Lenne, E. Manyasa and S. Sreenivasaprasad), Projects R8030 & 8445, UK Department for international development – Crop Protection Programme held on September 13–14, 2005, at Nairobi.

Wanyera, N.M.W. (2007) Facilitating the promotion of improved and blast resistant finger millet varieties to enhance production. In *Proceedings of the First International Finger Millet Stake-holders Workshop* (eds M.A. Mgonja, J.M. Lenne, E. Manyasa and S. Sreenivasaprasad), Projects R8030 & 8445, UK Department for International Development – Crop Protection Programme held on September 13–14, 2005, at Nairobi, pp. 66–67.

Zake, V.M. and Khizzah, B. W. (1986) Finger millet improvement in Uganda, in *Small Millets in Global Agriculture* (eds A. Seetharam, K.W. Riley and G. Harinarayana). Proceedings of the First International Small Millets Workshop, Bangalore India, October 29–November 2, 1986, Oxford & IBH Publishing Co. Pvt. Ltd., New Delhi.

Zake, V.M., Khizzah, B.W., Odelle, S.E. *et al.* (1984) *Progress Report 1981–1983. Sorghum and Millets Research in Uganda*, Uganda Agriculture and Forestry Research Organisation.

4

Foxtail Millet, *Setaria italica* (L.) P. Beauv.

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4.1 Introduction

Foxtail millet is one of the oldest cultivated crops known to man and the oldest of the cultivated millets (Oelke *et al.*, 1990). This cereal has been cultivated in Northern China since Neolithic times (8000 years ago), and remains a staple food crop (Fogg, 1983). Carbonised foxtail millet has been identified in archaeological sites in China, with various reports of its origination date. Archaeological data (de Wet *et al.*, 1979; Li and Wu, 1996) show that it has also been cultivated since ancient times (6000 years ago) in Eurasia. It is cultivated in about 23 countries in Asia, Africa and America, especially where climatic hazards do not permit the cultivation of other cereals. It is an important cereal crop grown as a staple food in China, India and Japan, and for silage and hay or bird feed in North and South America, Australia and North Africa (Wanous, 1990; Baltensperger, 2002; Diao, 2005, 2007; Doust *et al.*, 2009). It is a self-pollinating cereal ($2n = 2x = 18$), belonging to the family Poaceae. There are many wild and cultivated types, and the latter are divided into many cultivars with differences in height, habit, structure of inflorescences, number and colour of grain (Prasada Rao *et al.*, 1987; Brink, 2006).

Foxtail millet ranks second in the total world production of millets and continues to have an important place in the world agriculture providing approximately 6 million t of food to millions of people, mainly on poor or marginal soils in southern Europe and in temperate, subtropical and tropical Asia (Marathee, 1993). Its grain is used for human consumption and as feed for poultry and caged birds. Major producers of foxtail millet are China and India. Production statistics for foxtail millet are scarce because they are usually combined with those of other millets. In the early 1990s, it was estimated that foxtail millet represented about 18% of grain millet production, with about 5 million t of grains (ICRISAT and FAO, 1996). China is the main producer, and foxtail millet is next to rice and wheat in importance. China still ranks first in foxtail millet production in the world (4.6 million t), and it provides approximately 15–17% of the total food consumed in China (Baltensperger, 2002).

In India, because of the drought tolerance, foxtail millet was once an indispensable crop of vast rainfed areas in semi-arid regions. At present, foxtail millet is cultivated on a limited area in the states of Andhra Pradesh, Karnataka, Maharashtra, Tamil Nadu, Rajasthan, Madhya Pradesh, Uttar Pradesh and northeastern states. The area under

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foxtail millet in India has come down by more than half during the 1990s mainly due to the introduction of more remunerative crops such as sunflower and soybean in black soils. At present foxtail millet is grown in an area of 0.98 lakh ha (2005–2006) producing about 0.56 lakh t of grains with an average productivity of 565 kg/ha, and the important growing states are Andhra Pradesh (0.17 lakh t), Karnataka (0.14 lakh t), Rajasthan (0.05 lakh t), Maharashtra (0.05 lakh t), Arunachal Pradesh (0.05 lakh t), Tamil Nadu (0.01 lakh t) and Madhya Pradesh (RESMISA, 2012).

In Africa, foxtail millet can be found in the upland areas in East Africa, in Cameroon and Southern Africa (Brink, 2006). In Europe, where it used to be cultivated as a summer crop until the seventeenth century, it has become marginal, and Central Europe is now the main area of production (Panaud, 2006). In the United States, foxtail millet was introduced from the old world about the middle of the nineteenth century as a forage crop, and now cultivated as a catch crop, especially for fodder and pet food for caged and wild birds (Baltensperger, 2002).

The foxtail millet is valued as a crop of short duration, which is good as food, feed and fodder. Its cultivation is successful even in areas with low precipitation, and altitudes from sea level up to 2000 m above mean sea level (Oduori, 1993; Brink, 2006). It is mainly grown as a rainfed crop but does well under irrigation. It is fairly drought-tolerant crop and its water use efficiency (WUE) has been found to be higher than maize, wheat and sorghum (Zhang *et al.*, 2007). Its drought tolerance has been accredited to the association between increased WUE and its several morphological characteristics such as dense root system, thick cell walls, epidermal cell arrangements and minuscule leaf areas (Li, 1997). For producing 1 g of dry biomass, foxtail millet requires only 257 g of water, which is much lower than maize (470 g) and wheat (510 g) (Diao, 2007; Li and Brutnell, 2011). Foxtail millet cannot tolerate water logging. Though it has a low water requirement, and can grow rapidly in warm weather and in semi-arid conditions, sometimes it does not recover well from drought conditions because of shallow root system (Hancock Seed, 2014). It is adapted to a wide range of elevations, soils and temperatures. It can grow in sandy to loamy soils with pH from 5.5 to 7 (Sheahan, 2014). It has a high level of tolerance to salinity (Krishnamurthy *et al.*, 2014).

The maturity duration in foxtail millet varies from 60 to 120 days. It grows better in places where annual rainfall ranges from 500 to 700 mm and where rains fall during summer. However, it keeps growing at 300–400 mm annual rainfall also in semi-arid areas (Brink, 2006). Foxtail millet is frost-sensitive and grows better between 16 and 26°C, though it has much larger temperature tolerance (5–35°C). It thrives on soils ranging from sandy to heavy clay soils (except saline soils) provided they are in the range of 5.5–8.3 in pH and are not water logged (Brink, 2006; Ecocrop, 2011; FAO, 2011).

Grains can be harvested manually or mechanically by cutting off the panicles followed by threshing (trampling by cattle or stone roller). Foxtail millet harvested for grain yields 800–900 kg grain/ha (up to 1800 in China) and 2.5 t straw/ha (Brink, 2006; FAO, 2011). Under irrigated conditions, grain yields have reached 11 t/ha in experiments in China (Brink, 2006). After harvest, the grain is susceptible to heating and spoiling and should be dried thoroughly (Heuzé *et al.*, 2015). The grain of foxtail millet is ovoid in shape, 2 mm long, pale yellow to orange, red, brown or black in colour. It is enclosed in thin hulls and should undergo de-husking before being stored as husks are attractive to insects and processed for food (Brink, 2006; Ecoport, 2011; FAO, 2011). De-husking can be done by beating the grains in a mortar with pestle, or by using a rice processing apparatus such as a cone polisher or a centrifugal sheller (Ravi, 2004; Brink,

2006; FAO, 2011). The grain can be cooked in the same manner as rice and has many food applications (porridge, pudding, breads, cakes, flour, chips, rolls, noodles, etc.). It is an important staple food in India and Northern China. Foxtail millet is fermented to make vinegar and wine in China and to make beer in Russia and Myanmar. Sprouted grains are eaten as vegetable (Brink, 2006).

Foxtail millet is largely grown to meet the domestic needs of the rural people in selected pockets. It is widely used as an energy source for pregnant and lactating women, and also for sick people and children, especially for diabetics (Sema and Sarita, 2002). Like other small millets, foxtail millet is highly nutritious and even superior to fine cereals in certain nutrient constituents (Table 4.1). Grains of foxtail millet have low glycaemic index (GI) and high fibre content (Geervani and Eggum, 1989; Pawar and Pawar, 1997). The protein content is higher among millets and major cereals (Rao *et al.*, 2011) and also the amount of fibres (as β-glucans; 42.6 %) (Amadou *et al.*, 2011). These β-glucans increase the metabolism of sugar and cholesterol to induce hypoglycemic and hypocholesterolaemic effects and hence are beneficial for prevention of diabetes and cardiovascular diseases (Krishnakumari and Thayumanvan, 1997; Itagi *et al.*, 2012). Therefore, foxtail millet is used in the preparation of low GI foods for treating diabetics, particularly type 2 diabetes (Anju and Sarita, 2010; Thathola *et al.*, 2010; Chhavi and Sarita, 2012; Itagi *et al.*, 2012; Jali *et al.*, 2012) and cardiovascular diseases (Choi *et al.*, 2005).

Table 4.1 Nutritive value of foxtail millet vs. rice and wheat (per 100 g).

Item	Foxtail millet	Wheat (whole)	Rice (raw, milled)
Carbohydrates (g)	60.9	71.2	78.2
Protein (g)	12.3	11.8	6.8
Fat (g)	4.3	1.5	0.5
Energy (KCal)	331	346	345
Crude fibre (g)	8	1.2	0.2
Mineral matter (g)	3.3	1.5	0.6
Amylose (%)	17.5	25	12–19
Amylopectin (%)	82.5	75	88–81
Ca (mg)	31	41	10
P (mg)	290	306	160
Essential amino acid (mg/g of N)			
Arginine	220	290	480
Histidine	130	130	130
Lysine	140	170	230
Tryptophan	60	70	80
Phenyl Alanine	420	280	280
Tyrosine	—	180	290
Methionine	180	90	150
Cystine	100	140	90

Table 4.1 (Continued)

Item	Foxtail millet	Wheat (whole)	Rice (raw, milled)
Threonine	190	180	230
Leucine	1040	410	500
Isoleucine	480	220	300
Valine	430	280	380
Vitamins (mg/100 g)			
Thiamin	0.59	0.41	0.41
Niacin	3.2	5.1	4.3
Riboflavin	0.11	0.1	0.04
Vitamin A (carotene) (μg/100g)	32	64	0
Vitamin B6	—	0.57	—
Folic Acid	15	36.6	8
Vitamin B5	0.82	—	—
Vitamin E	31	—	—
Micronutrients (mg/100 g)			
Fe	2.8	5.3	0.7
Zn	2.4	2.7	1.4
Mg	81	138	90
Na	4.6	17.1	—
K	250	284	—
Cu	1.4	0.68	0.14
Mn	0.6	2.29	0.59
Mb	0.07	0.051	0.058
Cr	0.03	0.012	0.004
S	171	128	—
Cl	37	47	—
Fatty acids			
Palmitic	6.4	24.5	15
Palmoleic	—	0.8	—
Stearic	6.3	1	1.9
Oleic	13	11.5	42.5
Linoleic	66.5	56.3	39.1
Linolenic	—	3.7	1.1

Source: Nutritive value of Indian foods (2007), National Institute of Nutrition, India.

The use of foxtail millet grains as livestock feed is limited, though numerous studies investigating its value in poultry diets have been undertaken. This has been the case in India, where changes in food habits of the rural populations due to easy availability and affordability of fine cereals, has resulted in a greater availability of millet grains for feed

use (Rao *et al.*, 2000). Foxtail millet may also appear as a less expensive energy source for livestock when maize prices increase (Rao *et al.*, 2004). In developed countries, the grain is mainly used as bird feed. Products from foxtail millet processing, such as the bran resulting from de-hulling, can also be used in animal feeds (Brink, 2006; Heuzé *et al.*, 2015).

Foxtail millet because of its self-pollinating nature, small diploid genome size (~515 Mb) and low content of repetitive DNA, and close phylogenetic relationships with several important bio-fuel crops, such as switchgrass, Napier grass and pearl millet has been considered to be an appropriate model species for bio-fuel crops (Lata *et al.*, 2013). It is also an excellent model species for studies of C4 photosynthesis and abiotic stress tolerance mechanisms, especially for salinity and dehydration stresses (Li and Brutnell, 2011; Lata *et al.*, 2013). The recent release of its genome sequence by Beijing Genomics Institute, China, and the US Department of Energy—Joint Genome Initiative has put the crop on a fast-track to transforming into a model for studying functional genomics and to probe plant architecture, genome evolution, drought tolerance and physiology in the bioenergy grasses (Dekker, 2003; Diao, 2011; Bennetzen *et al.*, 2012; Lata *et al.*, 2013).

4.2 Origin and Taxonomy

Foxtail millet has the longest history of cultivation among the millets, having been grown in China since sometime in the sixth millennium BC. Some records from China indicate that foxtail millet originated there, while other varieties arrived in China from Africa. Carbonised foxtail millet has been identified in archaeological sites in China, with various reports of origination date. Its planting has been mentioned in Chinese records as early as 2700 BC (Vinall, 1924). Foxtail millet was the most important plant food in the Neolithic culture in China, and its domestication and cultivation was the earliest identifiable manifestation of this culture, the beginning of which has been estimated at over 4000 years ago (Chang, 1968). The earliest archaeological remains of foxtail millet are found in Northern China, in the Cishan and Peiligang ruins in the Yellow River Valley, approximately 7400 years before present and 7935 years before present, respectively (Li and Wu, 1996). A succession of sites in the Yiluo valley of Northern China show that foxtail millet was the dominant grain for 4 millennia, before becoming part of the current North China farming-tradition of millets, wheat and legume rotations by 3600–3300 years before present (Lee *et al.*, 2007).

In Russia, foxtail millet has been cultivated since ancient times and there is evidence that it was grown as long as 1500 years ago (Movsisyants, 1950). According to Vavilov (1926), the principal centre of diversity for foxtail millet is East Asia, including China and Japan. Based on the archaeological evidence, Harlan (1975) suggested an independent domestication centre in Europe, and de Wet and Harlan (1975) suggested that foxtail millet was domesticated in China and in Europe independently. Though several hypotheses concerning the origin and domestication of foxtail millet have been proposed, a multiple domestication hypothesis (de Wet *et al.*, 1979) is widely accepted. It probably spread from the highlands of Central China or Central Asia to India and European countries (Oelke *et al.*, 1990). Foxtail millet can now be found all over the world.

The cultivation of foxtail millet about 4000 years ago in Europe, itself supports the hypothesis of a second centre of domestication in Europe, since no archaeological evidence of migration or exchange between Europe and China during the Neolithic period

has ever been discovered. The crop in Europe, however, is more recent than that in China and is associated in European archaeological sites with cereals coming from the Middle East. The use of different isozyme systems such as esterase (Kawase and Sakamoto, 1984) did not lead to any clear conclusion regarding the history of foxtail millet domestication (Wang *et al.*, 1995). Furthermore, Li *et al.* (1995), using morphological traits, suggested that there was a third centre of domestication in an area ranging from Afghanistan to Lebanon (Le Thierry d'Ennequin *et al.*, 1999).

The geographical origin of foxtail millet based on cytological studies indicated that the wild ancestor of foxtail millet is *S. viridis* (Li *et al.*, 1945). Its diversity, wide geographical distribution and strong competitiveness in disturbed habitats make the green foxtail millet a highly successful weed. It spontaneously hybridises with *S. italica* (Li *et al.*, 1945). Phylogenetic analyses using both chloroplast and nuclear genes show foxtail and green millets (*S. viridis*) as close relatives (Giussani *et al.*, 2001; Doust *et al.*, 2007), consistent with the hypothesis that foxtail millet is a domesticated version of green millet (Li *et al.*, 1945; de Wet and Harlan, 1975; Wang *et al.*, 1995; Le Thierry d'Ennequin *et al.*, 1999). Three main groups of cultivated foxtail millet gene pool were suggested, namely, Chinese (from China, Japan and Korea), tropical (from Taiwan, India and Kenya) and the European group, on the basis of isozyme studies in accessions of *S. italica* and *S. viridis*, respectively (Jusuf and Pernes, 1985; Panaud, 2006). Though cytological and hybridisation studies have shown that green foxtail is the wild ancestor of foxtail millet (Kihara and Kishimoto, 1942; Li *et al.*, 1942), the geographical origin of domesticated foxtail millet could not be determined from the distribution of green foxtail, since it is found commonly in various areas of Europe and Asia (Li *et al.*, 2012).

The genus *Setaria* belongs to the tribe Paniceae in the sub-family Panicoideae, and consists of approximately 125 species extensively dispersed in warm and temperate regions worldwide (Dwivedi *et al.*, 2012). It contains crops, wild and weed species with different breeding systems, life cycles and ploidy levels (Li *et al.*, 2012). Foxtail millet is the most economically valuable of the genus (Baltensperger, 1996). Green foxtail millet, *S. viridis*, the closest wild relative (de Wet *et al.*, 1979) is a weedy annual. Yellow foxtail (*S. pumila* (Poiret) Roemer & Schultes or *S. glauca* (L.) P. Beauv.) is also occasionally cultivated as a cereal crop across southern India. Bristly foxtail (*S. verticillata* (L.) P. Beauv.) has been harvested as a wild cereal by local people in Africa, Asia, South America and Australia (de Wet *et al.*, 1979; Austin, 2006). Bristly foxtail, giant foxtail (*S. faberii* Herrm), green foxtail (*S. viridis* (L.) P. Beauv.), knotroot foxtail (*S. geniculata* (Lamarck) Beauv.) and yellow foxtail are the most widely distributed weedy foxtail species worldwide (Rominger, 1962). Some of these wild forms are difficult to control in crop fields even with herbicides (Dekker, 2003). Malm and Rachie (1971) thoroughly reviewed the domestication of foxtail millets and the taxonomy. They report the use of subspecies by Scholz (1960) based on papillae on the epidermal cells of the glumes (*moharia*) and no papillae (*maximas*). Understanding the phylogenetic relationships in the *Setaria* complex is useful for successful parent selection and hybridisation for breeding, as well as to organise germplasm, identify cultivars and ensure sampling from a broad range of genetic variability (Li *et al.*, 1998).

On the basis of inflorescence morphology foxtail millet is classified into two species *S. pumila* and *S. italica*. The species *S. italica* is classified into two sub-species *viridis* and *italica*. The sub-species *italica* is classified into three races and ten sub-races on the basis of inflorescence morphology (Prasada Rao *et al.*, 1987). The race *Moharia* (common in Europe, Southeast Russia, Afghanistan and Pakistan) is divided into sub-races *Aristata*,

Fusiformis, *Glabra*; race *Maxima* (common in Eastern China, Georgia (Eurasia), Japan, Korea, Nepal and Northern India (it has also been introduced in the USA)) is divided into sub-races *Compacta*, *Spongiosa*, *Assamense*; and race *Indica* (remaining parts of India and Sri Lanka) is divided into sub-races *Erecta*, *Glabra*, *Nana* and *Profusa*.

Foxtail and green foxtail millets are genetically close to several other millets and cereals, such as pearl millet (*Pennisetum glaucum*), common millet (*Panicum miliaceum*), maize (*Zea mays*), sugarcane (*Saccharum officinarum*) and sorghum (*Sorghum bicolor*). They are also closely related to candidate bio-fuel grasses with complex genomes, such as switch grass (*Panicum virgatum*) and Napier grass (*Pennisetum purpureum*) (Doust *et al.*, 2009). They are in the same sub-family as maize, sugarcane and sorghum, but in a different tribe, having diverged from the maize lineage roughly 28 million years ago (Gaut and Doebley, 1997). Green foxtail millet is believed to be one of the world's worst weeds of the arable land (Harlan, 1992). Domestication of foxtail millet led to the production of larger inflorescences with a more complex branching pattern, as well as a reduction in basal (tillering) and axillary vegetative branching (Harlan, 1992; Doust and Kellogg, 2002; Doust *et al.*, 2004).

An interesting feature of modern foxtail millet diversity is the global distribution of two phenotypically different varieties – the waxy and the non-waxy grain type (Van *et al.*, 2008). Waxiness is caused by lowered levels of amylose in the grain endosperm, which gives the grain a sticky texture when cooked (Van *et al.*, 2008). Geographical occurrence of these two types of foxtail millet varieties coincides with the ethnological preferences of local human populations. In East and Southeast Asia, where some local communities prefer sticky cereals (e.g. glutinous rice), the waxy foxtail millet phenotype is more commonly found. The non-waxy grain phenotype is more widespread, cultivated throughout Eurasia and parts of Africa (Kawase *et al.*, 2005). Control of the phenotype is due to transposable-element (TE) insertion events interrupting amylose production, and foxtail millet has been suggested as a model for studying TE-mediated evolution (Kawase *et al.*, 2005).

Only limited studies on genetic diversity and population structure have been reported in foxtail millet. Wang *et al.* (2012) reported four sub-groups in 250 landraces, which are in good accordance with eco-geographical distribution in China. Hirano *et al.* (2011) did population structure analysis by transposon display, which classified foxtail millet landraces into eight clusters that are closely related with geographic origins and suggest a monophyletic origin of foxtail millet domestication. Liu *et al.* (2011) investigated the population structure of foxtail millet and identified six groups, which matches with their pedigree information, in general, but not with their geographic origins.

4.3 Germplasm Resources and Utilisation

4.3.1 International Status

There is wide genetic diversity available in foxtail millet, and characterising these resources is a prerequisite for the genetic improvement of its cultivars. Collection of foxtail millet landraces in China started in the 1920s and more than 26000 accessions, 90% of which are landraces, are currently preserved at the Chinese National Genebank in Beijing (Doust *et al.*, 2009). More than 30000 germplasm accessions of foxtail millet have been conserved in different germplasm consortium all over the world viz., Chinese

National Gene Bank (CNGB), (26670 accessions), International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru (1535 accessions from 26 countries), National Institute of Agro-biological Sciences (NIAS), Tsukuba, Japan (1279 accessions) and the Plant Genetic Resources Conservation Unit (PGRCU), USDA-ARS (766 accessions) (Doust *et al.*, 2009) (Table 4.2). At the Consultative Group for International Agricultural Research (CGIAR) genebanks 9494 accessions of foxtail millet have been conserved, while at Svalbard Genebank, Norway 1442 accessions have been conserved (Padulosi *et al.*, 2009). Phenotypic characterisation of the collected materials has indicated that foxtail millet germplasm is highly diverse (Li and Wu, 1996; Reddy *et al.*, 2006). As in finger millet, there is an abundance of foxtail millet germplasm available to the scientific community (Goron and Raizada, 2015).

4.3.2 National Status

At National Genebank maintained at the National Bureau of Plant Genetic Resources, New Delhi, a total of 4473 accessions including 94 exotic accessions have been conserved,

Table 4.2 Status of some of the significant foxtail millet germplasm collections.

Organisation	Location	No. of accessions	Resource
Chinese National Genebank (CNGB)	Beijing, China	26670	Wang *et al.* (2012) http://icgr.caas.net.cn/cgris_english.html
National Bureau of Plant Genetic Resources (NBPGR)	New Delhi, India	4473	Umesh Chandra *et al.* (1987) www.nbpgr.ernet.in
ORSTOM-MONTP	Montpellier, France	3500	Dwivedi *et al.* (2012)
Project Coordinating Unit, AICSMIP	Bangalore, India	2821	http://www.smallmillets.res.in/
Svalbard Global Seed Vault	Norway	2505	http://www.nordgen.org/sgsv/
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)	Patancheru, India	1535	www.icrisat.org/crop-foxtailmillet.htm
National Institute of Agrobiological Sciences (NIAS)	Kannondai, Japan	1299	http://www.gene.affrc.go.jp/index_en.php
North Central Regional Plant Introduction Station, USDA-ARS	Ames, USA	1000	Dwivedi *et al.* (2012)
Biologie Végétale Appliquée, Institut Louis Pasteur (IUT)	l'Argonne-Strasbourg, France	850	Dwivedi *et al.* (2012)
Kenya Agricultural Research Institute (KARI)	Muguga, Kenya	772	Dwivedi *et al.* (2012)
Plant Genetic Resources Conservation Unit (PGRCU) of the USDA-ARS	Griffin, USA	762	http://www.ars-grin.gov/npgs/index.html
Tamil Nadu Agricultural University (TNAU)	Coimbatore, India	741	www.tnau.ac.in/
Estación de Iguala, Instituto Nacional de Investigaciones Agrícolas (INIA)	Iguala, Mexico	350	Dwivedi *et al.* (2012)

and catalogue has been published (Umesh Chandra *et al.*, 1987). At the University of Agricultural Sciences (UAS), Bangalore, India, National Active Germplasm Site (NAGS) for small millets was established in 1992. A total of 2821 accessions of foxtail millet, mainly landraces and cultivars from 13 states in India, Afghanistan, the United States, Russia, Turkey, Taiwan and African countries are being conserved at UAS, Bangalore. Out of these, catalogue on evaluation of 1482 accessions for 14 and 11 qualitative and quantitative descriptors, respectively, has been published. The Tamil Nadu Agricultural University (TNAU), Coimbatore, India, is also conserving germplasm resources of foxtail millet. Characterisation efforts have revealed considerable diversity among 741 accessions maintained for all the agronomic characters (Nirmalakumari and Vetriventhan, 2010).

4.3.3 Core Collection

As the grain yield levels of foxtail millet are low in comparison with other staple cereals, greater use of diverse germplasm in breeding is suggested as a means to improve the productivity of the crop. To utilise the diversity concealed in the ICRISAT foxtail millet collection from 26 countries in research, Upadhyaya *et al.* (2008) developed a core collection (10% of the entire collection) consisting of 155 foxtail millet accessions using passport information and data on 23 morphological descriptors on 1474 accessions. The germplasm accessions were stratified into three taxonomic races as *indica*, *maxima* and *moharia*. Principal coordinate analysis was performed on 12 qualitative traits for each of the biological races, separately that resulted in the formation of 29 clusters. From each cluster, 10% of the accessions were selected to constitute a core collection of 155 accessions. Different statistical analyses indicated that the diversity from the entire collection was optimally represented in the core collection.

In the core collection developed, the accessions from race *indica* were predominant (102 accessions; 65.8%), while those from race *maxima* were 15.5% (24 accessions) and *moharia* were 18.7% (29 accessions). The predominant sub-races were *nana* (81 accessions, 52.2%) and *glabra* (16 accessions, 10.3%) in race *indica*; *compacta* (20 accessions, 12.9%) and *spongiosa* (three accessions, 1.9%) in race *maxima*; and *glabra* (17 accessions, 10.9%) and *aristata* (11 accessions, 7.1%) in race *moharia*, while accessions from other sub-races were represented by 0.6–2%. Geographically, accessions from South and Southeast Asia were represented by 66.5% (103 accessions), while those from West Asia and East Asia were 12.9% (20 accessions) and 7.1% (11 accessions), respectively. Europe and Africa were each represented by 2.6% (four accessions), while those from Russia and Commonwealth of Independent States (CIS) countries were only 4.5% (seven accessions) (Upadhyaya *et al.*, 2008).

The abundant variation in the foxtail millet core collection provides an important reservoir of genetic diversity and potential sources of beneficial alleles for its improvement (Upadhyaya *et al.*, 2008). From the core collection, 25 foxtail millet accessions with better grain yield and early maturity have been identified. Twenty-three accessions flowered significantly early (25–40 days) and 19 (990–1760 kg/ha) produced greater grain yields than control SiA 326 (48 days; 980 kg/ha). Cluster analysis based on the first five principal components indicated that the selected accessions were diverse than the control cultivars. Some of the promising accessions of foxtail millet are given in Table 4.3.

Multi-location evaluation of core collection (155 accessions) for trait-specific germplasm has resulted in identification of a number of diverse germplasm accessions with agronomically (earliness and high grain yield) and nutritionally (high seed protein,

Table 4.3 Promising germplasm accessions and other entries of foxtail millet.

Trait	Promising accessions
High grain yield	ISe 710, ISe 969, ISe 1820, ISe 388, ISe 842, ISe 49, ISe 1888, ISe 90, ISe 364, ISe 1767, ISe 362, ISe 1808
Early flowering	ISe 1151, ISe 1161, ISe 1161, ISe 1201, ISe 1227, ISe 1227, ISe 1234, ISe 1254, ISe 1258, ISe 1286, ISe 1286, ISe 1312, ISe 1320, ISe 1335, ISe 1647, ISe 1658
Tall	ISe 769 and ISe 1434
High tillering (more basal tillers)	ISe 1433 and ISe 1434 , ISe 796, ISe 1009, ISe 1026, ISe 1134, ISe 1408 and ISe 1892
High panicle exertion	ISe 719, 827, 1151, 1161, 1163, 1227, 1286, 1312, 1320, 1547, 1563, 1593 and 1655
Longer inflorescence length and grain yield	ISe 785, ISe 1780 , ISe 1433 and ISe 1434, ISe 1593, ISe 701
High protein (≅17%),)	ISe 1312, ISe 1227, ISe 1789, ISe 1254, ISe 1541, ISe 827, ISe 748, ISe 1305, ISe 1647, ISe 1335, ISe 751, ISe 1118, ISe 1134
High Ca (≥200 mg/kg Ca)	ISe 1227, ISe 1181, ISe 1059, ISe 1419, ISe 827, ISe 751, ISe 1474, ISe 1685, ISe 1277, ISe 1418, ISe 1161
High Fe (≥62 mg/kg Fe)	ISe 1151, ISe 1286, ISe 1400, ISe 1305, ISe 1332, ISe 1059, ISe 1581, ISe 1320, ISe 748, ISe 1387, ISe 1511
Zn (≥55 mg/kg Zn)	ISe 1286, ISe 748, ISe 1387, ISe 195, ISe 1134, ISe 1408, ISe 1419, ISe 1161, ISe 900, ISe 1820, ISe 1511
Blast (leaf spot) resistance	ISe 1181, ISe 1547, ISe 1067, ISe 1575
Sheath blight resistance	RFM 29, RFM 84, GS 162, GS 1204, SiA 1827, SiA 2566, SiA 2667, SiA 2863, ISe 1488
Shoot fly tolerant	SIA 1538, SIA 1533, SIA 1507, SIA 1581, SIA1566, SIA 1549
Other promising accessions	ISe 941, ISe 905, ISe 781, ISe 1363, ISe 426, ISe 1135, ISe 989, ISe 1013, ISe 1042, ISe 1077, ISe 184, ISe 275, ISe 941, ISe 905, ISe 781, ISe 1363, ISe 426, ISe 1135, ISe 989, ISe 1013, ISe 1042, ISe 1077, ISe 148, ISe 275

calcium, iron and zinc) superior traits. The hierarchical cluster analysis of data using phenotypic distances resulted in 25 clusters, from each cluster, ~10% or a minimum of one accession was selected to form a mini core, which comprised of 35 accessions. Statistical tools revealed that the mini core indeed captured adequate variability from the core collection. This mini core collection is an ideal pool of diverse germplasm for studying population structure and diversity, and identifying new sources of variation for use in breeding and genomics studies in foxtail millet (Upadhyaya *et al.*, 2011).

The foxtail millet core collection established at ICRISAT is being used for different genetic and genomic studies. Fingerprinting of these 155 accessions using 84 markers (81 SSRs and three EST-SSRs) showed the presence of greater molecular diversity in the foxtail millet core collection (Vetriventhan *et al.*, 2012). The 84 markers detected a total of 1356 alleles with an average of 16.14 alleles (4–35) per locus. Of these, 368 were rare alleles, 906 common alleles and 82 the most frequent alleles. Sixty-one unique alleles that were specific to a particular accession and useful for germplasm identification were

also detected. The genetic diversity of foxtail millet was fairly correlated well with racial classification, and the race *indica* showed a greater genetic distance from the races *maxima* and *moharia*. Two hundred and fifty pairs of genetically most diverse accessions were identified. This large molecular variation observed in the core collection could be utilised effectively by breeders or researchers for the selection of diverse parents for breeding cultivars and the development of mapping populations (Vetriventhan *et al.*, 2012). In another study, Vetriventhan *et al.* (2014) genotyped the ICRISAT foxtail millet core collection using 72 SSR markers and investigated genetic diversity, population structure and linkage disequilibrium (LD). A high degree of molecular diversity with an average of 16.69 alleles per locus and LD decay of less than 40 cM of genetic distance in the accessions were observed and the study proved that the foxtail millet core collection of ICRISAT is an invaluable resource for trait association mapping, crop breeding and germplasm management. STRUCTURE analyses classified the accessions into four sub-populations based on SSR allelic diversity. The neighbour-joining clustering and the principal coordinate analysis were in accordance with the racial classification. The distribution of molecular genetic variation among and within the four sub-populations and three races showed high degree of variability within each group, and low level of genetic distance among the groups (Vetriventhan *et al.*, 2014).

4.4 Genetics and Cytogenetics

4.4.1 Inheritance of Agronomic Traits

Information on the inheritance of important agronomic traits of foxtail millet, including susceptibility to key diseases, is limited. Genetic studies have been conducted on several morphological characters and disease response (Malm and Rachie, 1971). Most of the previous work has focussed on estimating broad-sense heritability and realised genetic gains, with little attention directed to measuring levels of heterosis or to assessing the relative importance of different types of gene action (Athwal and Singh, 1966; Singh and Athwal, 1966; Gill and Randhawa, 1975; Vishwanatha *et al.*, 1981; Gurunadha Rao *et al.*, 1984; Prasada Rao *et al.*, 1985).

Darmency *et al.* (1987) studied 19 morphological and reproductive descriptors using different generations of an inter-specific cross between the cultivated foxtail millet and its wild relative *S. viridis*. The multivariate analysis of the diploid F2 showed two complex associations of characters: one concerning developmental traits (organs dimensions and flowering) and the other dealing with taxonomical characteristics (tillering, seed shedding and seed weight). The tetraploidisation resulted in a shift in characteristics towards the crop species, especially a two-fold increase in seed weight. However, artificial tetraploidisation has often resulted in altered characteristics, which have precluded the commercial use of polyploid cultivars in most crops (Dewey, 1980). There is only rare record of cultivation of the polyploid *S. glauca* as a crop (Kimata *et al.*, 2000), but this species is not genetically related to the foxtail millet gene pool (Benabdelmouna *et al.*, 2001). Non-additive effects were found for most characters, except for the seed shedding, which was found to be encoded by at least four loci. In another similar study, auto-tetraploid material was induced by colchicine treatment of a pure line of foxtail millet and an inter-specific hybrid between foxtail millet and giant green foxtail (Ahanchede *et al.*, 2004). Compared with diploid material, tetraploids

were smaller, flowered later and had a two-fold reduced fertility (number of grain per cm of spike). Grain weight showed 20% increase with polyploidy, but total grain yield had decreased by 46%. Hence, scope of breeding polyploidy lines of foxtail millet that are of agronomic use is limited.

Important agronomic traits in foxtail millet include not only grain yield, days to heading, days to maturity and plant height, but also number of tillers and spike length. When foxtail millet is used as forage, tillering is a desirable trait. However, non-tillering cultivars are preferred for use in producing birdseed because the seeds typically are larger. Spike length also is correlated with seed size. Correlation and path coefficient analysis revealed that straw yield per plant and harvest index were the major determining characters for grain yield among foxtail genotypes (Murugan and Nirmalakumari, 2006). Highest heritability, genotypic coefficient of variation and genetic advance as per cent of mean was recorded in grain yield per plant and the lowest was recorded in days to 50% flowering in another study (Nirmalakumari and Vetriventhan, 2010). Days to 50% flowering, plant height, total number of tillers, number of productive tillers, panicle length and days to maturity exhibited highly significant positive correlations with grain yield. Characters such as flag leaf area and 1000-grain weight were also observed to influence yield. The association of protein content and calcium content with grain yield was in negative direction. The association of carotene with grain yield was negative. So simultaneous improvement of these traits along with grain yield may not be possible (Lakshmi Prasanna *et al.*, 2013).

4.4.2 Genetic Control of Branching

When crops are domesticated from their wild progenitors, reduction in vegetative branching is a common observation, presumably as a result of selection for increased allocation to seeds (Harlan *et al.*, 1973). Doust *et al.* (2004) identified genetic loci responsible for these changes in foxtail millet. Quantitative trait locus (QTL) analysis and comparative genomics revealed that basal branching (tillering) and axillary branching were partially controlled by separate loci, and that the orthologue of *teosinte branched1*, the major gene controlling branching phenotype in maize, had only a minor and variable effect. They identified other candidate genes for control of branching, including a number of hormone biosynthesis pathway genes. The results suggested that similar phenotypic effects may not be produced by orthologous loci, even in closely related species, and that results from well-characterised model systems such as maize must be reviewed critically before being applied to other related species. Several QTL of major effect that control vegetative branching were identified (Doust *et al.* 2004), for each of which hypotheses of candidate genes have been proposed through examining the sequenced rice genome corresponding to the QTL regions on foxtail millet, using common markers mapped on both the rice and foxtail millet genomes.

4.4.3 Genetic Control of Flowering and Inflorescence Branching

Unlike sorghum and maize, which are panicoid crops that were domesticated in short-day environments, foxtail millet was domesticated from green millet (*S. viridis*) in the northern part of China, with more pronounced seasonal changes in photoperiod (Li and Wu, 1996; Bettinger *et al.*, 2010). Green millet is adapted to multiple photoperiod regimes, including both short- and long-day cycles (Holm, 1997; Dekker, 2003).

Inflorescence architecture is one of the most useful and conspicuous characteristics for distinguishing among the nearly 10000 species, and variation in inflorescence architecture is important in determining yield of cereal grains (Doust *et al.*, 2005). Even among closely related species the structure of the inflorescence may vary in the number of branches, the number of orders of branching, and the extent of elongation of various axes (Kellogg, 2000; Doust and Kellogg, 2002). Doust *et al.* (2004) had identified several QTL of major effect that control vegetative branching and for each of these QTL the authors had hypotheses of candidate genes.

Many genes have been found to affect inflorescence development in model system like maize and these are all possible candidates for the control of inflorescence morphology in other grass species, especially those with economic importance. However, developmental evolution of maize may not be representative of other grass species as several aspects of the morphology of maize are highly different within the grasses (Doust *et al.*, 2005).

Grass species differ in many aspects of inflorescence architecture, but in most cases the genetic basis of the morphological difference is unknown. Doust *et al.* (2005) undertook a developmental and QTL analysis of inflorescence differences between grain foxtail millet and its presumed progenitor green millet to investigate the genes underlying the inflorescence morphology. They pointed out that inflorescence differences between these two species were the result of changes in primary branch number and density, spikelet number and bristle (sterile branchlet) number. These differences also account for inflorescence variation within the group of more than 300 species that share the presence of bristles in the inflorescence. The authors detected 14 replicated QTL for the above four inflorescence traits, and these are suggested to represent genes that control differences between the species. The location of QTL that control inflorescence branching, was compared to that of vegetative QTL. Comparative mapping using common markers from rice and maize allowed a number of candidate genes from maize to be localised to QTL regions in the Setaria genome. Searches of regions of the sequenced rice genome orthologous to QTL regions on foxtail millet identified a number of transcription factors and hormone pathway genes that may be involved in control of inflorescence branching (Doust *et al.*, 2005).

The genetic control of flowering time and QTL that control differences in flowering time between foxtail and green millet in a variety of environments were investigated by Mauro-Herrera *et al.* (2013) using a recombinant inbred line mapping population derived from a cross between foxtail and green millet. Many of the QTL identified across trials undertaken in different environments co-localised, suggesting that the genetic control of flowering in *Setaria* is robust across a range of photoperiod and other environmental factors. A detailed comparison of QTL for flowering in genus *Setaria*, sorghum and maize indicated that several of the major QTL regions identified in maize and sorghum are syntenic orthologs with *Setaria* QTL. Several *Setaria* QTL intervals were composed of multiple syntenic blocks, suggesting that observed QTL represent multiple tightly linked loci.

4.4.4 Cytogenetic Studies

A complete set of nine primary trisomics ($2n + 1$) for cv. 'Yugu No. 1' of foxtail millet was identified cytologically from progenies derived from crosses between auto-triploids ($2n = 2x = 27$) and their diploid counterparts. Five auto-triploid plants were identified

from 2100 seedlings derived from 4*x*–2*x* crosses; the reciprocal crosses (2*x*–4*x*) failed to produce auto-triploids. Auto-triploids grew vigourously and were morphologically very similar to diploids. The primary trisomics ($2n = 2x = 19$) constituted ≅ 32.5% of the total progeny from the 3*x*–2*x* crosses, whereas 59.8% of the descendants were aneuploids with chromosome numbers ranging from 20 (double trisomics and tetrasomics) to 37 ($2n = 4x + 1$; or auto-tetraploid with one additional chromosome). The nine primary trisomics identified were self-fertile; seven had characteristic morphology, whereas trisomics VIII and IX resembled the disomics. The seed set for trisomic V was the lowest (20%), and trisomic VIII the highest (74%). Other aneuploids with 20 or more somatic chromosomes were either self-sterile or partially fertile with various, but low, levels of seed set. Each of the primary trisomics showed its unique transmission rate when self-pollinated; trisomic IX had the highest (45.8%), whereas trisomic V had the lowest (19.6%) transmission rate (Wang *et al.*, 1999).

4.4.5 Molecular Markers and Genetic Maps

In foxtail millet, two complete genetic maps were created in the late 1990s using RFLP markers (Devos *et al.*, 1998; Wang, Devos *et al.*, 1998). The first was generated from an inter-varietal cross within foxtail millet, whereas the second was generated in an inter-specific cross between foxtail millet and green millet. Wang, Devos *et al.* (1998) was the first to report markers in foxtail millet, where an RFLP-based map consisting of 160 loci was constructed in an inter-varietal cross. These markers were proven useful in constructing comparative genetic maps of foxtail millet and rice (Devos *et al.*, 1998). Although wide crosses often lead to a reduction in recombination, map lengths were found very similar in the intra- and inter-specific crosses (Wang, Devos *et al.*, 1998). The inter-specific map used foxtail millet markers and 111 rice and five wheat RFLPs. The comparison of the position of common markers on the foxtail millet and rice genetic maps showed that the two genomes were highly colinear, with six foxtail millet chromosomes that were orthologous to single rice chromosomes and three foxtail millet chromosomes that were each orthologous to two rice chromosomes (Devos *et al.*, 1998).

Jia *et al.* (2007) demonstrated the importance of EST-derived simple sequence repeat (EST-SSR) markers in foxtail millet. Thirty SSRs were identified in 1213 foxtail millet EST sequences and primers were designed for 26 SSRs. Of the 26 primers, two primers showed polymorphism in 12 foxtail millet and a green foxtail accessions with 10 alleles detected for four loci at an average of 2.5 alleles per locus (Jia *et al.*, 2007). The first SSR-linkage map of foxtail millet was reported by Jia, Zhang *et al.* (2009). The authors constructed two genomic libraries enriched for (GA)n and (CA)n and identified 100 polymorphic SSR markers. Further, the SSR linkage map was constructed by integrating 81 developed SSR markers with 20 RFLP anchored markers, and the genetic diversity was analyzed in 40 foxtail millet accessions (Jia, Zhang *et al.*, 2009). Heng *et al.* (2011) reported 45 polymorphic SSR markers from RAPD-enriched library and showed their applications in genetic diversity and cross-species transferability analyses. Using a drought- and salt-tolerant foxtail millet cv. 'Prasad', Gupta *et al.* (2012) constructed (CA)n, (AAC)n and (ATG)n enriched library to develop around 172 novel genomic SSRs. In addition to demonstrating their use in genetic studies, comparative mapping of the developed genomic SSRs onto the genomes of rice, maize and sorghum had also been performed (Gupta *et al.*, 2012). The same group had also constructed a (GA/CT) n microsatellite-enriched library to develop 78 SSR markers and substantiated the role

of these markers in diverse genotyping applications, resolving QTL, establishing phylogenetic relationships and transferability among several important grass species (Gupta *et al.*, 2013). Using 50 SSR markers reported by Jia, Zhang *et al.* (2009) and Pandey *et al.* (2013) in 184 foxtail millet accessions from diverse geographical locations, significant association ($R^2 = 18\%$) of eight SSR markers ($p < 0.01$) with nine agronomic traits (overall 18% association potential) was revealed by Gupta *et al.* (2014). These trait-associated SSR markers, can be used for identification of genes/QTL regulating the agronomic traits upon validation, and eventually for marker-assisted genetic improvement in foxtail millet. The SSR b129 along with SSR p75 on chromosome 5 showed significant association with grain weight and yield traits. Also, SSRs b225 and p61 showed association with inflorescence compactness and grain shape, respectively, which could also be considered as candidate markers to study grain quality and yield (Muthamilarasan and Prasad, 2015).

Gupta *et al.* (2011) reported 98 potential intron length polymorphic (ILP) markers in foxtail millet by exploiting the EST sequences of dehydration- and salinity-stressed suppression subtractive hybridisation (SSH) libraries (Lata *et al.*, 2010; Puranik *et al.*, 2011). They also demonstrated the high level of cross-species transferability and the utility of these ILP markers in germplasm characterisation and in studying genomic relationships in millet and non-millet species (Gupta *et al.*, 2011). Further, Muthamilarasan, Theriappan *et al.* (2013) and Muthamilarasan, Suresh *et al.* (2013) have developed 5123 ILP markers and demonstrated their utilities in germplasm characterisation, transferability, phylogenetics and comparative mapping studies in millets, cereals and bio-energy grass species (Muthamilarasan and Prasad, 2015).

4.5 Reproductive Biology

4.5.1 Inflorescence Morphology

Foxtail millet forms a slender, erect, leafy stem varying in height from 1–5 ft, and produces an inflorescence terminally (Plate 4.1). There is a very quick transition period from vegetative growth to flower-development (Baltensperger, 1996). The inflorescence is a spike with short side branches bearing spikelets and bristles (Plate 4.2). The compressed hairy panicle, 10–40 cm long with a diameter of 2–4 cm, resembles yellow foxtail, green foxtail, or giant foxtail. The spikelets are glabrous, elliptic to obovate, consists of a pair of glumes that embrace two minute flowers (about 1 mm in length); the lower one sterile and the upper one bisexual and fertile, with three stamens and a long oval smooth ovary with two long styles, that terminate in a brush like stigma (Hector, 1936). A spikelet is about 2 mm long. Both foxtail millet and green foxtail species produce sterile inflorescence branches, commonly called bristles. From one to three bristles develop at the base of each spikelet (Vinall, 1924). The length and density of these bristles on the panicle depend on the varieties. The bristles generally terminate the various inflorescence axes and also appear to be approximately paired with spikelets (Doust and Kellogg, 2002). When first initiated, spikelets and bristles appear to be paired and, if all spikelets grew to maturity, the numbers of spikelets and bristles would be approximately equal. However, a number of spikelets cease development and persist as tiny rudiments.

The panicle can be compared to a primary cluster made up of several secondary clusters (Sc), small rounded spikes. The second-order clusters are made up of third-order

Plate 4.1 Foxtail millet – field view. (*See color plate section for the color representation of this figure*.)

Plate 4.2 Foxtail millet – a single panicle. (*See color plate section for the color representation of this figure*.)

clusters (Tc), and are arranged in a helicoidal disposition on the panicle. The third-order clusters consist of a few spikelets (up to 10). The secondary clusters are generally sparse at the bottom of the inflorescence and densely aggregated at the top (Blaise *et al.*, 1992). A diagrammatic description of the mature panicle and a spikelet diagram are given in Figures 4.1a and 4.1b.

4.5.2 Anthesis, Flowering Behaviour and Seed

Anthesis in foxtail millet generally takes place near midnight and in the morning, but varies significantly with the environment (Malm and Rachie, 1971). The rate of anthesis is generally favoured by low temperature and high humidity. Morphology and anthesis behaviour make foxtail millet one of the most difficult species to cross-pollinate. Foxtail millet is largely a self-pollinating species, with cross-pollination averaging about 4% (Li *et al.*, 1935). Out-crossing rates have been estimated from 0.0 to only 1.4% for plants separated by 0.30 m (Till-Bottraud *et al.*, 1992), although Li *et al.* (1935) reported rates as high as 5.6% for some varieties under certain conditions. Siles, Baltensperger and

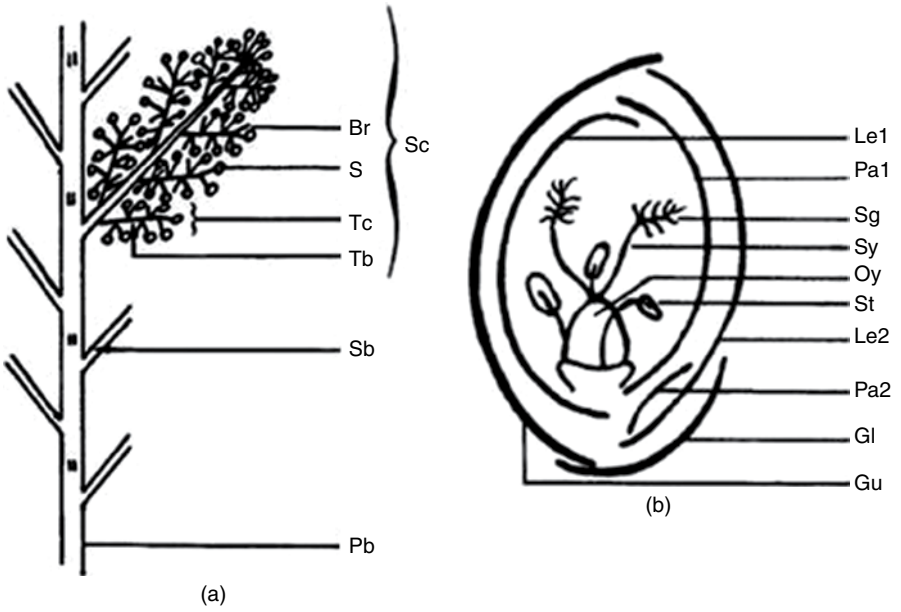

Figure 4.1 (a) Organisation of a mature panicle (basal 1/3 region) of foxtail millet. Pb – primary branch; Sb – secondary branch; Tb – tertiary branch; Sc – secondary cluster; Tc – tertiary cluster; S – spikelet; Br – bristle. (b) Spikelet diagram. Gl – lower glume; Gu – upper glume; Le1 – lemma of floret 1; Le2 – lemma of floret 2; Pa1 – palea of floret 1; Pa2 – palea of floret 2; St – stamen; Oy – ovary; Sg – stigma; Sy – style.

Nelson (2001) described an artificial technique of hybridisation that resulted in 67.5% hybrid seed set per flower crossed.

The small seeds, around 2 mm in diameter, are encased in a thin, papery hull, which is easily removed after threshing. The seed coat and husk of foxtail are generally of single entity with glossy appearance. The grains are very similar to paddy rice in grain structure. They contain an outer husk, which needs to be removed in order to be used. Seed colour varies greatly between genotypes, and usually yellowish in colour.

4.6 Breeding Objectives

4.6.1 Agronomic Traits

Crop improvement in small millets as a whole have received less priority in the past, both at national and international levels. The ultimate goal of breeding small millets remains improvement of grain yield including maximisation of biomass and the harvest index. Foxtail millet mature early, and, therefore, provide one first harvest for human consumption. Genotypes need to be tailored for maturity-early, mid-late and late, depending on the location-specific requirements of soil, rainfall, temperature, humidity, day length and cropping patterns (Harinarayana, 1989). One of the important selection needs is fertiliser use efficiency, particularly nitrogen, both native and applied apart from enhanced water-use efficiency. Breeding dwarf varieties is an objective of intensive

cultivation. Post-harvest technology demands free threshing grain for minimising human drudgery (Harinarayana, 1989). Seed colour may also be an important factor if grain is used for bird feed. Panicle size is another criterion as large individual heads are preferred for caged birds (Baltensperger, 2002).

4.6.2 Biotic and Abiotic Factors

One of the major constraints for the production of foxtail millet, especially in Northern China and India, is blast disease caused by pathogenic fungus, *Magnaporthe grisea* (Nakayama *et al.*, 2005). Blast affects both forage and grain production in foxtail millet. Symptoms of the disease appear as circular spots with straw-coloured centres on leaf blades. The spots are small and scattered, and are 2–5 mm in diameter, surrounded by a dark brown margin. When the disease appears in severe form during humid weather conditions, especially with a dense plant stand, the leaves wither and dry. Plants are infected at all growth stages (Gaikwad and D'Souza, 1986); lower leaves are the most severely affected. Node, neck and stem tissues are also infected in addition to leaf sheaths. The pathogen is variable, but highly specialised in its host range. Thus, *M. grisea* strains from rice or any other hosts do not infect foxtail millet, and *vice versa*. Other frequently occurring diseases in foxtail millet are sheath blight, downey mildew and rust. Another important disease affecting foxtail millet is leaf spot, which is caused by at least three species of *Helminthosporium*, that is, *H. setariae* Sawada, *H. turcicum* Pass. and *H. carbonum* Ullstrup (Haenseler, 1941; Robert, 1962).

Among the insect pests, shoot fly (*Atherigona atripalpis* wiede) is one of the important pests in foxtail millet. Shoot fly do not prefer the genotypes possessing lower moisture, crude protein and total sugar content for its oviposition and dead heart infestation (Sanjeev *et al.*, 2011), and hence these traits can be used as selection criteria in breeding efforts aimed at shoot fly tolerance. Foxtail millet is known to harbour wheat curl mites (*Eriophyes tullipae* Keifer), which may transmit wheat streak mosaic to winter wheat. Cutting the foxtail millet for hay early and complete removal of stubbles prevent it from acting as a host (Oelke *et al.*, 1990).

Lodging is another important yield- and quality-reducing factor depending on the environmental conditions, and weak stems and poorly developed anchored roots always result in crop lodging. Studies have demonstrated that lodging is associated with stem quality rather than plant height and inter-node length at the stem base. The most important trait that directly impacted on lodging coefficient was mechanical strength of the stem and plant height in the landraces, while the weights of the above- and underground tissues, in combination with mechanical strength of the stem, were the most important contributors to lodging coefficient in the improved cultivars (Tian *et al.*, 2010).

4.7 Breeding Methods

4.7.1 Pure-Line Selection

Pure-line selection remained the most important breeding method for improving performance, particularly grain yield till recently. Single plants were selected from landraces and improved varieties of farmers, and the progeny was tested. Superior progenies,

mostly for earliness, pest and disease resistance and grain yield were evaluated in multi-location trials, and released as varieties. Pure-line selection has resulted in the development and release of maximum number of foxtail millet varieties in India.

4.7.2 Recombination Breeding

Recombination breeding efforts in the early stages of organised crop improvement were very limited, largely due to the anthesis behaviour and difficulty in artificial emasculation and crossing. Very low degree of natural cross-pollination was observed in foxtail millet (Patil, 1952). This has led to the occurrence of natural hybrids in germplasm to some extent. In some of the earliest attempts to enhance the chances of natural cross-pollination, panicles of selected plants were enclosed in a parchment bag before flowering (contact method) (Ayyangar, 1934), which had resulted in a low frequency (1.5%) of true hybrids (Mahishi *et al.*, 1982). The technique of controlled hybridisation with removal of anthers and artificial pollination, though very difficult because of the small flower, started yielding improved cultivars by mid-1990s.

4.7.3 Heterosis Breeding and Male Sterility

Though foxtail millet is mainly autogamous (less than 2% out-crossing), Wang *et al.* (1997) reported that pollen from a 5-m diameter plot could fertilise a fertile variety up to 24 m away, and a male-sterile variety up to 40 m. Pollen competition for available target ovules was observed up to 2 m away from a 1 m diameter pollen source. The ability to hybridise foxtail millet opened other options to breeders besides selecting from landraces. When non-additive gene action is important, either mid- and/or high-parent heterosis may be sufficient to justify the production and use of varietal crosses (Siles *et al.*, 2004). In a study to determine whether sufficient high-parent heterosis is expressed in foxtail millet for grain yield and other key traits, on the basis of the estimate of average heterosis the expected yield of the F_1 generation was 68% greater than the average yield of the parental cultivars. This high level of heterosis for grain yield suggested that varietal crosses or other types of cultivars with relatively high amount of heterozygosity would provide a significant yield benefit over non-hybrid cultivars. Although significant heterotic effects were observed, additive effects were more important. Significant correlations between traits of estimates of additive and/or variety heterosis effects suggested that at least some of the genes controlling grain yield, plant height and spike length were either the same or in coupling phase linkage (Siles *et al.*, 2004).

For exploitation of heterosis various male-sterility lines have been identified in China such as dominant and recessive genic highly male-sterility lines and photo-(thermo-) sensitive nuclear lines (GMS) (Cui *et al.*, 1979; Wang, 1991; Wang *et al.*, 1993, 2002; Zhao *et al.*, 1996; Hao *et al.*, 2009), gene interaction male-sterility lines (GIMS) (Hu *et al.*, 1986), cytoplasmic male sterility (CMS) (Zhu *et al.*, 1991) and cytoplasmic-nuclear male-sterility type (CGMS) (Zhi *et al.*, 2007). Wang *et al.* (2002) considered the male-sterile line 1066A as a genic highly male-sterile line; its inbred seeding rate is about 5%, and the sterility trait was controlled by a recessive gene located on the chromosome VI using primary trisomics positioning method. On chromosome VI, a photo-(thermo-)sensitive male-sterile gene has also been reported by Hao *et al.* (2011). Wang *et al.* (2010) identified a highly genic sterile line Gao146A adapting to spring-sown late maturing ecological zones of China, showing 95% sterility rate and not sensitive to light

and temperature, and the F_1 generation showed fertile reaction and the segregation ratio of fertility to sterility was 3:1 in F_2 generation, which showed that the sterile trait of Gao146A was mainly controlled by a single recessive gene. The recessive gene tentatively named as *ms1*, linked to SSR marker *b234* with genetic distance of 16.7 cM, was mapped on the chromosome VI. Fine mapping of this highly male-sterile gene and improvement of highly male-sterile lines by using molecular-marker-assisted breeding is in progress (Wang *et al.*, 2013). The genetic basis of most male-sterile lines used for the hybrid production is still an area to be elucidated.

Exploitation of heterosis has been proven to be the most important genetic factor in increased foxtail millet yields in China. Hybrid cultivars yielding up to 12 t/ha have been developed. However, most of the currently released Chinese spring foxtail millet male-sterile lines were derived from Chang10A, whose cytoplasm was contributed by Qinyuanmujizui (Liu *et al.*, 2011; Wang, Li *et al.*, 1998), while most summer foxtail millet male-sterile lines were derived from Huangmi1A with the cytoplasm from Dahuanggu (Liu *et al.*, 1996; Liu *et al.*, 2006). Lack of genetic diversity in cytoplasmic sources is a serious problem for effective utilisation of heterosis and use of a single source of cytoplasm in male-sterile lines may pose future threats of epidemics of the disease leading to devastating losses in hybrid crop production due to quick development of specific cytoplasm-related pathogen race. Thus, discovery and deployment of novel types of cytoplasm in male-sterile lines is urgently needed. As in breeding programmes, locally adapted cultivars are usually used as the female parent in crosses, and introduced cultivars from other regions are usually used as male parents to contribute to the nuclear genome, to diversify cytoplasmic types in breeding programmes, introduced cultivars should also be used as female parents in breeding crosses (Liu, Zhang *et al.*, 2014).

4.7.4 Disease Resistance Breeding

Blast is an important disease, and genetic resistance against this disease is being explored. The evaluation of core collection against blast pathogen has resulted in identification of two accessions, ISe 1547 and ISe 1181, of race *maxima* resistant to all the four isolates of *M. grisea* indicating a high level of resistance in race *maxima* to different populations of *M. grisea* adapted to foxtail millet (Sharma *et al.*, 2014). ISe 1419, which is resistant to sheath, neck and head blast against all the four isolates and has leaf blast resistance to two isolates. Some of the blast resistant accessions are ISe 1059, ISe 1181, ISe 1685, ISe 1059 and ISe 1187 (Upadhyaya *et al.*, 2011). Some of the promising accessions (<10%) for sheath blight are RFM 29, RFM 84, GS 162, GS 1204, SiA 1827, SiA 2566, SiA 2667, SiA 2863 and ISe 1488.

4.8 Breeding Efforts in the United States

The majority of the foxtail millet breeding work took place over the period 1930–1965 in the former USSR, China and India (Malm and Rachie, 1971; Rachie, 1975). Foxtail millet breeding has been very limited in the United States until the past several years (Siles, Baltensperger and Nelson, 2001). Nearly all foxtail millet cultivars grown in the United States are the result of selections from landraces rather than designed crosses and selections as foxtail millet is one of the most difficult species to cross-pollinate

(Baltensperger, 1996; 2002). Identification of lines with longer photoperiod and adaptation to eastern Nebraska or adaptation to the High Plains were the preliminary objectives (Baltensperger, 2002). The primary limitation of foxtail millet production in the High Plains of the United States was that it served as a carrier for both the wheat curl mite, the carrier for wheat streak mosaic virus and the virus itself. While adapted cultivars of foxtail millet were not seriously impacted by the disease, the crop served as an over-summering host and adjacent wheat fields were frequently severely impacted. Germplasm has been identified with much higher levels of resistance (Marcon, 1994), and several advanced lines with wheat streak mosaic resistance, increased head size, and improved seed yield have been developed (Siles, Baltensperger, Nelson *et al.*, 2001).

4.9 Breeding Efforts in China

Many regional breeding organisations were established during the 1950s in China. Since the 1920s landraces of foxtail millet were collected and selections were carried out; by the end of the 1940s, several varieties such as Yanjing No. 811, Huanong No. 4 and Biangu No. 1 were released for cultivation (Jiaju, 1989). In the early part of the 1950s, many local varieties were evaluated and distributed to farmers. Single-ear selection was effective in the early stages, particularly in the landraces having many derivative forms. However, continuous selection was not so effective in pure lines or homogeneous landraces. From the later part of the 1950s to early 1960s, pedigree selection became a primary approach.

During the 1950s, hot water emasculation technique was developed and widely used. Normally a dominant marker character was also used to identify true F_1s. Rapid generation advancement (RGA) and overstepped advancement of selection were widely followed (Jiaju, 1989). In 1959, the first variety 'Xinnongdong No. 2' was bred through hybridisation. By the 1970s, 50% of the varieties used in cultivation were derived from hybridisation breeding, which has been the main method of foxtail millet improvement in China. Mutation breeding by irradiation also started in the 1970s. From 1949 to 1979, 158 varieties, developed by breeding, were grown in a total area of 4.5 million ha (Jiaju, 1989). Extensive use of improved varieties has greatly increased productivity of foxtail millet in China. Improved varieties were popular in all areas except in mountainous regions. In certain locations, varieties were renewed two to three times. Apart from grain yield, the level of resistance to lodging, diseases, insects and various forms of stress in improved varieties have been increased. Development of early maturing varieties has facilitated the improvement in cropping systems. Early varieties could be sown after the harvest of winter wheat and they mature before the sowing time for the next crop of winter wheat. Super-early maturing varieties (50–60 days) have been developed at Japan and China (Liu *et al.*, 2006). Besides ordinary types, special types with glutinous, or white or green or grey endosperm and with good seed quality were also developed.

Another important landmark in the foxtail millet improvement in China is the development of hybrids. Male-sterile lines have been developed, and lines with high male sterility (more than 95%) have been reported, and F_1 hybrid seeds could be produced by the two-line method. Most of the landraces could restore fertility when crossed with the male-sterile line. Since some 5% seeds could be harvested from the

sterile line under open pollination, no maintainer line is necessary. Heterosis utilisation research has made a number of breakthroughs in China since 1967 (Tian *et al.*, 2009). Due to lack of knowledge on heterotic classes and the genetic relationship among these classes, foxtail millet hybrid cultivars have been largely developed in China by crossing sterile lines to conventional cultivars or sterile lines to cultivars that are geographically distant from the sterile lines (Liu, 2010). However, due to extensive exchange of germplasm among different ecological regions and intensive use of a few common parents such as Yugu 1, Qingdaolao, Zhaogu 1, Qinyuanmujizui and Moligu (Liu *et al.*, 2006, 2011; Zhang, 2007; Jiang *et al.*, 2008) in almost all Chinese hybrid breeding programmes, the yield levels in current hybrid cultivars is far from the potential yield. Therefore, investigating heterotic classes and determining best heterotic class combinations, or heterotic patterns, can provide a guideline for effective use of heterosis in hybrid breeding, and to further improve the level of heterosis in hybrids (Liu, Bai *et al.*, 2014).

In recent times, heterosis has been used in developing very high-yielding hybrid cultivars. Zhangzagu5, a hybrid cultivar for example, was released from Zhangjiakou Academy of Agricultural Sciences, Hebei Province, China, and yielded 12159 kg/ha versus conventional cultivars ranging from 4500 to 6000 kg/ha in 2007 (Liu, Zhang *et al.*, 2014). More recently, several attempts have been made on construction of evolutionary trees to investigate the evolution and genetics of foxtail millet germplasm (Wang *et al.*, 2006; Jia, Tan *et al.*, 2009; Jia, Zhang *et al.*, 2009), and on assembling heterosis groups through population structure analysis (Liu, 2010; Liu *et al.*, 2011).

4.10 Breeding Efforts in India

Post-independence, the research needs of small millets to a limited extent were looked after under the erstwhile PIRCOM of the Government of India. Though the crop improvement work on small millets in India under the coordinated programme started in 1964, the launching of a separate coordinated millet improvement project in 1969 helped in giving greater attention to these crops with a few centres established in different states for specific millets. Five crop-specific lead centres were established in 1978–1979 with the International Development Research Centre (IDRC), Canada, assistance at Dholi in Bihar for proso millet, Dindori in Madhya Pradesh for kodo millet, Nandyal in Andhra Pradesh for foxtail millet, Semiliguda in Orissa for little millet and at Almora in Uttar Pradesh for barnyard millet. The establishment of these centres has greatly assisted in building the necessary infrastructure and manpower for these crops. These efforts have started bearing fruit and many new technologies and varieties are now undergoing critical evaluation in different parts of the country (Harinarayana, 1989). The major goal during the VII Five-Year Plan was to further consolidate the outcome of these research efforts and stabilise the productivity of small millets at a higher level. As an important step in this direction, a separate All India Coordinated Small Millets Improvement Project (AICSMIP) was launched in 1986 with its headquarters at UAS, Bangalore, and the IDRC centres became part of AICSMIP. The AICSMIP centre at Regional Agricultural Research Station, Acharya N.G. Ranga Agricultural University (ANGRAU), Nandyal, Andhra Pradesh, is exclusively working on foxtail millet. Other cooperating centres are located at Palem

(Mahbubnagar, Telangana); Dahod (Anand, Gujarat); and Hanumanamatti, Hagari and Gulbarga (Karnataka). With the establishment of AICSMIP, the varietal development in foxtail millet gained momentum.

Pure-line selection remained the prime breeding method for improving performance, particularly grain yield of foxtail millet. As foxtail millet is largely self-pollinated and out-crossing is very much limited, and because of the anthesis behaviour recombination breeding could not gather much research efforts compared to other crops. Progress through hybridisation has been extremely limited, in India. This has been chiefly due to difficulties in emasculation and pollination, in identification of true hybrids, limited heterosis in inter-varietal crosses (Srivastava and Yadav, 1977), and the availability of unexploited genetic resources. Identification of natural hybrids by contact method resulted in a low frequency of true hybrids (Mahishi *et al.*, 1982). Use of marker-plant types such as foxtail millet dwarfs or other distinctly distinguishable lines in germplasm and breeding nurseries for identification of natural hybrids (Harinarayana *et al.*, 1984) through grow-out tests met with limited success. Some of the early efforts in crop improvement of foxtail millet have resulted in the release of improved varieties as early as 1940s. For example Co 1, Co 2 and Co 3 were released in 1943; H1 and H2 were released in 1948; and T4 was released in 1949. Since 1978, the Centre for the Improvement of Small Millets, established at Nandyal by ICAR with the assistance of IDRC, Canada, is devotedly working towards the improvement of foxtail millet. Till date (1942–2015) about 32 varieties have been released, of which 14 were released before establishment of AICSMIP (1986) and 18 after 1986. Pure-line selection has resulted in the development and release of maximum number of foxtail millet varieties – till 1985, 13 varieties were developed (Harinarayana, 1989), and between 1986 and 2015, 11 varieties were developed. One hybrid derivative of foxtail millet, CO 5 (Co 1 × A 113/2) was released in Tamil Nadu (Raveendran *et al.*, 1979) and notified at the central level in 1982. Between 1986–2015, six varieties were released following recombination breeding and one through mutation breeding.

4.10.1 Improved Varieties

A number of varieties with high yield potential have been released for different states of India (Table 4.4). Some of the recent varieties with yield potential, area of adaptation and special features are listed in Table 4.5. Till date, 28 foxtail millet varieties have been notified by the Government of India, of which 13 are central releases and rest are state releases. The list of notified varieties is given in Table 4.6. New short-duration varieties SiA 3085 and SiA 3088 (Surya Nandi) are becoming popular in the major cultivated areas. Because of the short-duration nature, instead of fallow followed by chickpea cropping system, foxtail-chickpea has increased income significantly in Kurnool district of the Andhra Pradesh state of India. In paddy fallows also, short-duration foxtail is becoming popular in Kurnool in view of limited water supply. New varieties have a yield potential of 2000–2500 kg/ha. Under AICSMIP, the foxtail varietal evaluation trials are taken up at about a dozen locations across the major growing states of Andhra Pradesh (Nandyal, Vizianagaram, Chintapalle), Telangana (Palem), Bihar (Dholi), Karnataka (Bangalore, Mandya, Hiriyur, Dharwad, Hanumanamatti, Gulbarga and Hagari), Madhya Pradesh (Rewa), Jharkhand (Ranchi), Tamil Nadu (Coimbatore) and Uttarakhand (Pantnagar). The latest national checks are SiA 326 (Pure-line selection, Nandyal) and SiA 3156 (Selection from SiA 2871, Nandyal).

Table 4.4 State-wise high-yielding foxtail millet varieties in India.

State	Foxtail millet varieties
Andhra Pradesh	SiA 326, Chitra, PS 4, TNAU 186, Narasimharaya, Krishnadevaraya
Bihar	SiA 326, PS 4
Jharkhand	SiA 326, PS 4
Karnataka	SiA 326, PS 4, TNAU 186
Maharashtra	SiA 326, PS 4
Madhya Pradesh	SiA 326, PS 4
Chattisgarh	SiA 326, PS 4
Tamil Nadu	Co 5, K 3, Co 4, PS 4, K 2, TNAU 186, TNAU 43
Uttar Pradesh	Nischal, PS 4
Uttaranchal	PRK 1
Rajasthan	SR 51, SR 11, SR 16

Source: http://smallmillets.res.in/

4.11 New Tools for Genetic Improvement

A major development in the recent years in the area of foxtail millet genomics is the release of the first assembled reference genome of foxtail millet and green foxtail in the year 2012 by two independent groups (Bennetzen *et al.*, 2012; Zhang *et al.*, 2012). Zhang *et al.* (2012) sequenced the foxtail millet cv. 'Zhang gu' using Illumina second-generation sequencers (~86% genome coverage) with a predicted genome size of ~485 Mb. A photo-thermo-sensitive male-sterile line 'A2' was also sequenced and comparison of both the genomes revealed several thousand single-nucleotide polymorphisms (SNPs), insertion/deletion polymorphisms (InDels) and structural variations (SVs) between the two cultivars. The sequence analysis also showed the presence of 38801 genes, out of which ~82% were expressed. Foxtail millet accession 'Yugu1' and green foxtail accession 'A10' were sequenced by Bennetzen *et al.* (2012) using ABI3730xl capillary sequencer that achieved a genome coverage of ~80%. The availability of foxtail millet genome sequence in public domain has facilitated large-scale development of genomic resources such as SSRs and high-density physical maps (Pandey *et al.*, 2013; Zhang *et al.*, 2014).

The Joint Genome Institute of the US Department of Energy and the Center for Integrative Genomics had constructed a public domain database PHYTOZOME (http://phytozome.jgi.doe.gov/pz/portal.html) to provide online resources for foxtail millet genomics with unrestricted public access. Presently, the PHYTOZOME v10 provides access to 46 sequenced and annotated plant genomes including foxtail millet (annotation version 2.1) (Bennetzen *et al.*, 2012). The whole genome-sequence information of foxtail millet annotated by Bennetzen *et al.* (2012) is also available in Gramene v39 (http://www.gramene.org/; Monaco *et al.*, 2013) and PlantGDB (SiGDB; Duvick *et al.*, 2008). The genome data generated by Beijing Genomics Institute (Zhang *et al.*, 2012) are available in the Foxtail Millet Database (http://foxtailmillet.genomics.org.cn/).

Table 4.5 Improved foxtail millet varieties released in India with characteristics.

Sl. No.	Name of variety	Pedigree	Institute where developed	Year of release	Maturity (days)	Average Yield (kg/ha)	Area of adaptation	Special features
1.	Nischal	Selection from accessions of Basti district	CSAUA&T, Kanpur	1988	—	1100–1500	Uttar Pradesh	High seed yield
2.	K 3	Selection from SiA 2567	TNAU, Coimbatore	1989	85–90	1500–1800	Tamil Nadu	High seed yield
3.	AK 132-1	Pure-line selection	APAU, ARS Ananthpur	1990	82–85	1800–2000	Andhra Pradesh	Drought tolerance, high seed yield, suitable for Rayal Seema
4.	Krishnadevaraya	Selection from SiA 2593	APAU, ARS Nandyal	1993	85–96	2000–2200	Andhra Pradesh	High seed yield
5.	TNAU 43	Co 5 × ISe 30	TNAU, Coimbatore	1994	80–85	1500–1600	Tamil Nadu	—
6.	Gavari (SR 11)	Selection from local germplasm	RAU, Rajasthan	1995	75–80	1500–1600	Rajasthan	High seed yield
7.	PS 4	SiA 2616 (0.2% EMS induced mutant)	GBPUA&T, Pantnagar, Uttarakhand	1998	80–85	1800–2000	All States	Wider adaptability and high yield
8.	TNAU 43	Co 5 × ISe 30	TNAU, Coimbatore	1998	80–85	1500–1600	Andhra Pradesh, Tamil Nadu, Karnataka	
9.	TNAU 186	Co-5 × SiA 326	TNAU, Coimbatore	1998	85–90	1800–2000	Tamil Nadu, Andhra Pradesh, Karnataka	
10.	Meera (SR 16)	Pure-line selection	MPUA&T, Udaipur	2001	75–80	1500–1700	Rajasthan	Stay green character, tolerant to downy mildew

11.	Sri Lakshmi	Pure-line selection	ANGRAU, Hyderabad	2002	75–80	2000–2300	Andhra Pradesh	High seed yield
12.	Prathap kangni 1 (SR-1)	Selection from local germplasm	MPUA&T, Udaipur	2003	65–70	1800–2000	Rajasthan	Extra early maturity
13.	SR 51	Pure-line selection	MPUA&T, Udaipur	2003	62–68	1800–2000	Rajasthan	Bold seeds
14.	PRK 1	Selection from Tehri collection	GBPUA&T, Ranichauri	2000	75–80	1900–2000	Uttarakhand	—
15.	TNAU 196	Co 5 × ISe 248	TNAU, Coimbatore	2005	85–90	1800–2000	Tamil Nadu	—
16.	HMT-100-1	PS 3 × RS 118	ARS, Hanumanamatti	2007	90	2000–2500	Karnataka	Resistant to lodging
17.	SiA 3085	Selection from SiA 2644	RARS, ANGRAU, Nandyal	2012	75–82	3000–3200	Andhra Pradesh, Karnataka, Tamil Nadu, Bihar, Madhya Pradesh and Uttarakhand	Resistant to blast and downy mildew
18.	SiA 3156	Selection from SiA 2871	RARS, ANGRAU, Nandyal	2012	85–90	2000–2500	All states	High seed yield, tolerant to shootfly

Source: http://seednet.gov.in/; http://smallmillets.res.in/

Table 4.6 List of notified foxtail millet varieties in India.

Sl.No.	Variety name	Year of release	Notification date	Notification No.	State of release
1	Co.3	1942	01/01/1944	—	Tamil Nadu
2	Co.2	1942	01/01/1944	—	Tamil Nadu
3	Co.1	1942	01/01/1944	—	Tamil Nadu
4	H.2	1948	01/01/1950	—	Karnataka
5	H.1	1948	01/01/1950	—	Karnataka
6	Arjun	1969	01/01/1971	—	Andhra Pradesh
7	RS-118	1976	02/02/1976	S.O.786	Karnataka
8	RC-128	—	02/02/1976	786	Central
9	K-221-1	1970	02/02/1976	786	Karnataka
10	Co-4	1973	19/12/1978	19	Central
11	K.2	1978	14/01/1982	19(E)	Central
12	Co-5	1979	14/01/1982	19(E)	Central
13	Chitra	1982	01/01/1984	—	Andhra Pradesh
14	Nellamale Korra	1985	09/04/1985	295(E)	Central
15	SIC-3 (548-79K)	1985	01/01/1987	—	Central
16	Nischal	—	13/04/1989	280(E)	Central
17	K-3	—	31/07/1989	599(E)	Central
18	Lepakshi (AK-132-1)	—	17/08/1990	639(E)	Central
19	Krishna devaraya	—	04/05/1995	408(E)	Central

20	Gavari (SR-11)	1995	01/01/1996	1(E)	Central
21	TNAU 43	1994	01/05/1997	360(E)	Tamil Nadu
22	Pant Setaria-4 (PS 4)	1998	08/06/1999	S.O. 425(E)	Central
23	Meera (SR-16)	1999	02/02/2001	92(E)	Rajasthan
24	Pratap Kangni-1 (SR-51)	2003	04/02/2004	161(E)	Rajasthan
25	Co(Te) 7	2005	25/04/2006	599(E)	Tamil Nadu
26	HMT-100-1	2007	11/02/2009	S.O. 449(E)	Karnataka
27	SiA 3085	2011	10/04/2013	S.O. 952(E)	Andhra Pradesh
28	SiA 3156	2012	30/07/2014	S.O. 1919 (E)	Central

Source: http://seednet.gov.in/

4.12 Future Prospects

Foxtail millet has invited considerable attention in terms of both structural and functional genomics research as a model crop, and three prime areas of stress biology, C4 photosynthesis and bio-energy research have gained momentum in the recent years. Notably, foxtail millet research has now provided numerous scientific leads to proceed further towards crop improvement of millets, cereals and bio-energy grasses. The major research areas that need to be further explored are structural genomics, genome-wide studies of gene families, which play crucial role in abiotic stress tolerance, epigenetic mode of gene expression regulation and studies on nutritional genomics (Shaik and Ramakrishna, 2012; Sahu *et al.* 2013; Muthamilarasan and Prasad, 2015).

As foxtail millet is nutritionally superior to conventional food grains, and is also known for its therapeutic potential, understanding the genetics and genomics of nutritional traits is a new thrust area. Concerted efforts are needed in exploring grain characteristics, and studying genetic variations of grain characteristics in the foxtail millet germplasm using genomics and biochemical phenotyping. Further, combining the strengths of phenomics and metabolomics, and genome wide association studies will assist in identification of SNPs and candidate genes controlling nutritional content in the grains which will ultimately help in introgression into other graminaceous species through comparative genomics (Muthamilarasan and Prasad, 2015).

Promotion of foxtail millet cultivation through appropriate policy interventions can ensure food, nutrition, fodder and livelihood security. It is a climate-change-compliant crop because of the potential abiotic stress tolerance characteristics and, hence, can ensure ecological security. The availability of genetic and genomic resources would accelerate crop-improvement programmes not only in foxtail millet but also in other cereal grasses indirectly through the wealth of basic information generated in the area of gene expression and functional genomics.

References

Ahanchede, A., Poirier-Hamon, S. and Darmency, H. (2004) Why no tetraploid cultivar of foxtail millet? *Genet. Resour. Crop Ev.*, **51**, 227–230.

Amadou, I., Amza, T., Yong-Hui, S. and Guo-Wei, L. (2011) Chemical analysis and antioxidant properties of foxtail millet bran extracts. *Songklanakarin J. Sci. Technol.*, **33**, 509–515.

Anju, T. and Sarita, S. (2010) Suitability of foxtail millet (*Setaria italica*) and barnyard millet (*Echinochloa frumentacea*) for development of low glycemic index biscuits. *Malays. J. Nutr.*, **16**, 361–368.

Athwal, D.S. and Singh, G. (1966) Variability in Kangni-1. Adaptation and genotypic and phenotypic variability in four environments. *Indian J. Genet. Plant Breed.*, **26**, 142–152.

Austin, D.F. (2006) Foxtail millets (*Setaria*: Poaceae) – Abandoned food in two hemispheres. *Econ. Bot.*, **60**, 143–158.

Ayyangar, G.N.R. (1934) Recent work in the genetics of millets in India. *Madras Agric. J.*, **22**, 16–26.

Baltensperger, D.D. (1996) Foxtail and proso millet, in *Progress in New Crops* (ed. J. Janick), ASHS Press, Alexandria, VA, pp. 182–190.

Baltensperger, D.D. (2002) Progress with proso, pearl and other millets, in *Trends in New Crops and New Uses* (eds J. Janick and A. Whipkey), ASHS Press, Alexandria, VA, pp. 100–103.

Benabdelmouna, A., Shi, Y., Abirached-Darmency, M. and Darmency, H. (2001) Genomic in situ hybridization (GISH) discriminates between the A and the B genomes in diploid and tetraploid Setaria species. *Genome*, **44**, 685–690.

Bennetzen, J.L., Schmutz, J., Wang, H. *et al.* (2012) Reference genome sequence of the model plant Setaria. *Nat. Biotech.*, **30**, 555–561.

Bettinger, R.L., Barton, L., Morgan, C. *et al.* (2010) The transition to agriculture at Dadiwan, People's Republic of China. *Curr. Anthropol.*, **51**, 703–714.

Blaise, M.O., Girardin, P. and Millet, B. (1992) Developmental stages and oral ontogenesis of foxtail millet *Setaria italica* (L.) P. Beauv. *Agronomie*, **12**, 141–156.

Brink, M. (2006) *Setaria italica* (L.) P. Beauv. record from Protabase, in *PROTA (Plant Resources of Tropical Africa / Ressources végétales de l'Afrique tropicale)* (eds M. Brink and G. Belay), Wageningen, Netherlands (http://www.prota4u.org).

Chang, K. (1968) Archeology of ancient China. *Science*, **162**, 519–526.

Chhavi, A. and Sarita, S. (2012) Evaluation of composite millet breads for sensory and nutritional qualities and glycemic response. *Malays. J. Nutr.*, **18**, 89–101.

Choi, Y., Osada, K., Ito, Y. *et al.* (2005) Effects of dietary protein of Korean foxtail millet on plasma adinopectin, HDL-cholesterol and insulin levels in genetically type 2 diabetic mice. *Biosci. Biotechnol. Biochem.*, **69**, 31–37.

Cui, W.S., Du, G. and Zhao, Z.H. (1979) The selection and utilization of male sterile line Shanxi 280 of foxtail millet. *Scien. Agric. Sinica*, **12**, 43–46. (In Chinese.)

Darmency, H., Ouin, C. and Pernes, J. (1987) Breeding foxtail millet (*Setaria italica*) for quantitative traits after interspecific hybridization and polyploidization. *Genome*, **29**, 453–456.

de Wet, J.M.J. and Harlan, J.R. (1975) Weeds and domesticates: evolution in the man-made habitat. *Econ. Bot.*, **29**, 99–107.

de Wet, J.M.J., Oestry-Stidd, L.L. and Cubero, J.I. (1979) Origins and evolution of foxtail millet (*Setaria italica*). *J. d'Agric. Trad. et de Bota (Journal d'Agriculture Tropicale et de Botanique Appliquée)*, **26**, 53–64.

Dekker, J. (2003) Evolutionary biology of the foxtail (*Setaria*) species group, in *Principles and Practices in Weed Management: Weed Biology and Management* (ed. K. Inderjit), Kluwer Academic Publishers, The Netherlands, pp. 65–114.

Devos, K.M., Wang, Z.M., Beales, J. *et al.* (1998) Comparative genetic maps of foxtail millet (*Setaria italica*) and rice (*Oryza sativa*). *Theor. Appl. Genet.*, **96**, 63–68.

Dewey, D.R. (1980) Some applications and misapplications of induced polyploidy to plant breeding, in *Polyploidy, Biological Relevance* (ed. W.H. Lewis), Plenum Press, New York, pp. 445–470.

Diao, X. (2005) Advances in foxtail millet biotechnology and its future directions. *J. Hebei Agric. Sci.*, **9**, 61–68.

Diao, X. (2007) Foxtail millet production and future development direction in China, in *Reports on Minor Grain Development in China* (eds Y. Chai and S.H. Wan), Chinese Agricultural Science and Technology Press, Beijing, pp. 32–43.

Diao, X.M. (2011) Current status of foxtail millet production in China and future development directions, in *The Foxtail Millet Production in China and the Industrial Technology System* (ed. X.M. Diao), Chinese Agricultural Science and Technology Press, Beijing, pp. 20–30 (in Chinese).

Doust, A.N., Devos, K.M., Gadberry, M.D. *et al.* (2004) Genetic control of branching in foxtail millet. *Proc. Natl. Acad. Sci. USA*, **101**, 9045–9050.

Doust, A.N., Devos, K.M., Gadberry, M.D. *et al.* (2005) The genetic basis for inflorescence variation between foxtail and green millet (Poaceae). *Genetics*, **169**, 1659–1672.

Doust, A.N. and Kellogg, E.A. (2002) Inflorescence diversification in the panicoid 'bristle grass' clade (Paniceae, Poaceae): evidence from molecular phylogenies and developmental morphology. *Am. J. Bot.*, **89**, 1203–1222.

Doust, A.N., Kellogg, E.A., Devos, K.M. and Bennetzen, J.L. (2009) Foxtail millet: a sequence-driven grass model system. *Plant Physiol.*, **149**, 137–141.

Doust, A.N., Penly, A.M., Jacobs, S.W. and Kellogg, E.A. (2007) Congruence, conflict, and polyploidization shown by nuclear and chloroplast markers in the monophyletic 'Bristle clade' (Paniceae, Panicoideae, Poaceae). *Syst. Bot.*, **32**, 531–544.

Duvick, J., Fu, A., Muppirala, U. *et al.* (2008) PlantGDB: a resource for comparative plant genomics. *Nucleic Acids Res.*, **36**, D959–D965.

Dwivedi, S., Upadhyaya, H., Senthilvel, S. *et al.* (2012) Millets: genetic and genomic resources, in *Plant Breed Reviews*, vol. **35** (ed. J. Janick), John Wiley & Sons, Inc., USA, pp. 247–375.

Ecocrop (2011) *Ecocrop database, FAO* (http://ecocrop.fao.org/ecocrop/srv/en/home)

Ecoport (2011) *Ecoport database* (http://www.ecoport.org) (http://www.feedipedia.org/node/6346; http://www.feedipedia.org/node/382)

FAO (2011) *Grassland Index. A searchable catalogue of grass and forage legumes*. Food and Agriculture Organization, Rome (http://www.fao.org/ag/AGP/AGPC/doc/GBASE/Default.htm)

Fogg, W.H. (1983) Swidden cultivation of foxtail millet by Taiwan Aborigines: a cultural analogue of the domestication of *Setaria italica* in China, in *The Origin of Chinese Civilization* (ed. D.N. Keighty), University of California Press, Berkeley, California, pp. 97–115.

Gaikwad, A.P. and D'Souza, T.F. (1986) Studies on blast disease of Rala. *Setaria italica. J. Maharashtra Agric. Univ.*, **11**, 108–109.

Gaut, B.S. and Doebley, J.F. (1997) DNA sequence evidence for the segmental allotetraploid origin of maize. *Proc. Natl. Acad. Sci. USA*, **94**, 68090–68094.

Geervani, P. and Eggum, B.O. (1989) Nutrient composition and protein quality of minor millets. *Plant Foods Hum. Nutr.*, **39**, 201–208.

Gill, A.S. and Randhawa, A.S. (1975) [*Setaria italica* (L.) P. Beauv.] Heritable variation and interrelationships in foxtail millet. *Madras Agric. J.*, **62**, 253–258.

Giussani, L.M., Cota-Sanchez, J.H., Zuloaga, F.O. and Kellogg, E.A. (2001) A molecular phylogeny of the grass subfamily Panicoideae (Poaceae) shows multiple origins of C4 photosynthesis. *Am. J. Bot.*, **88**, 1993–2012.

Goron, T.L. and Raizada, M.N. (2015) Genetic diversity and genomic resources available for the small millet crops to accelerate a new Green Revolution. *Front. Plant Sci.*, **6**, 157. doi: 10.3389/fpls.2015.00157

Gupta, S., Kumari, K., Das, J. *et al.* (2011) Development and utilization of novel intron length polymorphic markers in foxtail millet [*Setaria italica* (L.) P. Beauv.]. *Genome*, **54**, 586–602.

Gupta, S., Kumari, K., Muthamilarasan, M. *et al.* (2013) Development and Utilization of Novel SSRs in Foxtail Millet [Setaria italica (L.) P. Beauv.]. *Plant Breed.*, **132**, 367–374.

Gupta, S., Kumari, K., Muthamilarasan, M. *et al.* (2014) Population structure and association mapping of yield contributing agronomic traits in foxtail millet. *Plant Cell Rep.*, **33**, 881–893.

Gupta, S., Kumari, K., Sahu, P.P. *et al.* (2012) Sequence based novel genomic microsatellite markers for robust genotyping purposes in foxtail millet (*Setaria italica* [L.] P. Beauv.). *Plant Cell Rep.*, **31**, 323–337.

Gurunadha Rao, Y., Anjanappa, M. and Appa Rao, P. (1984) Genetic variability in yield and certain yield components of foxtail millet (*Setaria italica* Beauv.). *Madras Agric. J.*, **71**, 332–333.

Haenseler, C.H. (1941) Helminthosporium leaf spot on millet in New Jersey. *Plant Dis. Rep.*, **25**, 486.

Co, H.S. (2014) *German Foxtail Millet Seed*, Hancock Seed Company, Dade City, FL.

Hao, X.F., Wang, J.Z., Wang, G.Q. *et al.* (2009) AFLP analysis of photosensitive male sterile gene in millet. *J. Shanxi Agric. Sci.*, **37**, 3–5, 10. (In Chinese.)

Hao, X.F., Wang, Z.M., Wang, G.Q. *et al.* (2011) SSR analysis of photosensitive male sterile gene of millet. *Acta Agron. Bor.-Sin.*, **26**, 112–116. (In Chinese.)

Harinarayana, G. (1989) Breeding and varietal improvement of Small Millets in India, in *Small Millets in Global Agriculture*, Proceedings of the First International Small Millets Workshop (eds A. Seetharama, K.W. Riley and G. Harinarayana), Bangalore. Oxford and IBH publishing Co. Pvt. Ltd, New Delhi, pp. 59–70.

Harinarayana, G., Navale, P.A. and Mungse, H.B. (1984) Dwarf genotypes of foxtail millet. *J. Maharashtra Agric. Univ.*, **9**, 343–344.

Harlan, J.R. (1975) *Crops and Man*, American Society of Agronomy, Madison, Wisconsin, p. 295.

Harlan, J.R. (1992) *Crops and Man*, 2nd edn, American Society of Agronomy and Crop Science Society of America, Madison, Wisconsin, USA, p. 284.

Harlan, J.R., de Wet, J.M.J. and Price, E.G. (1973) Comparative evolution of cereals. *Evolution*, **27**, 311–325.

Hector, J.H. (1936) Introduction to the botany of field crops. Millets, in *Cereals. South African Agri. Series, Vol. I*, Central New Agency Johannesburg, South Africa, pp. 307–319.

Heng, L., Chih, C., Song, C. and Chang, K. (2011) Development of simple sequence repeats (SSR) markers in *Setaria italica* (Poaceae) and cross-amplification in related species. *Int. J. Mol. Sci.*, **12**, 7835–7845.

Heuzé, V., Sauvantm D., Tranm G. *et al.* (2015) *Foxtail millet* (*Setaria italica*), *grain*. Feedipedia.org. A programme by INRA, CIRAD, AFZ and FAO. http://www.feedipedia.org/node/725 Last updated on March 26, 2015

Hirano, R., Naito, K., Fukunaga, K. *et al.* (2011) Genetic structure of landraces in foxtail millet (*Setaria italica* (L.) P. Beauv.) revealed with transposon display and interpretation to crop evolution of foxtail millet. *Genome*, **54**, 498–506.

Holm, L.G. (1997) *World Weeds: Natural Histories and Distribution*, Wiley, New York, Chichester.

Hu, H.K., Ma, S.Y. and Shi, Y.H. (1986) The discovery of a dominant male-sterile gene in millet (Setaria italica). *Acta Agron. Sin.*, **12**, 73–78. (In Chinese.)

ICRISAT and FAO (1996) *The World Sorghum and Millet Economies: Facts, Trends and Outlooks.* ICRISAT and FAO (http://www.fao.org/es/esc/common/ecg/63/en/Sor_Mil.pdf), p. 68.

Itagi, S., Naik, R., Bharati, P. and Sharma, P. (2012) Readymade foxtail millet mix for diabetics. *Int. J. Sci. Nat.*, **3**, 131–134.

Jali, M., Kamatar, M., Jali, S. *et al.* (2012) Efficacy of value added foxtail millet therapeutic food in the management of diabetes and dyslipidamea in type 2 diabetic patients. *Recent Res. Sci. Tech.*, **4**, 7.

Jia, X., Shi, Y., Song, Y. *et al.* (2007) Development of EST-SSR in foxtail millet (*Setaria italica*). *Genet. Resour. Crop Ev.*, **54**, 233–236.

Jia, X.P., Tan, X.J., Li, Y.X. *et al.* (2009) A study on the genetic diversity of foxtail millet cultivars by SSR markers. (In Chinese). *Acta Agric. Uni. Jiangxi.*, **31**, 633–638.

Jia, X.P., Zhang, Z.B., Liu, Y.H. *et al.* (2009) Development and genetic mapping of SSR markers in foxtail millet [*Setaria italica* (L.) P. Beauv.]. *Theor. Appl. Genet.*, **118**, 821–829.

Jiaju, C. (1989) Breeding and varietal improvement of foxtail millet in China, in *Small Millets in Global Agriculture*, Proceedings of the First International Small Millets Workshop, Bangalore (eds A. Seetharama, K.W. Riley and G. Harinarayana), Oxford and IBH publishing Co. Pvt. Ltd, New Delhi, pp. 101–104.

Jiang, Z.K., Liu, J.R., Wang, S.Y. *et al.* (2008) Analysis on genetic bases and pedigree evolution of foxtail millet variety in Henan province. *Anhui Agric.*, **5**, 124–127.

Jusuf, M. and Pernes, J. (1985) Genetic variability of foxtail millet (*Setaria italica* [L.] P. Beauv): Electrophoretic study of five isoenzyme systems. *Theor. Appl. Genet.*, **71**, 385–391.

Kawase, M., Fukunaga, K. and Kato, K. (2005) Diverse origins of waxy foxtail millet crops in East and Southeast Asia mediated by multiple transposable element insertions. *Mol. Genet. Genom.*, **274**, 131–140. doi: 10.1007/s00438-005-0013-8

Kawase, M. and Sakamoto, S. (1984) Variation, geographical distribution and genetic analysis of esterase isozymes in foxtail millet, *Setaria italica* (L.) Beauv. *Theor. Appl. Genet.*, **67**, 529–533.

Kellogg, E.A. (2000) Molecular and morphological evolution in Andropogoneae, in *Proceedings of the Second International Conference on the Comparative Biology of the Monocotyledons, Vol. 2* (eds J.E. Everett and S.W.L. Jacobs), Symposium on Grass Systematics and Evolution. CSIRO, Melbourne, pp. 149–158.

Kihara, H. and Kishimoto, E. (1942) Bastarde zwischen *Setaria italica* und *S. viridis*. *Bot. Mag. TOKYO*, **56**, 62–67. (in Japanese.)

Kimata, M., Ashok, E.G. and Seetharam, A. (2000) Domestication, cultivation and utilization of two small millets, *Brachiaria ramosa* and *Setaria glauca* (Poaceae), in south India. *Econ. Bot.*, **54**, 217–227.

Krishnakumari, S. and Thayumanvan, B. (1997) Comparative study of resistant starch from minor millets on intestinal response of blood glucose, serum cholesterol and triglycerides in rats. *J. Sci. Food Agric.*, **73**, 296–302.

Krishnamurthy, L., Upadhyaya, H.D., Gowda, C.L.L. *et al.* (2014) Large variation for salinity tolerance in the core collection of foxtail millet (*Setaria italica* (L.) P. Beauv.) germplasm. *Crop Pasture Sci.*, **65**, 353–361. http://dx.doi.org/10.1071/CP13282

Lakshmi Prasanna, P., Samba Murthy, J.S.V., Ramakumar, P.V. and Srinivasa Rao, V. (2013) Studies on correlation and path analysis in exotic Genotypes of Italian millet [*Setaria italica* (L.) Beauv]. *Electronic J. Plant Breed.*, **4**, 1080–1085.

Lata, C., Gupta, S. and Prasad, M. (2013) Foxtail millet: a model crop for genetic and genomic studies in bioenergy grasses. *Crit. Rev. Biotech.*, **33**, 328–343.

Lata, C., Sahu, P.P. and Prasad, M. (2010) Comparative transcriptome analysis of differentially expressed genes in foxtail millet (*Setaria italica* L.) during dehydration stress. *Biochem. Biophy. Res. Commun.*, **393**, 720–727.

Le Thierry d'Ennequin, M., Toupance, B., Robert, T. *et al.* (1999) Plant domestication: a model for studying the selection of linkage. *J. Evol. Biol.*, **12**, 1138–1147.

Lee, G.A., Crawford, G.W., Liu, L. and Chen, X.C. (2007) Plants and people from the Early Neolithic to Shang periods in North China. *Proc. Natl. Acad. Sci. USA*, **104**, 1087–1092.

Li, C.H., Pao, W.K. and Li, H.W. (1942) Interspecific crosses in *Setaria*. II. Cytological studies of interspecific hybrids involving 1, *S. faberii* and *S. italica*, and 2, a three way cross, F2 of *S. italica*, *S. viridis* and *S. faberii*. *J. Hered.*, **33**, 351–355.

Li, H.W., Li, C.H. and Pao, W.K. (1945) Cytological and genetical studies of the interspecific cross of the cultivated foxtail millet, *Setaria italica* (L.) Beauv., and the green foxtail millet, *S. viridis* L. *J. Am. Soc. Agron.*, **37**, 32–54.

Li, H.W., Meng, C.J. and Liu, T.N. (1935) Problems in the breeding of millet (*Setaria italica* (L.) Beauv.). *J. Am. Soc. Agron.*, **27**, 963–970.

Li, P. and Brutnell, T.P. (2011) *Setaria viridis* and *Setaria italica*, model genetic systems for the Panicoid grasses. *J. Exp. Bot.*, **62**, 3031–3037.

Li, W., Zhi, H., Wang, Y. *et al.* (2012) Assessment of Genetic Relationship of Foxtail Millet with Its Wild Ancestor and Close Relatives by ISSR Markers. *J Integrat. Agric.*, **11**, 556–566.

Li, Y., Jia, J.Z., Wang, Y.R. and Wu, S.Z. (1998) Intraspecific and interspecific variation in setaria revealed by RAPD analysis. *Genet. Resour. Crop Ev.*, **45**, 279–285.

Li, Y. and Wu, S.Z. (1996) Traditional maintenance and multiplication of foxtail millet [*Setaria italica* ([L.) Beauv] landraces in China. *Euphytica*, **87**, 33–38.

Li, Y., Wu, S. and Cao, Y. (1995) Cluster analysis of an international collection of foxtail millet [*Setaria italica* (L.) P. Beauv]. *Euphytica*, **83**, 79–85.

Li, Y.M. (1997) Breeding for foxtail millet drought tolerant cultivars (in Chinese), in *Foxtail Millet Breeding* (ed. Y. Li), Chinese Agr. Press, Beijing, pp. 421–446.

Liu, Z., Sun, S., Cheng, R. *et al.* (2006) Development of a new foxtail millet germplasm with super early maturity and high iron content. *Agric. Sci. China*, **5**, 558–562.

Liu, Z., Zhang, T., Li, C. and Bai, G. (2014) Genetic diversity and classification of cytoplasm of Chinese elite foxtail millet [*Setaria italic* (L.) P. Beauv.] Germplasm. *Crop Sci.*, **54**, 659–666.

Liu, Z.L. (2010) Establish method of heterotic group in foxtail millet and its research progress. *J. Hebei Agric. Sci.*, **14**, 102–104. (In Chinese.)

Liu, Z.L., Bai, G.H., Zhang, D.D. *et al.* (2011) Genetic diversity and population structure of elite foxtail millet [*Setaria italica* (L.) P. Beauv.] germplasm in China. *Crop Sci.*, **51**, 1655–1663. http://dx.doi.org/10.2135/cropsci2010.11.0643

Liu, Z.L., Bai, G.H., Zhang, D.D. *et al.* (2014). Heterotic classes and utilization patterns in Chinese foxtail millet [*Setaria italica* (L.) P. Beauv]. *Agric. Sci.*, **5**, 1392–1406. http://dx.doi.org/10.4236/as.2014.514150

Liu, Z.L., Cheng, R.H. and Li, X.Y. (1996) The pedigree analysis and evaluation of north China summer millets. *Crops*, **5**, 24. (In Chinese).

Liu, Z.L., Cheng, R.H., Zhang, F.L. *et al.* (2006) Millet variety in boreali-sinica summer millets region and its pedigree evolution and analysis on genetic foundation. *Acta Agric. Boreali-Sin., Suppl.*, **21**, 103–109. (In Chinese.)

Mahishi, D.M., Aradhya, K.M., Seetharam, A. and Gowda, B.T.S. (1982) Efficacy of contact method for hybridization in foxtail millet. *MILWAI Newsletter*, **1**, 16.

Malm, N.R. and Rachie, K.O. (1971) *Setaria Millets: A Review of the World Literature. S.B. 513*, University of Nebraska, College of Agriculture, Agricultural Experiment Station, Lincoln, p. 133.

Marathee, J.P. (1993) Structure and characteristics of the world millet economy, in *Advances in Small Millets* (eds K.W. Riley, S.C. Gupta, A. Seetharam and J.N. Mushonga), Oxford & IBH, New Delhi, India, pp. 159–178.

Marcon, A. (1994) Wheat streak mosaic virus resistance in foxtail millet, *Setaria italica* L. Beauv., and factors related to resistance, in *MS thesis*, University of Nebraska, Lincoln.

Mauro-Herrera, M., Wang, X., Barbier, H. *et al.* (2013) Genetic control and comparative genomic analysis of flowering time in Setaria (Poaceae). *Gene Genome Genet.*, **3**, 283–295.

Monaco, M.K., Stein, J., Naithani, S. *et al.* (2013) Gramene 2013: comparative plant genomics resources. *Nucleic Acids Res.*, **42**, D1193–D1199.

Movsisyants, A.P. (1950) Foxtail millet – A valuable forage crop. *Sotsialist. Zhivotn.*, **12**, 60–63.

Murugan, R. and Nirmalakumari, A. (2006) Genetic divergence in foxtail millet [*Setaria italica* (L.) Beauv.]. *Indian J. Genet.*, **66**, 339–340.

Muthamilarasan, M. and Prasad, M. (2015) Advances in Setaria genomics for genetic improvement of cereals and bioenergy grasses. *Theor. Appl. Genet.*, **128**, 1–14. doi: 10.1007/s00122-014-2399-3

Muthamilarasan, M., Suresh, B.V., Pandey, G. *et al.* (2013) Development of 5123 intron-length polymorphic markers for large-scale genotyping applications in foxtail millet. *DNA Res.*, **21**, 41–52. doi: 10.1093/dnares/dst039

Muthamilarasan, M., Theriappan, P. and Prasad, M. (2013) Recent advances in crop genomics for ensuring food security. *Curr. Sci.*, **105**, 155–158.

Nakayama, H., Nagamine, T. and Hayashi, N. (2005) Genetic variation of blast resistance in foxtail millet (*Setaria italica* (L.) P. Beauv.) and its geographic distribution. *Genet. Resour. Crop Ev.*, **52**, 863–868.

Nirmalakumari, A. and Vetriventhan, M. (2010) Characterization of foxtail millet germplasm collections for yield contributing traits. *Electronic J. Plant Breed.*, **1**, 140–147.

Oduori, C. (1993) Small millets production and research in Kenya, in *Advances in Small Millets* (eds K.W. Riley, S.C. Gupta, A. Seetharam and J.N. Mushonga), Oxford & IBH Publ. Co. Pvt. Ltd., New Delhi, pp. 67–73.

Oelke, E.A., Oplinger, E.S., Putnam, D.H. *et al.* (1990) Millets, in *Alternative Field Crops Manual*, University of Wisconsin, Cooperative Extension and University of Minnesota, Center for Alternative Plants & Animal Products and Minnesota Extension Service. (https://www.hort.purdue.edu/newcrop/afcm/millet.html)

Padulosi, S., Mal, B., Bala Ravi, S. *et al.* (2009) Food security and climate change: role of plant genetic resources of minor millets. *Indian J. Plant Genet. Resour.*, **22**, 1–16.

Panaud, O. (2006. Foxtail millet, in *Cereals and Millets. Genome Mapping and Molecular Breeding in Plants, Vol. 1* (ed C. Kole), Springer-Verlag Berlin Heidelberg, France, pp. 325–332.

Pandey, G., Misra, G., Kumari, K. *et al.* (2013) Genome-wide development and use of microsatellite markers for large-scale genotyping applications in foxtail millet [*Setaria italica* (L.)]. *DNA Res.*, **20**, 197–207.

Patil, J.A. (1952) Natural cross-pollination in rala (*Setaria italica* Beauv). *Poona Agric. Col. Magazine*, **43**, 151–154.

Pawar, V.S. and Pawar, V.D. (1997) Malting characteristics and biochemical changes of foxtail millet. *J. Food Sci. Technol.*, **34**, 416–418.

Prasada Rao, G.P., Nagaraja Rao, M. and Anjanappa, M. (1985) Genetic variability in setaria. *Andhra Agric. J.*, **32**, 34–56.

Prasada Rao, K.E., de Wet, J.M.J., Brink, D.E. and Mengesha, M.H. (1987) Intraspecific variation and systematics of cultivated *Setaria italica*, foxtail millet (Poaceae). *Econ. Bot.*, **41**, 108–116.

Puranik, S., Bahadur, R.P., Srivastava, P.S. and Prasad, M. (2011) Molecular cloning and characterization of a membrane associated NAC family gene, SiNAC from foxtail millet [*Setaria italica* (L.) P. Beauv.]. *Mol. Biotechnol.*, **49**, 138–141.

Rachie, K.O. (1975) *The millets. Importance, utilization and outlook*, ICRISAT, Hyderabad, India, p. 63.

Rao, B.R., Nagasampige, M.H. and Ravikiran, M. (2011) Evaluation of nutraceutical properties of selected small millets. *J. Pharm. Bioallied. Sci.*, **3**, 277–279.

Rao, S.V.R., Raju, M.V.L.N, Reddy, M.R. and Panda, A.K. (2004) Replacement of yellow maize with pearl millet (*Pennisetum typhoides*), foxtail millet (*Setaria italica*) or finger millet (*Eleusine coracana*) in broiler chicken diets containing supplemental enzymes. *Asian-Aust. J. Anim. Sci.*, **17**, 836–842.

Rao, S.V.R., Reddy, M.R., Prarharaj, N.K. and Shyam Sunder, G. (2000) Laying performance of broiler breeder chickens fed various millets or broken rice as a source of energy at a constant nutrient intake. *Trop. Anim. Health Prod.*, **32**, 329–338.

Raveendran, T.S., Nagarajan, C., Natarajan, U.S. and Appadurai, R. (1979) Tenai CO 5 – a high yielding rust resistant variety suitable for Tamil Nadu. *Madras Agric. J.*, **66**, 771–773.

Ravi, S.B. (2004) *Neglected millets save the poor from starvation*. LEISA India, Valuing crop diversity. *AME Foundation, Bangalore, India*, **1**, 34–36.

Reddy, V., Upadhyaya, H.D. and Gowda, C.L.L. (2006) Characterization of world's foxtail millet germplasm collections for morphological traits. *J. SAT Agric. Res.*, **2**, 1–3.

RESMISA (2012) Supporting Millets in India: Policy Review & Suggestions for Action. *Revalorising Small Millets in Rainfed Regions of South Asia (RESMISA)*. Prepared by DHAN foundation, Plot No. 8, Sixth Street, Rajaji Nagar, Phase II, Krishnagiri, Tamil Nadu, India. (http://www.dhan.org/smallmillets/)

Robert, A.L. (1962) New hosts for three Helminthosporium species from corn. *Plant Dis. Rep.*, **46**, 321–324.

Rominger, J.M. (1962) *Taxonomy of Setaria (Gramineae) in North America*, Illinois Biological Monographs No. 29, University of Illinois Press, Urbana, Illinois, USA.

Sahu, P.P., Pandey, G., Sharma, N. *et al.* (2013) Epigenetic mechanisms of plant stress responses and adaptation. *Plant Cell Rep.*, **32**, 1151–1159.

Sanjeev, U., Jagadish, P.S., Mahendra, R. *et al.* (2011) Biochemical basis of resistance to shoot fly (*Atherigona atripalpis* Wiede) in foxtail millet. *Int. Jr. of Agril., Env. Biotech.*, **4**, 221–222.

Scholz, H. (1960) A contribution to knowledge of cultivated plants. *Ber. Dtsch. Bot. Ges.*, **73**, 471–476.

Sema, A. and Sarita, S. (2002) Suitability of millet-based food products for diabetics. *J. Food Sci. Technol.*, **39**, 423–426.

Shaik, R. and Ramakrishna, W. (2012) Bioinformatic analysis of epigenetic and microRNA mediated regulation of drought responsive genes in rice. *PLoS ONE*, **7**(11), e49331. (http://dx.doi.org/10.1371/journal.pone.0049331)

Sharma, R., Girish, A.G., Upadhyaya, H.D. *et al.* (2014) Identification of Blast Resistance in a Core Collection of Foxtail Millet Germplasm. *Plant Disease* **98**, 519–524.

Sheahan, C.M. (2014). *Plant Guide for Foxtail Millet (Setaria italica)*. USDA-Natural Resources Conservation Service, Cape May Plant Materials Center, Cape May, NJ.

Siles, M.M., Baltensperger, D.D. and Nelson, L.A. (2001) Technique for artificial hybridization of foxtail millet [*Setaria italica* (L.) Beauv.]. *Crop Sci.*, **41**, 1408–1412.

Siles, M.M., Baltensperger, D.D., Nelson, L.A. *et al.* (2001) Registration of five genetic marker stocks for foxtail millet. *Crop Sci.*, **41**, 2011–2012.

Siles, M.M., Ken Russell, W., Baltensperger, D.D. *et al.* (2004) Heterosis for grain yield and other agronomic traits in foxtail millet. *Crop Sci.*, **44**, 1960–1965.

Singh, G. and Athwal, D.S. (1966) Variability in Kangni-2 genotype x environment interaction, heritability and genetic advance. *Indian J. Genet. Plant Breed.*, **26**, 153–161.
Srivastava, D.P. and Yadav, A. (1977) Heterosis in *Panicum miliare* Lam. *Curr. Res.*, **6**, 66–67.
Thathola, A., Srivastava, S. and Singh, G. (2010) Effect of foxtail millet (*Setaria italica*) supplementation on serum glucose, serum lipids and glycosylated hemoglobin in type 2 diabetics. *Diabetol. Croat.*, **40**, 23–28.
Tian, B., Wang, J., Zhang, L. *et al.* (2010) Assessment of resistance to lodging of landrace and improved cultivars in foxtail millet. *Euphytica*, **172**, 295–302.
Tian, G., Wang, Y.W., Li, H.X. *et al.* (2009) Breeding and studies of foxtail millet hybrid Changzagu 2 with herbicide resistance. *J. Agric. Sci. Technol.*, **11**, 138–141. (In Chinese.)
Till-Bottraud, I., Reboud, X., Brabant, P. *et al.* (1992) Outcrossing and hybridization in wild and cultivated foxtail millets: Consequences for the release of transgenic crops. *Theor. Appl. Genet.*, **83**, 940–946.
Chandra, U., Thomas, T.A., Sapra, R.L. and Paroda, R.S. (1987) *Catalogue on Foxtail Millet (Setaria italica L.) Germplasm*, NBPGR Publication, New Delhi, p. 80.
Upadhyaya, H.D., Pundir, R.P.S., Gowda, C.L.L. *et al.* (2008) Establishing a core collection of foxtail millet to enhance the utilization of germplasm of an underutilized crop. *Plant Genet. Resour.*, **7**, 177–184.
Upadhyaya, H.D., Ravishankar, C.R., Narasimhudu, Y. *et al.* (2011) Identification of trait-specific germplasm and developing a mini core collection for efficient use of foxtail millet genetic resources in crop improvement. *Field Crops Res.*, **124**, 459–467.
Van, K., Onoda, S., Kim, M.Y. *et al.* (2008) Allelic variation of the *Waxy* gene in foxtail millet (*Setaria italica* (L.) P. Beauv.) by single nucleotide polymorphisms. *Mol. Genet. Genom.*, **279**, 255–266.
Vavilov, N.I. (1926) Studies on the origin of cultivated plants. *Bull. Applied Bot.*, **16**, 1–248.
Vetriventhan, M., Upadhyaya, H.D., Anandakumar, C.R. *et al.* (2014) Population structure and linkage disequilibrium of ICRISAT foxtail millet (*Setaria italica* (L.) P. Beauv.) core collection. *Euphytica*, **196**, 423–435.
Vetriventhan, M., Upadhyaya, H.D., Anandakumar, C.R. *et al.* (2012) Assessing genetic diversity, allelic richness and genetic relationship among races in ICRISAT foxtail millet core collection. *Plant Genet. Resour.*, **10**, 214–223.
Vinall, H.N. (1924) *Foxtail millet: its culture and utilization in the United States*, USDA. Farmers Bull, p. 793.
Vishwanatha, J.K., Mallanna, K.N., Aradhya, K.M. *et al.* (1981) Genetic variability in a world collection of germplasm of foxtail millet. *Setaria italica Beauv. Mysore J. Agric. Sci.*, **15**, 234–238.
Wang, C., Jia, G., Zhi, H. *et al.* (2012) Genetic diversity and population structure of Chinese foxtail millet [*Setaria italica* (L.) Beauv.] landraces. *Gene Genome Genet.*, **2**, 769–777.
Wang, J., Wang, Z., Yang, H. *et al.* (2013) Genetic analysis and preliminary mapping of a highly male-sterile gene in foxtail millet (*Setaria italica* L. Beauv.) using SSR markers. *J. Integr. Agric.*, **12**, 2143–2148.
Wang, J.Z., Hao, X.F., Wang, G.Q. *et al.* (2006) Study of genetic diversity of millet germplasm resources by molecular markers. (In Chinese.) *Biotechnology*, **16**, 12–16.
Wang, R., Gao, J. and Liang, G.H. (1999) Identification of primary trisomics and other aneuploids in foxtail millet. *Plant Breed.*, **118**, 59–62.

Wang, R.L., Wendel, J.F. and Dekker, J.H. (1995) Weedy adaptation in Setaria spp. I. Isozyme analysis of genetic diversity and population genetic structure. *Setaria viridis. Am. J. Bot.*, **82**, 308–317.

Wang, R.Q., Gao, J.H., Mao, L.P. *et al*. (2002) Chromosome location of the male-sterility and yellow seedling gene in line 1066A of foxtail millet. *Acta Bot. Sin.*, **44**, 1209–1212. (In Chinese.)

Wang, T. (1991) Studies and utilization of a high nuclear male sterile line in foxtail millet. *J. Hebei Agric. Univ.*, **14**, 60–66.

Wang, T., Du, R.H. and Hao, F. (1993) Studies and utilization of highly male sterility of summer millet (*Setaria italica*). *Sci. Agric. Sinica.*, **26**, 88. (In Chinese.)

Wang, T.Y., Chen, H.B. and Darmency, H. (1997) Pollen-mediated gene flow in an autogamous crop: foxtail millet (*Setavia italica*). *Plant Breed.*, **116**, 579–583.

Wang, Y.W., Li, H.X., Tian, G. and Shi, Q.X. (2010) Study on innovation and application of highly male-sterile line with high outcrossing rate in millet. *Sci. Agric. Sinica*, **43**, 680–689. (In Chinese.)

Wang, Y.W., Li, H.X., Wang, G.H. and Tian, G. (1998) Breeding of foxtail millet highly sterile line "Chang10A". (In Chinese). *Gansu Agr. Sci. and Techn.*, **12**, 12–13.

Wang, Z.M., Devos, K.M., Liu, C.J. *et al.* (1998) Construction of RFLP-based maps of foxtail millet, *Setaria italica* (L.) P. Beauv). *Theor. Appl. Genet.*, **96**, 31–36.

Wanous, M.K. (1990) Origin, taxonomy and ploidy level of foxtail millet and minor cereals. *Plant Var. Seeds*, **3**, 99–112.

Zhang, G., Liu, X., Quan, Z. *et al.* (2012) Genome sequence of foxtail millet (*Setaria italica*) provides insights into grass evolution and biofuel potential. *Nat. Biotech.*, **30**, 549–554.

Zhang, H.J. (2007) The main millet variety pedigree analysis in Liaoning province. *Rain Fed Crop.*, **5**, 343–344.

Zhang, J.P., Liu, T.S., Zheng, J. *et al.* (2007) Cloning and characterization of a putative 12-oxophytodienoic acid reductase cDNA induced by osmotic stress in roots of foxtail millet. *DNA Seq.*, **18**, 138–144.

Zhang, S., Tang, C., Zhao, Q. *et al.* (2014) Development of highly polymorphic simple sequence repeat markers using genome-wide microsatellite variant analysis in foxtail millet [Setaria italica (L.) P. Beauv]. *BMC Genom.*, **2**, 15.

Zhao, Z.H., Cui, W.S., Du, G. and Yang, S.Q. (1996) The selection of millet photo-(thermo-) sensitive line 821 and study on the relation of sterility to illumination and temperature. *Sci. Agric. Sinica*, **29**, 23–31. (In Chinese.)

Zhi, H., Wang, Y.Q., Li, W. *et al.* (2007) Development of CMS material from intra-species hybridization between green foxtail and foxtail millet. *J. Plant Genet. Resour.*, **8**, 261–264.

Zhu, G.Q., Wu, Q.M. and Ma, Y.T. (1991) Breeding of Ve type CMS in foxtail millet. *Shaanxi Agric. Sci.*, **1**, 7. (In Chinese.)

5

Proso Millet, *Panicum miliaceum* (L.): Genetic Improvement and Research Needs

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5.1 Introduction

Proso millet (*Panicum miliaceum*, $2n = 4x = 36$) is one of the most ancient domesticated crops by mankind. It is also known by various names in different geographical regions. It is called *common millet* and *hog millet* in the United States; *broomcorn millet* in China; *common millet* in Japan, Korea and Asia Pacific countries; '*hersey' millet* in Germany; and *French white* in France (Rajput *et al.*, 2014). It is one of the most important crops in today's climate-change scenario and has high suitability for sustaining production in dry-land agriculture. In the past, it was one of the major cereals grown across Eurasia. Its importance decreased since eighteenth century owing to significant developments in other competing food crops (potato, rice, wheat, maize, etc.) and changing food habits more skewed towards bread and other baked products (Kalinova and Moudry, 2006).

Presently, it is cultivated in the United States (Nebraska, South Dakota and Colorado), China, India, Nepal, Sri Lanka, Pakistan, former USSR, Iran, Iraq, Syria, Afghanistan, Turkey and Romania. The crop is grown as minor millet on marginal lands with very meagre resources/inputs. Proso millet has a very short growing duration, of about 70–80 days. It has very high water-use efficiency, resulting in the lowest water requirement among all cereal crops. Nutritionally, it is very rich in protein, vitamins, minerals and micronutrients such as iron, zinc, copper and manganese, compared to other staple cereals (Table 5.1). Proso millet is high in protein content (>14%), with superior quality and optimum balance of essential amino acids (Dikshit and Sivaraj, 2013).

5.2 Origin and Taxonomy

Origin of proso and other millets from Neolithic China is well accepted. Husk phytoliths and biomolecular components discovered from recently excavated storage pits at the Neolithic Cishan site in China which were also identified as of proso millet. These were found to be between ~10300 and 8700 calibrated years before present (cal yr BP). This reveals that proso millet was the first crop to be domesticated in East Asia. It later spread to Russia, India, the Middle East and Europe (Lu *et al.*, 2009). Harlan (1971) also stated that the centre of origin of a particular species becomes more reliable when the plant evidence is incorporated with the archaeological evidence.

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Table 5.1 Nutrient composition of proso millet and cereals.

Food grain (per 100 g)	Protein (g)	Carbohy-drates (g)	Fat (g)	Crude fibre (g)	Mineral matter (g)	Calcium (mg)	Phosphorous (mg)	Fe (mg)
Proso millet	12.5	70.4	3.1	7.2	1.9	14	206	10.0
Wheat	11.8	71.2	1.5	1.2	1.5	41	306	5.3
Rice	6.8	78.2	0.5	0.2	0.6	45	160	—

Proso millet (*Panicum miliaceum*) is a member of the genus *Panicum* of Poaceae family, which is one of the largest grass families. Grasses in this family are mainly classified into two tribes (*Paniceae* and *Andropogoneae*). The tribe *Paniceae*, one of the largest tribes of the *Poaceae*, consists of about 84 genera, covering around 1500 species (Roshevits, 1980; Soreng *et al.*, 2015). The genus *Panicum* with about 450 annual and perennial grass species is one of the largest genus in *Paniceae* (Aliscioni *et al.*, 2003). This genus with its characteristics of thriving in harsh climates is widely distributed in tropical and subtropical regions around the world. Very few species are located in temperate regions also. There are mainly two groups in *Panicum maliaceum* described by various researches revealing its complex nature with various wild and cultivated types. Two groups as described are classified in to subsp. *ruderale* (Kitag.) Tzvelev, comprising all natural variants such as wild and weedy types, and subsp. *miliaceum* with cultivated types. Further, the cultivated types of *P. miliaceum* are commonly classified into five races, taking into account the inflorescence morphology (Lyssov, 1975). These are mainly recognised as races (Table 5.2) without any taxonomic validity.

5.3 Botany and Reproductive Biology

The cultivated types have sometimes been classified into cultivated types and wild types. The wild types have lax panicles, usually jointed spikelet stalks and narrow lemmas,

Table 5.2 Different races of proso millet.

Race	Inflorescence morphology	Characteristics
Miliaceum	Large, open inflorescences with sub-erect branches that are sparingly subdivided. Resembles wild *P. miliaceum* in inflorescence morphology.	These two races occur across the range of broomcorn millet cultivation, from Eastern Europe to Japan
Patentissimum	Its slender and diffused panicle branches are often difficult to distinguish from race *miliaceum*	
Contractum	Compact, drooping inflorescences	Highly evolved cultivars of broomcorn millet have more or less compact inflorescences
Compactum	Cylindrical-shaped inflorescences that are essentially erect	
Ovatum	Cultivars with compact and slightly curved inflorescences that are ovate in shape	

whereas the cultivated ones have either lax or compressed panicles, spikelet stalks without joints and wider lemmas. The true wild type is native to Central China and is considered to be the ancestor of the cultivated types. In temperate regions of Europe, Asia and the United States, however, wild types occur that differ from the wild type in China and are most probably derivatives of cultivated types which have regained the ability of natural seed dispersal and spread as weeds. Proso millet is considered as a short-day plant and usually an erect annual (30–100 cm height). Its stems and leaves are covered with slight to dense hairs/pubescence (Kaume, 2006).

5.3.1 Roots

The proso millet plant has two sets of roots, viz., (i) the seminal roots, and (ii) the adventitious or secondary roots. The seminal roots emerge from the germ and help the seedlings become established. These are produced by the young plants. They may remain functional for the life of the plant but form only small fraction of the total root system. The adventitious roots arise from the basal node which forms near the soil surface and eventually become the permanent root system.

5.3.2 Stem/Culm

This is usually a hollow, jointed cylindrical, simple or sparingly branched, glabrous to variously hairy with nodes and internodes. The upper internode bearing the spike is called peduncle. Tillers and lateral branches arise from the axillary buds at the lower internodes. The stem is reddish-green when the seed becomes mature.

5.3.3 Leaves

Leaves are alternate, simple; and consist of the sheath, blade and short ligule without auricles (Cobley, 1976). The leaves are arranged alternately on the culm. Blade are linear lanceolate, 10–42 cm long and 0.5–2.5 cm wide, variously hairy, with three–six veins on each side of the midrib. Ligule membranous (~1 mm) are long and ciliate. The uppermost leaf on the plant is called the flag leaf.

5.3.4 Panicle

After completion of vegetative phase, the plant produces drooping panicle usually 10–45 cm long that may be of open or compact type (Hulse *et al.*, 1980). Spikelets are solitary, stalked, ovoid–ellipsoid, 4–6 mm long, two-flowered, glabrous; glumes unequal, the upper as long as spikelet, many-veined; lower floret sterile, upper one bisexual with thick broad (~2 mm) lemma and palea, two lodicules, three stamens and superior ovary with two plumose stigmas. Fruit is caryopsis (grain), broadly ovoid, smooth, variously coloured but often white, enclosed by the persistent lemma and palea and shedding easily.

5.3.5 Seed

The seed is very small, botanically called as caryopsis. Proso millet seeds are smaller in size than major coarse grain cereals (sorghum and pearl millet). The seed size is about 3 mm in length and 2 mm width and typically oval in shape (Cardenas *et al.*, 1983). Uneven seed ripening where seeds mature at random in the entire panicle leads to delay

in harvesting and thereby causing yield loss as a result of seed shattering. (Theisen *et al*., 1978; Baltensperger *et al*., 1995). At threshing, mature seeds remain in hull, which are of various shades and colours (white, cream, yellow, orange, red and black to brown), with typical creamy white coloured seed coat.

Proso millet ($2n = 36$) is predominantly a self-pollinated crop, but more than 10% natural cross-pollination may occur (Popov, 1946). Proso millet produces an inflorescence as a drooping panicle. Flowers generally open between 1000 and 1200 hours. There is only a short duration of 7 minutes between the opening and closing of flowers. The flower opening starts from the tip of the panicle and proceeds downwards. For complete blooming of all the spikelets, it takes around 10 days. The floral morphology of proso millet (small florets with tightly held lemma and palea) makes emasculation prior to anthesis and artificial crossing difficult, but techniques were developed and a number of cultivars have been released using artificial hybridisation.

Emasculation in proso millet is usually done using hot water having 50°C temperature for 5 minutes. The panicles are immersed in hot water for deactivating the anthers and pollen grains. This method can be used effectively everywhere by optimising the temperature and duration of the treatment.

5.4 Growth and Development

Growth and development in proso millet can be divided mainly in to three distinct phases (Cardenas *et al*., 1983), viz., vegetative, reproductive and maturity/ripening, which may be further sub-divided into physiologically distinct stages. The vegetative phase, which is the period from germination to panicle initiation, may take about 16–20 days to complete determined by cultivars used and the prevailing climate in the growing area. In this phase, major development takes place with an increase in number of leaves, tiller primordia and plant height. The reproduction phase which starts from panicle differentiation and completed with the flowering of main stem. It usually takes about 20–25 days. During this phase, overall increase in the plant biomass takes place with increase in leaf area with more number of tillers. The maturity/ripening covering a period 20–30 days (which is almost same across cultivars), mainly characterised by the active accumulation of dry matter specifically in the grains. This phase starts at flowering to the end of physiological maturity. Even after grain maturity, the lower parts of the panicle and the stem and leaves remain green (Figure 5.1).

5.5 Cytogenetics

Panicum miliaceum is tetraploid millet, well known for high water-use efficiency. Till recently, its ancestors have not been identified. In one of the recent studies by Hunt *et al*. (2014) at University of Cambridge, United Kingdom, investigations on the origin of *P. miliaceum* were carried out to find out probable candidates with in this tetraploid genome. They used the nuclear and chloroplast DNA sequences from *P. miliaceum* and a wide array of diploid and tetraploid species relatives to delineate the phylogenies of the diploid and tetraploid species. Use of genomic DNA as a probe in chromosome

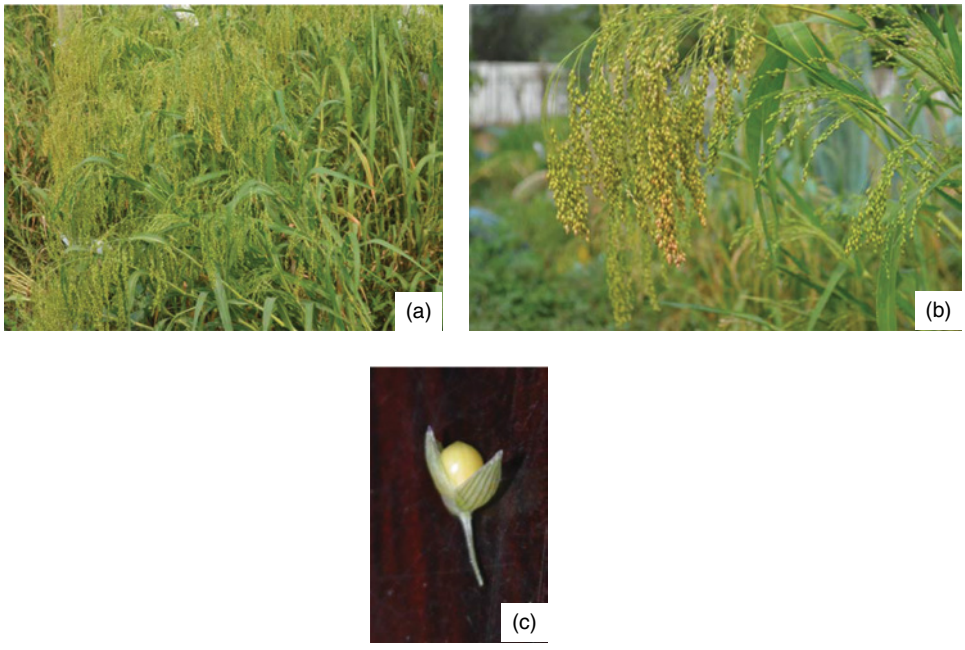

Figure 5.1 (a) Proso millet crop; (b) panicles; (c) seed enclosed in glumes and clasping lemma and palea. (*See color plate section for the color representation of this figure.*)

in situ hybridisation technique to characterise the two genomes *P. miliaceum* and *P. repens* revealed that half of the chromosomes of *P. miliaceum* hybridised more closely with labelled genomic DNA from *P. capillare*, and remaining half with labelled DNA from *P. repens*. DNA probes also differentiated two sets of 18 chromosomes in the tetraploid *P. repens*. It was concluded that the study supported the allotetraploid origin of *P. mimiaceum*, having maternal ancestor as *P. capillare* (or a close relative) and other genome shared with *P. repens*. Further, the *P. repens* accession used in the study was also allotetraploid with dissimilar but closely related genome with *P. sumatrense* as maternal genome. These findings gave insight in to the probable origin of allotetraploid *P. miliaceum*, but further suggested to include wide collection of *Panicum* species from the Old World (Figure 5.2) (Hunt *et al*., 2014).

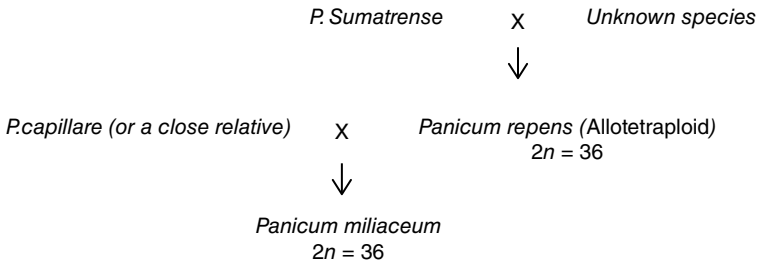

Figure 5.2 Probable origin of *Panicum miliaceum*. *Source*: Conceptualised from Hunt *et al*. (2014).

5.6 Genetic Resources and Utilisation

The utilisation of germplasm in small millets, as in most crops, is most important. In the case of small millets, the utilisation of germplasm is poor and has been drastically restricted by difficulties in artificial hybridisation. Systematic use of these resources for breeding can help in improving grain and fodder yield, grain quality with better composition and biotic and abiotic stress tolerance. World's total germplasm collection of *Panicum miliaceum* is about 29000 (Table 5.3); the largest collections are held in Russia (N.I. Vavilov All Russian Scientific Research Institute of Plant Industry, St. Petersburg, about 9000 accessions), followed by China (Institute of Crop Science, Chinese Academy of Agricultural Sciences [CAAS], Beijing, about 8500 accessions) and Ukraine (Institute of Plant Production, Kharkiv, about 1000 accessions; Ustimovskaya Experimental Station for Plant Cultivation, Ustimovka, about 4000 accessions). In India, about 3000 accessions are held at AICRP on Small Millets, International Crop Research Institute for Semi-Arid Tropics (ICRISAT) and National Bureau of Plant Genetic Resource (NBPGR). In tropical Africa, very few accessions are held in Kenya (National Genebank of Kenya, Crop Plant Genetic Resources Centre, KARI, Kikuyu).

Table 5.3 Proso millet germplasm accessions maintained worldwide.

Country	Institute	Accessions
Argentina	Banco Base de Germoplasma, Instituto de Recursos Biológicos, Instituto Nacional de Tecnología Agropecuaria	01
	Estación Experimental Agropecuaria 'Ing. Agr. Guillermos Covas'	01
Australia	Australian Tropical Crops & Forages Genetic Resources Centre	228
Austria	AGES Linz – Austrian Agency for Health and Food Safety/Seed Collection	05
	Genebank Tyrol/Tyrolean Government	08
	Office of the Styrian Regional Government, Department for Plant Health and Special Crops	01
Azerbaijan	Research Institute of Forage, Meadows and Pastures	10
Bangladesh	Plant Genetic Resources Centre, BARI	198
Bulgaria	Institute for Plant Genetic Resources 'K.Malkov'	489
Canada	Plant Gene Resources of Canada, Saskatoon Research Centre, Agriculture and Agri-Food Canada	23
China	Institute of Crop Science, Chinese Academy of Agricultural Sciences	8451
Czech Republic	Genebank Department, Division of Genetics and Plant Breeding, Crop Research Institute	171
Georgia	Biological Farming Association (NGO) ELKANA	03
Germany	Genebank, Leibniz Institute of Plant Genetics and Crop Plant Research	166
Hungary	Institute for Agrobotany	244
	Station of Ujmajor, Research Institute for Vegetable Crops	50

(*Continued*)

Table 5.3 (Continued)

Country	Institute	Accessions
India	AICRP on Small Millets	920
	International Crop Research Institute for the Semi-Arid Tropics	842
	National Bureau of Plant Genetic Resources	998
Japan	Department of Genetic Resources I, National Institute of Agrobiological Sciences	516
	Plant Germplasm Institute, Faculty of Agriculture, Kyoto University	62
Kenya	National Genebank of Kenya, Crop Plant Genetic Resources Centre – Muguga	06
Mexico	Estación de Iguala, Instituto Nacional de Investigaciones Agrícolas	400
Morocco	Centre Régional de la Recherche Agronomique de Settat	05
Nepal	Central Plant Breeding and Biotechnology Division, Nepal Agricultural Research Council	16
Pakistan	Plant Genetic Resources Program	54
Philippines	Crop Science Cluster – Institute of Plant Breeding, College of Agriculture, University of the Philippines, Los Baños College	01
Poland	Botanical Garden of Plant Breeding and Acclimatization Institute	354
	Plant Breeding and Acclimatization Institute	359
Portugal	Portuguese Bank of Plant Germplasm	01
Romania	Research Institute for Cereals and Technical Plants Fundulea	65
	Suceava Genebank	32
Russian Federation	N.I. Vavilov All-Russian Scientific Research Institute of Plant Industry	8778
Slovakia	Plant Production Research Center Piestany	57
Spain	Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria. Centro Nacional de Recursos Fitogenéticos	03
Sri Lanka	Dry Zone Agricultural Research Institute	04
	Plant Genetic Resources Centre (conservation, evaluation, data management)	27
Ukraine	Institute of Plant Production n.a. V.Y. Yurjev of UAAS	1046
	Ustymivka Experimental Station of Plant Production	3976
United Kingdom	Genetic Resources Unit, Institute of Biological, Environmental & Rural Sciences, Aberystwyth University	03
	Millennium Seed Bank Project, Seed Conservation Department, Royal Botanic Gardens, Kew, Wakehurst Place	01
United States	National Center for Genetic Resources Preservation	01
	North Central Regional Plant Introduction Station, USDA-ARS, NCRPIS	721
Uruguay	INIA La Estanzuela	03
Viet Nam	Plant Resources Center	01
	Total collections	**29301**

Source: http://apps3.fao.org/wiews/germplasm_report.jsp?

Table 5.4 Genetic resources identified for various traits in Indian programme.

Trait	Promising genotypes	Reference
Days to flower	IPM 40 , IPM 2125, IPM 2589, IPM 84 , IPM 273, IPM-982 , JPM 44, IC345024	NBPGR Annual Report, 1986, 1987
Grain yield (g)	IC 41847, IPM 36, IPM 33, IC 52792, IPM 364. IC 28829, EC 24114, EC 24113	NBPGR Annual Report, 2012
Panicle length	Shai Local, Rampur Local	NBPGR Annual Report, 2011
Blast, sheath blight, leaf blight, grain smut	TNAU 218, TNAU 164, DHPRMV 2769, TNAU 148	Anonymous, 2014
Rust	TNAU 145, TNAU 204, 218, 220 and CO 5	AICSMIP, 2014

Germplasm resources management is of prime importance for genetic improvement of any crop species. It helps in identifying accessions with novel traits and also the sources for various biotic and abiotic stresses (Table 5.4). Graybosch and Baltensperger (2009) evaluated 650 accessions of proso millet for presence of accession with waxy (amylase free) endosperm starch. They also performed crosses between waxy and non-waxy lines to assess the genetics of this trait. It was concluded that the waxy trait was governed by duplicate recessive alleles at two loci. The identified waxy accessions are being used for the introgression of this trait in to the elite breeding lines under cultivation in the Great Plains of North America.

The accessions with high protein content and high diversity for various morpho-agronomical characteristics were identified by Dikshit and Sivaraj (2013). A core collection comprising 106 proso millet accessions was developed by evaluating 833 accessions which is mainly constituted based on data of 20 qualitative and quantitative traits and geographic information (Upadhyaya *et al*., 2011). Reddy *et al*. (2007) characterised 842 germplasm accessions originating from 27 countries. The characterisation was carried out since 1977 onwards at ICRISAT, India. The characterisation data revealed high diversity for various traits, indicating superior trait-specific accessions from different countries.

Salini *et al*. (2010) evaluated 364 proso millet accessions maintained at Small Millets Section, Tamil Nadu Agricultural University (TNAU), Coimbatore, Tamil Nadu, India. Highest variability with high heritability estimates in addition to high genetic advance was observed for grain yield per plant and total number of productive tillers. Plant height, number of productive tillers and 100–1000 grain weight recorded positive direct effect indicating suitability of these characters to improve the grain yield. The various studies have revealed high variability with regards to morphological and yield-attributing traits in proso millet (Natrajan *et al.*, 1978; Manoharan and Sivasubramanian, 1982; Panwar and Kapila, 1992; Reddy *et al*., 2007).

Hawlader (1991) reported high genotypic and phenotypic coefficients for grain yield and total number of tillers, Chidambaram and Palanisamy (1995) for grain yield and Prasad *et al*. (1995) for total number of tillers. Heritability was more than 80% for all the characters studied indicating less influence of environmental conditions on these traits and selection would be effective on the basis of phenotype alone. Sasamala *et al*. (2011) recorded moderate to high estimates of heritability along with moderate to high genetic

advance (GA) and genotypic coefficient of variation (GCV) for grain yield and all the component traits except plant height and panicle number. Significant positive association of grain yield with plant height, flag leaf length, flag leaf area, panicle length, panicle weight, panicle yield, biological yield, harvest index and 1000-grain weight was observed. Flag leaf length, panicle weight, 1000-grain weight and plant height had maximum contribution towards the improvement of grain yield.

5.7 Genetic Improvement of Proso Millet: Achievements and Status

5.7.1 India

All India Coordinated Small Millets Improvement Project (AICSMIP) and SAUs have been screening the accessions/germplasm lines since inception of research for yield and other traits improvement. Few improved varieties (Table 5.5) of proso millet have been developed using conventional plant breeding techniques such as pure-line selection, pedigree breeding and back-crossing.

5.7.2 United States

The history and present status of proso millet improvement was briefly reviewed by Dipak Santra, alternative crops breeder at the Panhandle Research and Extension Center (PHREC) (http://panhandle.unl.edu/c/document_library/get_file?folderId=481640&name=DLFE- 979.pdf). In the United States, the focussed breeding programme for proso millet productivity improvement was started in the year 1972 under the alternative crops breeding programme at PHREC. It was started by Lenis Nelson at Scottsbluff with the establishment of the first proso millet breeding and research centre. That led to the significant improvement in proso millet productivity enhancement with the release of four cultivars, viz., Sunup, Dawn, Cerise and Rise. Of these cultivars, Dawn was the most commonly used parent in the various varietal development programmes. David Baltensperger in 1988 took over the proso millet breeding programme. He received significant recognitions for his cultivars, viz., Early bird, Hutsman, Sunrise and Horizon. These varieties are still grown extensively and are very popular. Recently, breeding programmes for alternative crops have been shouldered by Dipak Santra. The main objective of the proso millet improvement focussed on by Santra is the use of genomic tools to speed up the breeding programme and develop genomic resources for utilisation in marker-assisted selection (MAS).

5.7.3 Russia

Russia and the former Soviet Union countries account for about 45% of the world's proso millet production. As in other countries, here also major reduction (2–2.5 times) in area and production was recorded by the end of the twentieth century. That was resulted mainly because of the increase in area and production of maize and wheat. To increase the production of proso millet with declining area was the major challenge and that was addressed with the development of modern varieties with higher adaptability to various soil and environmental conditions and high yield potential of more than $4\,t\,ha^{-1}$. Proso millet breeding programmes in Russia mainly aim at increasing productivity, disease

Table 5.5 Improved varieties released in proso millet in India.

S.No.	Variety	Pedigree	Developing centre	Year	Duration (in days)	Grain yield (kg/ha)	State	Salient features
1	Ram Cheena	A pure-line selection	—	1960	65–95	2000–2500	Bihar	—
2	Shyam Cheena	A pure-line selection	—	1960	80	1200–1300	Bihar	—
3	V-27	—	Andhra Pradesh	1965	—	—	Andhra Pradesh	—
4	V-306	—	Andhra Pradesh	1965	—	—	Andhra Pradesh	—
5	K2	A selection from PV 1685	TNAU, Coimbatore	1980	68–70	1334	Tamil Nadu	Tolerant to major pests and diseases
6	K 1	Selection from local	TNAU, Coimbatore	1982	70–75	900–1000	Tamil Nadu	—
7	BR-7	Pure-line selection	—	1982	80–95	2200–2500	Bihar	Moderately resistant to *Helminthosporium* and shoot fly
8	CO-2	Pure-line selection from a local collection from *Manjanaikanur* in *Annamalai* block Coimbatore	TNAU, Coimbatore	1985	70–75	1600	Central	Shining yellow bold grain; densely pubescent
9	CO-3	Pure-line selection from the local collection maintained at TNAU	TNAU, Coimbatore	1985	—	1280	Central	Shining golden yellow grain drought tolerant, leaf pubescent
10	CO-4	Pure-line selection	TNAU, Coimbatore	1989	70–75	1200–1500	Tamil Nadu	—
11	Nagarjuna	Pure-line selection	ANGRAU, Hyderabad	1989	60–65	1500–1800	Andhra Pradesh	Early maturity
12	Sagar	Selection from local	ANGRAU, Hyderabad	1989	80–87	1800–2000	Andhra Pradesh	High seed yield

(*Continued*)

Table 5.5 (Continued)

S.No.	Variety	Pedigree	Developing centre	Year	Duration (in days)	Grain yield (kg/ha)	State	Salient features
13	Bhawna	Pure-line selection	CSAUAT, Kanpur	1992	70–75	1200–1500	Uttar Pradesh	Early maturity
14	Bhawna	Selection from genetic collections of *Deoria* district	Chandra Shekhar Azad University of Agriculture and Technology, Kanpur	1992	70–75	1200–1500	Central	Plants remain stout, erect and semi dwarf. All productive tiller come out
15	GPUP 8	S 7 × L 111	UAS, Dharwad	2001	70–75	1500–1600	Karnataka	Resistant to brown spot
16	GPUP 21	GPUP 14 × K 1	PC Unit, UAS, Bangalore	2003	67–75	1500–1800	Karnataka, Tamil Nadu	High yield, moderately tolerant to shoot fly
17	Pratap Chenna-1 (PR-18)	Pure-line selection	MPUA&T, Udaipur	2006	75–85	1500–1700	Central	For sub-marginal/shallow, undulating and hilly agro-ecological situations in Rajasthan
18	CO (PV) 5	Cross derivative of PV 1403 × GPUP 21	TNAU, Coimbatore	2007		2300–2400	Tamilnadu	Resistant to brown spot and tolerant to rust and grain smut
19	PRC-1	Selection from GPMS 519	GBPUA&T, Pantnagar	2008	90	1125	Uttarakhand	Resistant to *helminthosporium*
20	TNAU 145	Cross-derivate of PV 1454 × TNAU 96	TNAU, Coimbatore	2009	88	1800–1900	Central	Tolerant to rust and shoot fly
21	TNAU 151	TNAU 96 × PV 1673	TNAU, Coimbatore	2009	72	1800	Central	Tolerant to rust and shoot fly
22	TNAU 164	Derivate of TNAU 137 × CO4	TNAU, Coimbatore	2010	72	1890	Central	Resistant to rust and grain smut disease incidence
23	TNAU 202	PV 1453 × GPUP 16	TNAU, Coimbatore	2011	75	1800–2000	Central	Recommended for cultivation in dry lands of India

resistance (especially to smut) and grain quality (uniform size and shape, yellow endosperm with high carotenoid content). The main breeding method employed in Russia is intra-specific hybridisation. A series of varieties (50) were developed in proso millet, and the notable cultivars are 'Bistrove' and 'Krupnoskoroe' (ssp. *Subcoccineum*), which recorded more than 5 t ha^{-1} grain yield with very short duration. The variety 'Krupnoskoroe' has large and uniform grain size (9.3 g/1000 grains), which makes it suitable for processing, and it also benefits in getting rid of the small seeds of wild weedy proso millet (Kurzeva *et al.*, 2012).

With the advancement of new techniques of selection, specifically for smut disease and identification of genes for resistance, the improved varieties 'Sputnik' (ssp. *coccineum*) and 'Slavjanskoe' (spp. s*ubflavum*) were developed in 2006. These medium-duration varieties gave grain yield as high as 7 t ha^{-1}. For resistance to diseases, new medium-duration variety of proso millet the Sojuz (selection line l.1980) with effective race-specific resistance to smut and yield more than 6 t ha^{-1}, was developed. More emphasis was given for increasing the grain quality for food purpose with high-quality attributes (uniformity of grains, not less than 75%; output of ground millet, not less than 77%; millet should be of bright yellow colour with content of the struck kernel less than 0.8%; porridge should be friable, bright yellow with a high sensory score, etc.) giving high groat recovery coupled with excellent culinary advantages. In addition to these attributes, some more quality indicators (size, form, threshability of grains, kernel consistency, large and spherical grains, glassy kernel, etc.) were considered for breeding high-grain-quality cultivars. These kernels are strong and at processing are less split up and gives less waste. Improvement of quality of production of newly created varieties is one of leading directions of modern selection of millet. Varieties of millet for food purpose along with high yield should have high parameters of grain quality which provide high output of groats with excellent culinary advantages. Breeding of modern varieties is accompanied by constant monitoring of characteristics of quality (Zotikov *et al.*, 2012).

During 2006–2010, the new selection technologies based on mutant forms, dihaploid plants production, genotype identification with the use of storage proteins electrophoresis and PCR-based DNA markers were developed. As an outcome of this, a new variety 'Regent' was produced in 2011 using anther-culture technique and selection was done keeping in mind the productivity and grain-quality parameters. The variety has high yield, medium duration (95–105 days) and resistance to lodging and shattering. It is also resistant against majority of races of smut and also least affected by *melanosis* diseavse.

5.7.4 China

The proso millet was first domesticated in China, and it later spread to other regions of the world. Proso millet improvement programme was started around 1940. It was taken up by the two organisations the Agricultural Experiment Farms of the former province of Suyuan (currently Langshan town of Linhe District, Inner Mongolia) and the Guanghua Farm (the predecessor of the Yan'an Research Institute of Agricultural Sciences) of the Shan-Gan-Ning Region (region ruled by Chinese Communist Party before 1949). Here, they screened large numbers of proso millet germplasm and local land races as well. The well-performing varieties were selected and recommended for cultivation. The varieties, Langshan 462 and Micang 155, screened by the first Agricultural

Experiment Farm, were the earliest proso millet varieties adopted in the Qianshan region and Tumochuan Plain of Bayan Nur and Ulan Qab, Inner Mongolia, before 1965 (Yan *et al*., 2012).

The major work on germplasm collection, characterisation and evaluation was started after 1950 and the available germplasm was screened nationwide in 1957 at major institutes of agricultural sciences in proso millet production areas. After 1950, as required for the broomcorn millet production in China and the crop germplasm collection, sorting and evaluation of millets in China was carried out nationwide in 1957 by the major institutes of agricultural sciences. The Crop Breeding Institute of Heilongjiang Academy of Agricultural sciences, the Bayan Nur League Institute of Agricultural sciences of Inner Mongolia, the Crop Breeding Institute of Gansu Academy of Agricultural sciences, the Crop Science Institute of Ningxia Academy of Agricultural Sciences and the Yan'an Research Institute and Yulin Research Institute of Agricultural Sciences of Shaanxi first began variety improvement of broomcorn millet and from 1940 to 1970, there were 10 research organisations carrying out varietal improvement of proso millet, which successfully bred 42 proso millet varieties, accounting for about 31% of all the proso millet varieties bred in China. The varietal improvement using hybridisation technique was adopted for the first time by one of the major research organisations, the Crop Breeding Institute of Helongjiang Academy of Agricultural Sciences. This laid the foundation for hybridisation breeding in proso millet which bred 10 varieties, out of which 'Longshu 16' was the first broomcorn millet variety bred by hybridisation in China.

The proso millet breeding programme was stagnated due to the reduced funding from important research organisations. The proso millet area was gradually replaced by maize and soybean during 1970–2000 in Northeast China, and it was no longer cultivated as a main crop. The Second National Crop Germplasm Collection, Sorting, Evaluation and Exploitation of China was conducted in 1979, and this promoted the varietal improvement programme in this crop. About 62 varieties were bred in China during 1971–2000. Thereafter the long-term improvement efforts made in proso millet breeding by the research organisations during 2000–2012 attracted the attention of the Chinese Government and the governments of provinces. They supported the programme specifically in Northwest China. This gave new impetus to the varietal improvement and strengthened the overall proso millet breeding (Yan and Pengke, 2012).

5.7.5 Kenya

Among tropical African countries, Kenya has the proso millet improvement programme where some work on the improvement of proso millet has been carried out. The group at Kenya Agricultural Research Institute (KARI) started an initial improvement programme with a few selections within local line and lines from ICRISAT. The cultivar 'KAT/PRO-1' is recommended for cultivation in Kenya was developed by KARI. It is a selection from 'N40101', an introduction from the former Soviet Union received through ICRISAT. The cultivar 'KAT/PRO-1' was developed using mass-selection method with repeated selection cycles for common traits along high yield potential. The cultivar recorded an average yield of 1400 kg ha^{-1}, which was 50% higher than the local cultivars.

5.8 Breeding Objectives and Research Strategies

5.8.1 Development and Evaluation of Core Sets for Biotic and Abiotic Stresses as well as Quality Traits

Presently, the AICSMIP holds about 939 accessions of proso millet (AICSMIP, 2014). Out of these many germplasm accessions, there is need to identify the set of genotypes representing the overall diversity. The development of core collections and mini-cores will certainly boost the future breeding efforts for making notable advances in productivity. The recent development of the core collection using geographic and morphological data (Upadhyaya *et al.*, 2011) will provide a new avenue to access the germplasm for important agronomic traits and sources for various abiotic and biotic stresses. There is variability available for stover quality and quantity in the germplasm, offering scope for the improvement of the feed value of this crop.

5.8.2 DUS Characterisation of Varieties

There are about 24 varieties of proso millet released at the national level in India. As this crop is gaining importance as a health food, the private sector will definitely come up for the commercialisation aspect through development of value-added products, thereby increasing the seed demand for product-specific varieties. To protect the existing varieties at the national level, varieties need to be registered with the Protection of Plant Varieties and Farmers' Rights Authority (PPVFRA), India; and, for that purpose, distinctness, uniformity and stability (DUS) testing is mandatory. DUS testing is also useful for identifying novel traits in the existing cultivars, and it will restrict the development of similar varieties and give a boost for identifying new varieties with distinct traits. Development of detailed descriptors for the crop is necessary for DUS testing. *Panicum* descriptors developed by the International Bureau for Plant Genetic Resources (IBPGR) can be of great use as a base for further refining and developing new DUS testing guidelines for proso millet.

5.8.3 Identification of Location and Trait-Specific Germplasm for Utilisation in Crop Improvement

Genotypes require to be designed and developed for different maturity-duration groups depending upon the location-specific climatic parameters such as soil, rainfall, temperature, humidity, day length and cropping patterns. Some localities may prefer a variety for a particular trait such as grain colour and lustre, increased plant height, stover quality, etc. In such conditions, preferred varieties can be developed and supplied to the niche areas. Some proso millet varieties perform better in specific locations, making them popular among the farmers. All varieties may not produce significantly higher yield across locations since variety developments are mainly targeted for dry-land production.

5.8.4 Development of Varieties with Abiotic and Biotic Stress Tolerance/ Resistance

Varieties with high levels of tolerance to the abiotic stresses, viz., drought, heat, salinity, cold, etc., need to be evolved for sustaining the crop yields. The varieties with such resistance levels would fill the slot where the present cash crops fail to sustain the profitability.

Among insects, shoot fly (*Atherigona spp.*) is the only major pest reported in proso millet. Germplasm and the newly developed varieties in AICSMIP are evaluated for shoot fly resistance. In the recent evaluation studies under AICSMIP all-India testing, entries DHPVMV 21-64 and DHPVMV 27-21 exhibited high resistance to shoot fly over five locations in the year 2013–2014 (AICSMIP, 2014). Blast, sheath blight, leaf blight and grain smut are the important diseases recorded so far on this crop. Use of resistant germplasm to improve host-plant resistance in the high-yielding varieties is the key strategy to minimise losses.

5.8.5 Developing Lodging- and Shattering-Resistant Varieties

After attaining maturity, ripening in proso millet starts from the upper part of the panicle, and it is usually not uniform. Uneven ripening causes seeds remain green in the lower portion of the panicle (Matz, 1986). If harvesting is delayed until these grains are sufficiently dry, there is possibility of considerable losses on account of seed shattering. In Indian conditions, this is not of much concern during the rainy season crop, but, for post-rain and summer crops, this may affect the overall yields drastically. Threshing can be postponed until the grain moisture is less than 13% (Baltensperger *et al*., 1995).

5.8.6 Development of Varieties with Early Vigour and Short Duration

One of the most critical periods in growing small millet is the 2 weeks after planting. The small seed size and the resulting slow growth during the initial weeks make small millets comparatively poor weed competitors and thereby give lower yields when cultivated on weedy land. There is need to identify a germplasm with early vigour and highest per-day productivity. Short-duration genotypes will generally have high early vigour.

5.8.7 Identification of Elite Germplasm and Varieties with Superior Nutritional Traits and Bio-Fortification of Existing Elite Lines

Human consumption of proso millet is high in Asia, and it is also increasing in developed countries. The waxy proso millet genotypes are preferred in such markets because of their glutinous nature and greater properties of adhesion after cooking. Waxy forms of proso millet exist in the germplasm, and these can be used for developing the waxy proso millet cultivars. In addition to different grain-quality traits, the increase in seed size is of great value to diversify the utilisation. In addition to this trait, the brightness of the endosperm which contains carotenoids is of great value. Resistance to Melanos disease (blackening of endosperm due to bacterial infection) is also an important criterion. The yellowish, bright and lustrous traits of grains are directly related to the content of the carotenoids. Red-coated varieties are preferred mainly because they offer protection from light degradation of carotenoids under field conditions.

5.8.8 Grain Quality Improvement

The grain-quality traits in proso millet have a very complex inheritance. The quality traits exhibit reverse correlations between them (large grains are mainly affected by melanosis disease, bright yellow grains contain less amount of protein, etc.). Proso millet is gaining more attention worldwide as a health food. While developing various food products using proso millet grains, some novel end-use characteristics such as waxy starch, seed size, grain lustre, appearance, etc., can bring better market attention.

Heyduck *et al*. (2008) evaluated 18 experimental F_5 waxy lines derived from a cross of 'Hutsman' and PI436626 across seven locations to improve the existing elite lines with introgression of waxy endosperm trait. Chao *et al*. (2014) also examined the starch composition in four waxy proso millet varieties and found that they are rich in nutritional composition when compared to non-waxy genotypes. As a long-term research goal, reliable sources of large grain, thin glumes, high uniformity, high technology traits, excellent consumer and culinary advantages of millet are required to be determined. Their use in practical breeding would help in raising the degree of grain quality in varieties of new generation.

5.8.9 Protein Content and Quality

Among the small millets, proso has the highest protein content. The highest identified content of protein in proso millet grains is about 17%. This mainly depends on the variety and growing conditions. However, the usual range is from 11.3 to 12.7%. The dehulled grains contain 16% of protein in dry matter. Eight varieties of proso millet were evaluated for protein content and quality. Kalinova and Moudry (2006) highlighted the richness of proso protein in essential amino acids (leucine, isoleucine and methionine), which is better than wheat. The proso grain contained about $3.3\,g\,kg^{-1}$ of the limiting amino acid lysine. Dikshit and Sivaraj (2013) evaluated 18 diverse accessions of proso millet germplasm varying in morpho-agronomic trait and noticed high variability (coefficient of variation) for protein content, inflorescence length and days-to-maturity in proso millet germplasm collected from the Southern region of Ratnagiri district, Maharashtra, India, using DIVA-GIS grid maps.

5.8.10 Inducing Cytoplasmic Genetic Male Sterility

Availability of male sterility will offer a new gateway to exploit heterosis, thereby increasing the yield potential of the crop (Yang *et al*., 2012). As of now, there are no reports of stable male sterility in proso millet. Some efforts have been made to use the chemical mutagens such as N-ethyl-*N*-nitrosourea and diethyl sulfate for producing mutagenic populations (Konstantinov *et al.*, 1991). They isolated mutants resistant to smut disease in elite Ukrainian varieties.

5.8.11 Wide Hybridisation

The cultivated proso millet has a very narrow genetic base. To increase the yield potential and resistance levels for various biotic and abiotic stresses, there is necessity to introgress new genes in to the improved varieties. The wild species/wild relatives of this species can play an important role for exploiting the novel genes. The proso millet probable progenitors *Panicum capillare* or *Panicum repens* can be effectively used to broaden the genetic base and to identify the novel high adaptive genotype combinations (Hunt *et al*., 2014).

5.8.12 Improved Plant Type with High Harvest Index (HI)

Plant harvest index, the ratio of grain weight to total plant weight, is an important trait associated with the dramatic increases in crop yields that have occurred in the twentieth century, specifically in major cereal crops wheat, rice, maize, sorghum, etc. Harvest index reflects the partitioning of photosynthates between the grains and biomass of the

plant. Harvest index of intensively cultivated grain crops with the development of modern cultivars ranges within 0.40–0.60. Contrary to this, the scenario in small millets is quite different, around 0.25–0.35. This provides a large scope for improving the varieties of small millets to achieve HI of above 0.40.

5.8.13 Breeding Varieties for Intensive Cultivation and Suitable for Mechanical Harvesting

The availability of agriculture labour has decreased substantially; it is still continuously declining, making it very difficult to sustain farm production/profitability with increased cultivation cost. One of the solutions is mechanisation of the labour-intensive farm operations. Therefore, there is great necessity to develop varieties amenable to mechanical harvesting. Developing plant ideotype suitable for mechanical harvesting has manifold advantages. It would increase yield, as new plant architecture will assimilate more food as grains with increased photosynthetic activity. Erect genotypes with optimum height and well-arranged branching and panicle morphology are very useful for mechanical harvesting.

5.9 Future Prospects

Proso millet's lowest water requirement as compared to other cereals makes it a strong player under climatic fluctuations. It is a climate-resilient crop which can withstand very resource-poor soils, especially dry lands. This along with other small millets has great scope for sustaining agriculture production in near future. Nutritionally it is very rich in protein (>14%) content and has other nutritive components like fibre, vitamins and minerals. This gives it an additional advantage over other commonly used cereals. Till date, all the millets were neglected due to significant yield improvements in other cereals and cash crops (wheat, rice, maize, soybean, potato, etc.), but now things are changing and more people are coming forward to explore these old-world crops. Thus, proso millet's genetic improvement has great future to increase its productivity and develop superior cultivars with the added advantages of proteins and minerals. Technology developments in the form of new cultivars, cropping systems, agronomical interventions, plant protection strategies and mechanisation of farm processes are the key factors to be considered in future proso millet improvement programmes.

References

AICSMIP (2014) Annual Report 2013–2014 – All India Coordinated Small Millets Improvement Project (AICSMIP), Bengaluru, India.

Aliscioni, S.S., Giussani, L.M., Zuloaga, F.O. and Kellogg, E.A. (2003) A molecular phylogeny of *Panicum* (Poaceae: *Paniceae*): tests of monophyly and phylogenetic placement within the Panicoideae. *American Journal of Botany*, **90**, 796–821.

Anonymous (2014) *Status Paper on Coarse Cereals*, Directorate of Millets Development, Jaipur, Rajasthan, India, Department of Agriculture and Cooperation, Ministry of Agriculture, Government of India.

Baltensperger, D., Lyon, D., Anderson, R. *et al.* (1995) *Producing and Marketing Proso Millet in the High Plains*, University of Nebraska Cooperative Extension EC 95-137-C.

Cardenas, A., Nelson, L. and Neild, R. (1983) *Phenological Stages of Proso Millet. MP45*, University of Nebraska, Lincoln.

Chao, G., Gao, J., Liu, R. *et al.* (2014) Starch physicochemical properties of waxy proso millet (*Panicum miliaceum* L.). *Starch*, **66**, 1005–1012.

Chidambaram, S. and Palanisamy, S. (1995) Dry matter production and harvest index in relation to grain yield in Panivaragu – prosomillet (*Panicum miliaceum* L.). *Madras Agricultural Journal*, **82**, 13–15.

Cobley, L.S. (1976) *An Introduction to the Botany of Tropical Crops*, 2nd edn, Longman, London.

Dikshit, N. and Sivaraj, N. (2013) Diversity for protein and morpho-agronomical characteristics in proso millet germplasm collections of Ratnagiri district, Maharashtra, India. *Vegetos*, **26** (2), 164–170.

Graybosch, R.A. and Baltensperger, D.D. (2009) Evaluation of the waxy endosperm trait in proso millet (*Panicum miliaceum*). *Plant Breeding*, **128** (1), 70–73.

Harlan, J.R. (1971) Agricultural origins: Centers and Noncenters. *Science*, **174** (4008), 468–474.

Hawlader, M.S.H. (1991) Genetic variability and correlation study in proso millet (*Panicum miliaceum* L.). *The Annals of Bangadesh Agriculture*, **1** (2), 61–64.

Heyduck, R.F., Baltensperger, D.D., Nelson, L.A. and Graybosch, R.A. (2008) Yield and Agronomic Traits of Waxy Proso in the Central Great Plain. *Crop Science*, **48** (2), 741–748.

Hulse, J.H., Laing, E.M. and Pearson, O.E. (1980) *Sorghum and the Millets. Their Composition and Nutritional Value*, Academic Press, New York.

Hunt, H.V., Badakshi, F., Romanova, O. *et al.* (2014) Reticulate evolution in *Panicum* (Poaceae): the origin of tetraploid broomcorn millet. *P. miliaceum. Journal of Experimental Botany*, **65** (12), 3165–3175.

Kalinova, J. and Moudry, J. (2006) Content and quality of protein in proso millet (*Panicum miliaceum* L.) varieties. *Plant Foods for Human Nutrition*, **61**, 45–49.

Kaume, R.N. (2006) *Panicum miliaceum* L, in *PROTA 1: Cereals and pulses/Céréales et légumes secs* (eds M. Brink and G. Belay), [CD-Rom]. PROTA, Wageningen, The Netherlands.

Konstantinov, S.I., Linnik, V.M., Shapina, L.Ya. and Grigorashchenko, L.V. (1991) Breeding proso millet for resistance to diseases, in *Urozhaĭ i adaptivnyĭ potentsial ekologicheskoĭ sistemy polya*, Ukrainian Academy of Agrarian Sciences, Ukrain, pp. 112–117. (ISBN 5-7778-0012-2)

Kurzeva, A., Romanova, O. and Krylov, A. (2012) Genetic resources of common millet (*Panicum miliaceum L.*) at the Vavilov Research Institute of Plant Industry (VIR), in *Advances in Broomcorn Millet Research*, Proceedings of the 1st International Symposium on Broomcorn Millet held at Yangling, Shaanxi, People's Republic of China, August 25–31, 2012 (eds C. Yan and F. Baili), Northwest A&F University Press.

Lu, H., Zhang, J., Liu, K. *et al.* (2009) Earliest domestication of common millet (*Panicum miliaceum*), in *East Asia extended to 10,000 years ago*, *Proceedings of the National Academy of Sciences*, *USA*, **106** edn, National Academy of Science, USA, pp. 7367–7372.

Lyssov, B.H. (1975) Proso (*Panicum* L.), in *The USSR Flora of Cultivated Plants. 3. Croat Crops* (ed. A.S. Krotov), USSR, Kolos, Leningrad.

Manoharan, V. and Sivasubramanian, S. (1982) Variability studies in proso millet (*Panicum miliaceum* L.). *Madras Agricultural Journal*, **69** (5), 343–345.

Matz, S.A. (1986) *Millet, wild rice, adlay, and rice grass, in Cereal Science*, AVI Press, Westport, CT, pp. 225–229.

Natarajan, U.S., Raveendran, T.S. and Appadurai, R. (1978) A path coefficient analysis of yield and yield components in proso millet (*Panicum miliaceam* L.). *Madras Agricultural Journal*, **65** (7), 430–434.

NBPGR (1986) National Bureau of Plant Genetic Resources, India. *Annual Report*, **1986**, 131.

NBPGR (1987) National Bureau of Plant Genetic Resources, India. *Annual Report*, **1987**, 81.

NBPGR (2011) National Bureau of Plant Genetic Resources, India. *Annual Report*, 2010–2011.

NBPGR (2012) National Bureau of Plant Genetic Resources, India. *India. Annual Report*, 2012–2013.

Panwar, K.S. and Kapila, R.K. (1992) Variation and character association in proso millet. *Crop Improvement*, **19**, 130–133.

Popov, G.I. (1946) The Importance of diversity in millet. *Agrobiologiya*, **2**, 28–43.

Prasad, S.G., Nagaraja, T.E., Seetharam, A. and Gowda, B.T.S. (1995) Genetic variability and character association studies in proso millet. *Crop Improvement*, **22**, 225–227.

Rajput, S.G., Plyler-Harveson, T. and Santra, D.K. (2014) Development and characterization of SSR markers in proso millet based on switchgrass genomics. *American Journal of Plant Sciences*, **5**, 175–186.

Reddy, V.G., Upadhyaya, H.D. and Gowda, C.L.L. (2007) Morphological characterization of World's proso millet germplasm collection. *SAT e-Journal*, **3**, 1–4.

Roshevits, R.Y. (1980) *Grasses: An Introduction to the Study of Fodder and Cereal Grasses*, Indian National Scientific Documentation Centre, New Delhi.

Salini, K., Nirmalakumari, A., Muthiah, A.R. and Senthil, N. (2010) Evaluation of proso millet (*Panicum miliaceum* L.) germplasm collections. *Electronic Journal of Plant Breeding*, **1** (4), 489–499.

Sasamala, A.C., Sahoo, L.P., Mahapatra, K.C. and Pandey, S. (2011) Genetic variability and character association in common millet germplasm of Odisha. *Indian Journal of Plant Genetic Resources*, **24** (1), 82–86.

Soreng, R.J., Peterson, P.M., Romschenko, K. *et al.* (2015) A worldwide phylogenetic classification of the *Poaceae* (*Gramineae*). *Journal of Systematics and Evolution*, **53** (2), 117–137.

Theisen, A.A., Knox, E.G. and Mann, F.L. (1978) Feasibility of introducing food crops better adapted to environmental stress, in *Individual Crop Reports, Vol. II*, National Science Foundation Arlington, Virginia, USA, pp. 168–172.

Upadhyaya, H.D., Sharma, S., Gowda, C.L.L. *et al.* (2011) Developing proso millet (*Panicum maliaceum* L.) core collection using geographic and morpho-agronomic data. *Crop & Pasture Science*, **62**, 383–389.

Yan, C. and Pengke, W. (2012) Variety improvement of broomcorn millet in China, in *Advances in Broomcorn Millet Research*, Proceedings of the 1st International Symposium on Broomcorn Millet held at Yangling, Shaanxi, People's Republic of China, August 25–31 (eds C. Yan and F. Baili), Northwest A&F University Press.

Yan, C., Xiaoli, G. and Cui, L. (2012) Production of Proso Millet in China, in *Advances in Broomcorn Millet Research*, Proceedings of the 1st International Symposium on Broomcorn Millet held at Yangling, Shaanxi, People's Republic of China, August 25–31 (eds C. Yan and F. Baili), Northwest A&F University Press.

Yang, Q., Xiaodong, Z., Jia, C. *et al.* (2012) Effects of Different Chemical Hybridizing Drugs on Male Sterility of Proso Millet, in *Advances in Broomcorn Millet Research*, Proceedings of the 1st International Symposium on Broomcorn Millet held at Yangling, Shaanxi, People's Republic of China, August 25–31 (eds C. Yan and F. Baili), Northwest A&F University Press.

Zotikov, V.I., Sidorenko, V.S., Bobkov, S.V. *et al.* (2012) Area and Production of Proso Millet (*Panicum miliaceum* L.) in Russia, in *Advances in Broomcorn Millet Research*, Proceedings of the 1st International Symposium on Broomcorn Millet held at Yangling, Shaanxi, People's Republic of China, August 25–31 (eds C. Yan and F. Baili), Northwest A&F University Press.

6

Genetic Improvement in Little Millet

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6.1 Introduction

Little millet (*Panicum sumatrense* Roth. Ex. Roem and Schultz) is one of the important small millets native to the Indian subcontinent. The wild ancestor *Panicum psilopodium* too is reported to be present throughout the country. Little millet is generally confused with proso millet *Panicum miliaceum* L., but it has generally smaller panicles and seeds than *P. miliaceum*. It is widely cultivated mainly in the hilly tracts of India and in certain regions in Nepal and Western Burma. In India, the crop is widely grown in Madhya Pradesh, Chhattisgarh, Tamil Nadu, Karnataka, Orissa, Andhra Pradesh, Jharkhand and Bihar. The crop is reported to be predominantly grown in the eastern parts of India, where it forms part of tribal agriculture. The crop is drought-tolerant and provides good harvest even in low fertile soils and unfavourable weather conditions (Selvi *et al.*, 2014). The crop is cultivated both in the tropics and sub-tropics and can even come up well at altitudes of 7000 ft above mean sea level. The grains can be preserved for 10 years or more without much loss due to deterioration (Selvi *et al.*, 2014). And therefore the crop is recognized as important reserve food crop.

The area under little millet cultivation has reduced from about 0.5 million hectares during 2001–2002 to presently about 0.3 to 0.4 million hectares with a production of around 0.1 million tonnes. Exact figures on the area, production and productivity are not available. In India, Madhya Pradesh state occupies about 50% of the area, followed by Chhattisgarh, Tamil Nadu, Karnataka, Maharashtra, Orissa, Andhra Pradesh and Jharkhand (Table 6.1). The productivity is highest in Tamil Nadu (769 kg/ha) followed by Karnataka (664 kg/ha), while in other growing states it is less than 450 kg/ha. Chhattisgarh and Gujarat recorded the low productivity in the range of 165 and 186 kg/ha, respectively.

In general, incidence of disease is less in this crop, but occurrence of grain smut (*Macalpinomyces sharmae*) can lead to economic losses. The shootfly incidences are widely reported and are known to cause economic losses. However, shootfly incidence is less during post-rainy season. Nutritionally, the crop is comparable or even superior to some of the major cereals (Table 6.2). Little millet is known for the highest content of crude fibre in its grains. It is also a rich source of protein, fat, minerals and vitamins. The crop can be considered as an essential food for nutritional security. Little millet also has received considerably low attention from researchers; however, the crop comes

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Table 6.1 State-wise average area, production and productivity in India (2001–2006).

Sl. No	State	Area (lakh ha)	Production (lakh tonnes)	Productivity (kg/ha)
1	Andhra Pradesh	0.23	0.10	425
2	Chhattisgarh	0.67	0.12	186
3	Gujarat	0.02	0.00	165
4	Jharkhand	0.24	0.11	445
5	Karnataka	0.31	0.20	664
6	Madhya Pradesh	1.63	0.37	229
7	Maharashtra	0.25	0.09	371
8	Orissa	0.25	0.10	422
9	Tamil Nadu	0.41	0.32	769
	All India	***4.01***	***1.41***	***352***

Source: Status Paper on Millets, 2010.

Table 6.2 Proximate composition in comparison with other major cereals.

Sl. No	Crop	Carbohydrates (g)	Protein (g)	Fat (g)	Crude fibre (g)	Mineral matter (g)	Calcium (mg)	Phosphorous (mg)
1	Little millet	75.7	8.7	5.3	8.6	1.7	17	220
2	Sorghum	72.6	10.4	1.9	1.6	1.6	25	222
3	Rice	78.2	6.8	0.5	0.2	0.6	10	160
4	Wheat	71.2	11.8	1.5	1.2	1.5	41	306
5	Maize	66.2	11.5	3.6	2.7	1.5	20	348

Source: National Institute of Nutrition (NIN), Hyderabad.

fairly well under conditions where other crops cannot be grown profitably. It matures in 70–90 days time. The yields are generally less than 500 kg/ha, but under favourable conditions may reach close to 3000 kg /ha.

6.2. Floral Biology

Floral biology of the crop is given in the Royal Botanical Garden, Kew website as described by Clayton *et al.* (2006). The inflorescence of little millet is called as panicle. The panicle is contracted, oblong, nodding and is about 5–40 cm long and 1–5 cm wide. The primary branches are appressed and are about 3–15 cm long. The branches of panicle are scabrous. The spikelets are solitary, and the fertile spikelets are borne on a pedicel. Fertile spikelets comprise of one basal floret which is sterile and one fertile floret without rachilla extension. Spikelets are elliptic in shape, compressed dorsally, pointed, 2.5–3.5 mm long and persistent on plant. Glumes cover apex of florets, thinner than the fertile lemma; lower glume is ovate, 0.7–1.2 mm long, membranous, without keels and are 1–3-veined. The lateral veins of the lower glume are absent or obscure.

Lower glume apex is acute. Upper glume is ovate, membranous, without keels and 11–15-veined; tip of upper glume is acute. The basal florets are barren with presence of palea. The lemma of the lower sterile floret is similar to the upper glume, ovate, membranous, 9–13-veined and acute. Palea of lower sterile floret is almost length of lemma. Fertile lemma is elliptic, dorsally compressed, 2.2–2.5 mm long, indurate, dark brown, shiny and without keel. Lemma margins are involute, lemma apex is acute and palea is involute and indurate. Anthers are three in number and 1.5 mm long. Caryopsis is with adherent pericarp and is about 1.8–1.9 mm long.

6.3 Cytogenetics and Morphological Variation in the Genus

The Indian cereal *P. sumatrense* is known by different epithets such as *miliare* and *attenuatum.* De Wet *et al.* (1983) reported that the correct name for the Indian cereal is *P. Sumatrense* and this has been derived based on a specimen collected from Sumatra. The species is believed to be grown in Tanimbar Island (Backer, 1960) and was probably introduced to Indonesia as a crop by Indian immigrants. Very fewer efforts have been made to understand the cytogenetics of *P. sumatrense* and their wild relatives. The basic chromosome number is 9, and evidences have been presented to show that the basic chromosome number has originated from basic chromosome number $x = 10$ (Hiremath *et al.,* 1990). Polyploidy is common in this genus, (Chennaveeraiah and Hiremath, 1990). Knowledge on genome relations in these species is also not understood. *Panicum psilopodium* is believed to be the progenitor of *P. sumatrense* and is widespread in India. In the Eastern ghats of north Andhra Pradesh, it is reported to be grown as a weed in the little millet fields and forms fertile hybrids. Morphologically both the species *P. Sumatrense* and *P. psilopodium* are similar but can be distinguished based on several distinguishing characters. The hybrids formed among both these species were vigorous and fertile. Morphology of the hybrids developed between *P. Sumatrense* × *P. psilopodium* resembled more towards *P. sumatrense* with regard to the non-shattering nature of the spikelets and reported to be intermediate for quantitative characters like stem thickness, plant height, leaf width and spikelet number (Hiremath *et al.,* 1990). The hybrids resembled *P. Psilopodium* with respect to purple glumes colour and stigma. Evidences that support *P. psilopodium* as putative progenitor of *P. sumatrense* are the morphological similarity, sympatric distribution and formation of fertile hybrids (Hiremath *et al.,* 1990). The genome notation proposed is AABB. Meiotic behaviour studied among the hybrids was perfectly normal. In addition to these, occurrence of regular 18 bivalents in the hybrids strongly suggests the fact that *P. sumatrense* might have originated from wild taxon *P. psilopodium* through selection (Hiremath *et al.,* 1990). Occurrence of single quadrivalent in the hybrid indicated that the genomic divergence and differentiation among these two species through one reciprocal translocation has taken place (Hiremath *et al.,* 1990). de Wet *et al.* (1983) in their study on the systematic and domestication of *Panicum sumatrense* reported that the genus includes wild, weed and cultivated forms. They also reported that the species is divided into *P. sumatrense* subsp. *sumatrense* to include cultivated little millet or *sama*, and the subsp. *psilopodium* which includes the wild progenitor. These two subspecies cross with each other and they are sympatric to produce fertile hybrids, derivatives are often weedy types observed in little millet fields. Weedy types are the derivatives of hybrids between wild and cultivated types and escapes from cultivation that have the ability for

efficient natural seed dispersal(de Wet *et al*., 1983). *P. sumatrense* is extensively variable regard to growth habit and inflorescence morphology. Growth habits vary widely from decumbent to erect (de Wet *et al*., 1983). Decumbent plants root at the lower end of the nodes and produce erect flowering culms ranging from 60–170 cm in height. The plants are strongly branched, and produce as many as 46 flowering culms which are sub-branched from the upper nodes to develop into as much as eight secondary inflorescences (de Wet *et al.,* 1983). Erect plants do rarely root from the lower nodes and are said to produce as many as 26 flowering culms that are 120–190 cm tall, and secondary inflorescence are formed from the upper one or two nodes little below the terminal inflorescence (de Wet *et al.,* 1983). Inflorescences of cultivated *P. sumatrense* do not disarticulate at maturity. Inflorescences are generally well exerted from the upper leaf-sheaf during the maturity stage (de Wet *et al.,* 1983). Decumbent plants generally do have open type inflorescence, with a length up to 50 cm and with 14–50 spreading type branches arranged along the elongated primary axis (de Wet *et al.,* 1983). Erect plants either have open or compact inflorescences, and they are up to 46 cm long with the more compact type branches drooping down at time of maturity (de Wet *et al.,* 1983). Spikelets are in the range of 2.5 mm length, lanceolate, glabrous, with the lower glume about one-third of the spikelet length and the upper glume almost the length of the spikelet (de Wet *et al.,* 1983). Florets dis-articulate above the glumes in spontaneous types and are freely threshable from the glumes in cultivated types. The lemma and palea hold the grains tightly during maturity to develop into a shiny, white to near black fruitcase (de Wet *et al.,* 1983). Based on the morphological variation and distribution, two races of cultivated little millet are recognised, namely, *nana* and *robusta* (de Wet *et al.,* 1983). Race nana resembles wild subsp of *P.sumatrense* with regard to inflorescence morphology. Race nana includes plants with decumbent to almost prostrate culms that become erect at time of flowering. Inflorescences are large and open with the upper branches sometimes clumped and curved at time of maturity. Height of the plants ranges from 60 cm to 170 cm, with decumbent culms and generally root at the lower nodes. Terminal inflorescences size ranges from 14 to 50 cm in length, erect, open and are branched strongly, and sometimes branches get clumped at time of maturity (de Wet *et al.,* 1983). Race robusta are erect plants with large strongly branched open or compact inflorescences. Flowering culms grow tall and range between 120 and 190 cm and robust. Terminal inflorescence is in the range of 20–46 cm in length, open or compact and strongly branched. Open inflorescences appear erect, while compact types are curved at maturity. This race is grown in India in the north western regions of Andhra Pradesh and adjacent Orissa, where it crosses with race nana (de Wet *et al.*, 1983).

6.4 Improvement in Little Millet

Little millet is early maturing comparatively less incidence of pests and diseases as well as tolerant to poor agro-climatic conditions. The grains are the economic part which are nutritional and used in various food preparations, while the dry stover is used as cattle feed. The national active germplasm site located at Bangalore and the gene bank unit at International Crop Research Institute for Semi-arid Tropics (ICRISAT) located at Hyderabad each maintains more than 1000 germplasm accessions belonging to different countries for its utilization in research and development programmes. Compared to other fine cereals, reports on improvement in little millet is scanty. The

Major efforts towards improvement is carried out by the All India Coordinated Small Millets Improvement Programme (AICSMIP) in collaboration with different State agricultural university centres/stations such as Berhampur (Orissa), Coimbatore (Tamil Nadu), Dindori (Madhya Pradesh), Jagdalpur (Chhattisgarh), Kolhapur (Maharashtra), Ranchi (Jharkhand) and Rewa (Madhya Pradesh). AICSMIP, Bangalore, is the lead centre working on basic and applied aspects of little millet and other small millets. The lead centre mainly coordinates and monitors the research work in different regional centres and organizes research programs relevant to regional research needs. The lead centre along with the regional centres contribute by developing improved varieties along with refinement of production and protection technologies, conservation, evaluation and documentation of germplasm resources and to promote their utilisation in the research programs. The MS Swaminathan Research Foundation (MSSRF), Chennai, along with several agriculture research institutes and universities, non-governmental organization, Government organization and international agencies have been conducting series of participatory research programme on millets mainly aimed at reviving, conserving and enhancing sustainable use of millets for food and nutrition. The various activities include establishing community-based institutions for promotion of millets, strengthening millet seed-supply system, increasing yield through improving millet cultivation practices and participatory selection of high yielding and superior varieties. A centrally sponsored scheme, National Food Security Mission under Government of India aimed at promoting cereals including millets. Interventions in the proven crop production technologies developed by National Agricultural Research System are made available to the farmers through a series of planned interventions and financial incentives. The Centre of Excellence for Small Millets (CoE-SM) located at the University of Agricultural Sciences, Bengaluru sponsored by National Food Security Mission, Under Government of India, New Delhi, has undertaken various small millet promotional activities through training programmes, popularisation of the centre as an Incubation Centre and Research.

6.4.1 Genetic Variability

Major work reported so far is on screening of the germplasm and improved genotypes for yield and other important traits, germplasm diversity studies, identification of resistant sources for smut resistance, testing association among different traits influencing yield, proximate and mineral composition in grains, mutation studies and creation of new variation and identification of surrogate/adaptive traits and genotypes for drought tolerance.

6.4.2 Germplasm Variability for Various Economic Traits

The crop is classified broadly under race nana and robusta, based on panicle morphology. Race nana matures faster and generates less biomass than robusta (de Wet *et al.*, 1983). In the tribal area of the Indian Kolli Hills, diversity among locally grown landraces of little millet was found to be high for all morphological traits measured both within and between landraces (Arunachalam *et al.,* 2005). High diversity, heritability and genetic advancement were reported for yield and productive tillers in the collection of 109 landraces, indicating the crop as a good candidate for varietal development (Nirmalakumari *et al.*, 2010). Evaluation of 460 accessions of little millet held by ICRISAT revealed high genetic variation for most of the quantitative traits tested.

A core collection of 56 genotypes was identified, which was representative of the entire seed bank (Upadhyaya *et al.,* 2014). Increased heritable lodging resistance has been introduced to a population of little millet with γ-ray mutational breeding (Nirmalakumari *et al.*, 2007). Channappagoudar *et al.* (2007) identified important traits influencing grain yield potential in little millet and observed that taller genotypes were found to be of high-yielding capacity and shorter genotypes are medium to low yielding. DPI 1865 and TNAU 63 were recorded as taller 152 and 161 cm, respectively. Their studies also observed that leaf number and tillers per plant positively contributing towards higher grain yield. The leaf parameters were also recorded as important parameters for improving the yield and total dry matter as it gives indications of the efficiency of the photosynthetic system. They observed TNAU 63 (20.2 q/ha) and DPI 1869 (18.3 q/ha) and TNAU 18 (16.9 q/ha) were high yielding with high values for most morpho-physiological parameters. From the study on biophysical basis of productivity in little millet by Gollagi *et al.* (2013) they observed higher transpiration rate in low-yielding genotypes and low in high-yielding genotypes and observed that high-yielding genotypes had higher stomatal conductance, which could be due to higher stomatal frequency on abaxial surface leading to enhanced canopy photosynthesis. They also observed minimum inter-veinal distance and higher vein load frequency in high-yielding genotypes. Nirmalakumari and Ulaganathan (2013) used farmer's participatory approach of breeding to identify trait-specific genotypes. Twelve genotypes were evaluated along with the farmers on community plots managed by them at several sites in agro-ecological areas. Farmers evaluated and rated the varieties based on their preferences especially for panicle type, yield traits, seed size and lodging tolerance. Farmers showed more interests towards compact panicles possessing bold seeds, pest and disease free genotypes and non-lodging characteristics. Salini *et al.* (2014) analysed 105 germplasms for 17 quantitative and 12 qualitative traits and selected 12 promising germplasm as parents and developed a total of 132 cross combinations from the set of parents. They studied the gene action for 11 characters and reported non-additive gene action for most of the characters other than plant height where additive and non-additive gene action played equal role. High coefficient of variation was observed for grain yield and tillers per plant. Heritability per cent were high for most of the characters except flag-leaf sheath length. The nature of inheritance of the qualitative characters revealed monogenic simple dominant inheritance for traits except grain colour. From the stability analysis carried out for 12 germplasm in four environments for eight characters identified lines IPmr 1046 and IPmr 889 as stable genotypes for grain yield. Girish *et al.* (2013) conducted a study with six improved lines RLM 40, BL 4, RLM 186, DLM 14, GV-2-1 and RLM 141 to identify superior yielding genotypes along with checks JK 8 and OLM 203 during 2011–2012. The study identified two lines BL 4 (1141 kg/ha grain yield and 5 t/ha fodder yield) and DLM 14 (grain yield of 1292 kg/ha with fodder yield of 5 t/ha as promising compared to check JK 8, which yielded 994 kg/ha with 6 t fodder yield. DLM 44 was early with a plant height of 113 cm and suited for inter crop with red-gram. Sasamala *et al.* (2012) studied the genetic diversity (D square) among 22 little millet genotypes evaluated under 12 environments. The study identified KCM 42, KCM 102D, Sabar and Co 2 as most divergent with KCM 594 and RCM 4, indicating that hybridisation between these genotypes likely to give better recombinants in segregating generations.

MSSRF has taken lead initiatives to collect, conserve and evaluate little millet in the Kolli region of Tamil Nadu, where little millet was preferred by tribal farmers as they

provided sustainable benefits to them. In recent years, introduction of high-yielding varieties of other commercial crops such as cassava shifted to commercial production relegating cultivation of millets to an obscure background leading to genetic erosion of millet diversity. MSSRF laid efforts to bring millet cultivation and to revitalise the conservation of local landraces and cultivars. The participatory rural appraisal conducted with the farmers revealed interest of the farmers in millets, but cultivation are getting eroded due to the poor productivity of landraces that are under cultivation. There is a need to introduce scientific interventions to optimise their cultivation practices under site-specific constraints. A program under Swiss Development Corporation, was taken up for optimisation of cultivation practices under a participatory plant-breeding activity. A two-season operation of these initiatives has shown that: (i) the long discontinuation of small millet cultivation has not yet destroyed the inherent genetic diversity, (ii) the genetic integrity of short and long-duration landraces is still maintained, (iii) even out of the seven prevalent landraces sufficient genetic diversity existed giving four distinctly different genetic groups and (iv) introduction of improved practices into farmers' method of cultivation has improved the productivity up to 200% at no extra cost. Arunachalam *et al.* (2005) studied the stability of genetic diversity among little millet landraces of South India under MSSRF. Genetic divergence studies and principal component analysis revealed presence of high diversity among set of landraces studies analysed over two seasons. The study confirmed the sustained availability of the distinct divergence in little millet in Kolli Hills of Tamil Nadu. They observed site-specific expression among the landraces and suggested that breeding and selection to be done based on specific location. It was expected that the high level of diversity would be preserved at Kolli Hills as long as the micro (including traditional cultivation practices) and macro (such as edaphic and climatic factors, soil status and fertility) environments are left largely undisturbed.

6.4.3 Varietal Improvement

Varietal improvement has received less attention as the case in other small millets. The varieties released were developed mostly through mass selection or pure-line selection methods. Breeding for improved varieties using hybridisation techniques are meagre owing to small sized florets and difficulties encountered in crossing (Nirmalakumari *et al.*, 2007). Mutation breeding was used as one of the strategy in addition to conventional breeding methods for genetic improvement of little millet. A number of improved varieties have been developed and released for cultivation in different little millet-growing states. The improved varieties are developed to meet the specific requirements of different regions. In addition to yield as one of the major criterion for the development of new varieties, some varieties possess drought tolerance and blast and grain smut resistance. The varieties released in different states and popular in different little millet-growing states are given in Table 6.3.

6.4.4 Improvement in Grain Smut Resistance

For management of grain smut, Jain and Tripathi (2007) analysed different varieties differing for maturity and chemical methods for the management of grain smut (*Macalpinomyces sharmae*) in little millet. They observed average grain smut incidence ranging from 5.9 and 31.0%, and grain yield reduction ranging from 9.8 to 53.5% in different cultivars. The early cultivars (up to 70 days maturity), namely, OLM 20, OLM 23,

Table 6.3 List of improved varieties and their characteristics.

S. No	Variety Name	Central/ State	Date of Notification	Parentage	Maturity in Duration (days)	Pests and disease Reaction	Grain Yield (kg/ha)
1	OLM-208	Central	2010	Selection from Lajigada local	71–137	Resistant to blast and moderately resistant to rust, grain smut, sheath blight and shoot fly	1413–3407
2	Co4	Tamil Nadu	2007	Co2 × MS 1684	75–80	—	1500
3	OLM-20	Central	2004	Mutant of SS 81-1	46–77	Moderately resistant to shoot fly, moderately susceptible to grain smut; moderately resistant to sheath blight and brown spot	1196–2100
4	OLM-36	Central	2001	Mutant of SS81-1	77	Moderately resistant to grain smut and shootfly, resistant to brown spot and shoot fly	1091
5	OLM-203	Central	2001	Selection from a local cultivar (kl-2) of Koraput district	105–115	Resistant to blast and grain smut and moderately resistant to brown spot and shoot fly	—
6	Paiyur-2	Tamil Nadu	2000	Pure line selection from the germplasm accession pm 295	80–85	Less incidence of grain smut as compared to Co2, Co3 and Paiyur-1	744–800
7	Co3	Tamil Nadu	1997	Selection from germplasm	80–85	Tolerant to major diseases and pests	1066
8	TNAU-63	Central	1997	Single plant selection from germplasm MS 2369	69–104	Shoot fly incidence (8%), aphids (14%), brown spot (0.5% grade), smut incidence (3.4%)	1152
9	Birsa gundli-1	Central	1993	Selection from local germplasm	55–60	—	700–800
10	Paiyur-1	Central	1989	Pure-line selection from Sathur local		—	873

(*Continued*)

Table 6.3 (Continued)

S. No	Variety Name	Central/ State	Date of Notification	Parentage	Maturity in Duration (days)	Pests and disease Reaction	Grain Yield (kg/ha)
11	Jawahar kutki-2	Central	1987	Selection from local material named Gariyaband	75–80	—	700–1000
12	Jawahar kutki-8	Central	1987	Pedigree – single-plant selection from germplasm no. 8	80	Moderately resistant to shootfly	
13	PRC-3	Central	1986	Single-plant selection from GPM 97	61–93	Moderately resistant to shootfly	—
14	Gujarat vari-1	Gujarat	1985	A selection from local strain vari 8-3		—	1500
15	Gariya Band (Dindori-2)	Madhya Pradesh	1984	—	75–80	—	700–1000
16	K-1	Tamil Nadu	1982	Developed from culture no. Pm-368	90	—	1285
17	Co2	Central	1978	A pure-line selection from a local (pm -296) collection of Andhra Pradesh	80–85	Fairly tolerant to pests under field conditions	
18	Dindori-1	Madhya Pradesh	1973	Mutant of no. 50-1	125–130	No serious pest or disease observed	1500–2000
19	Co1	Tamil Nadu	1956	Pure-line selection from Anantpur selection	90–100	The incidence of shoot fly is similar to that of other varieties	400–500
20	Jawahar kutki-36 (2009)	Madhya Pradesh		Selection from local germplasm no. 36	76	Tolerant to grain smut and shoot fly	4600
21	V-15	Central		Pure-line selection	78– 80	Moderately resistant to diseases	1400–600
22	V-17	Central		Pure-line selection	78–80	Moderately resistant to disease	1400–1600

Source: AICSMIP, small millets, Bengaluru and http://smis.dacnet.nic.in/

OLM 45, DLM 80, DLM 93, DLM 314, DLM 369, RLM 36 and K 8, were susceptible to grain smut and confirmed that the conditions of weather prevailing during flowering time and floral characteristics were the reasons for high incidence. Cultivars having more than 100 days duration (Varisukdhara, RLM 13, RLM 14, OLM 203, VMLC 281, VLMC 296 and OLM 40) were reported to be free from grain smut. Seed treatment with chemicals such as carboxin @2 g per kg of seed and one foliar application of carbendazim (0.05%) was most effective for control of grain smut. From the studies carried out in Rewa region where little millet is grown, screening of 16 genotypes for grain smut, RLM 118 (4.0), Kutki No 2 × Co2 (4.7) and RLM 136 (4.8) recorded the least susceptibility index. In a different experiment, 50 elite entries along with two national checks were screened for grain smut. Incidence ranged from 0.0 to 81.8%, and susceptibility index ranged from 0 to 17. Nine entries PCGL 2, PCGL 6, PCGL 19, PCGL 20, 24, 25, 32, 35, 39 and national check OLM 203 were completely free from grain smut incidence. Seventeen entries showed <5 susceptibility index, and are considered as resistant.

6.4.5 Drought-Tolerance Studies

Drought-tolerance studies were conducted during pre-heading and post-heading water stress deficit on growth and grain yield of *P. sumatrense*, along with other millets such as *P. miliaceum*, *Setaria italica* and *Setaria glauca*. Comparing different millets, the grain yield loss under water stress was recorded lowest in *P. sumatrense* (20%), followed by *P. miliaceum* (36%), while it was highest in *S. italica* (80%) and *S. glauca* (70%). Higher osmotic adjustment was recorded in *S. glauca* and *P. sumatrense*, but did not result in higher productivity under water deficit. Increased root growth in *P. sumatrense*, *S. italica* and *S. Glauca* was recorded at water stress. One of the important findings include significant correlation between grain weight and root dry-weight, indicating root growth to be more important than osmotic adjustment for genetic improvement. Ajithkumar and Panneerselvam (2013) analysed the growth, chlorophyll pigments, osmotic adjustment and anti-oxidative enzymes activity in *P. Sumatrense* under drought stress. As in the earlier studies, the root length increased gradually in all drought treatments at all growth stages of *P. sumatrense*. The chlorophyll pigments and plant height showed a reduction in 13 DID treatment when compared to all treatment. Compatible solutes such as proline, glycine betaine and free amino acid increased in all drought treatment when compared to control at 70 DAS. Furthermore, stress treatment caused an increase in the activity of anti-oxidant enzymes such as superoxide dismutase, catalase and peroxidase. *Panicum sumatrense* possesses many growth and physiological drought tolerance characters which can be used in future breeding programmes.

Bhaskaran and Paneerselvam (2013) investigated response and regulation of the anti-oxidant defense system and the level of lipid peroxidation in *P. Miliacium* and *P. Sumatrense* under salt treatments. NaCl stress was imposed for 20 days after the sowing of two *Panicum* species. The changes in the anti-oxidant enzyme activities such as superoxide dismutase, catalase, peroxidase and ascorbate peroxidase and the rate of lipid peroxidation level in terms of malondialdehyde (MDA) were recorded in both *Panicum* species. A great correlation exists between the anti-oxidant enzymes and lipid peroxidation. The defence mechanism activated in *Panicum* species studied was confirmed by the increased anti-oxidant enzyme activities under progressive NaCl stress. MDA content remained close to control at moderate NaCl concentrations and increased

at higher salinities. Although lipid peroxidation increased in both *Panicum* species under salt stress the percentage of increase was low in *P. sumatrense*, indicating its salt-tolerant nature. Another possible conclusion is that improved tolerance to salt stress may be accomplished by increased capacity of the anti-oxidative system.

6.4.6 Nutritional Improvement

Nambi *et al.* (2012) studied the proximate and mineral composition of 18 genotypes obtained from the millet-growing regions of Tamil Nadu. The accessions varied for seed colour. Analysis was carried out using inductively coupled plasma (ICP) spectroscopic method. Among proximate compositions, carbohydrate (61.48–68.57 g/100 g), protein content ranged 6.36–9.15 g/100 g, ash (3.15–9.07 g/100 g), fibre (5.54–7.84 g/100 g) and fat (3.61–5.56 g/100 g). Among minerals, potassium content ranged 199.2–334 mg/100 g, phosphorous 184.3–389 mg/100 g, magnesium 131.3–186.6 mg/100 g, iron 7.84–90.8 mg/100 g, calcium 22.6–56.4 mg/100 g and zinc 1.52–2.14 mg/100 g. Overall analysis of the mineral composition showed that minerals were contained in the following order; potassium followed by phosphorous, magnesium, iron, calcium and zinc. Overall, high variability was recorded for all the proximate and mineral contents among the genotypes analysed indicated its scope for utilisation in breeding programmes. Usha *et al.* (2011) also analysed the variability for proximate and mineral compositions. Protein content in their study ranged between 9.8 and 12.49 g/100 g. Fat, ash, crude fibre and carbohydrates were in the range of 2.87–5.09, 0.98–4.78, 0.49–8.72 and 62.25–76.59 g/100 g, respectively. Micronutrients (mg/100 g) were present, such as calcium (18–24), phosphorous (215–232), iron (3.0–10.5), potassium (125–131), sodium (6.3–7.8), zinc (2.63–4.20), copper (0.6–1.0) and silicon (0.07–1.97).

6.4.7 Mutational Approaches

Among the various methods adopted mutation breeding has been widely used for creating new variability in millets, including little millet. The varieties released were developed mostly through mass-selection or pure-line selection methods. Breeding for new varieties using crossing techniques are least exploited owing to difficulties encountered in crossing due to tiny spikelets on brittle pedicels (Nirmalakumari *et al.*, 2007). Mutation breeding was used as complement approach to conventional breeding methods for genetic improvement of little millet. Nirmalakumari *et al.* (2007) carried out mutagenesis in Co3 and Co4 cultivars by using gamma rays. They observed maximum variability for characters like plant height and number of tillers in both the cultivars irradiated. High heritability per cent along with high genetic advance was recorded for number of tillers, lodging and the grain yield in the M_2 generation. Irradiated mutants obtained from 500 and 600 Gy exhibited maximum variability, heritability and genetic advance for plant height, number of tillers, number of nodes, inter-nodal length, culm thickness and grain yield indicating the selection efficiency of these characters for development of improved genotypes. Ganapathy *et al.* (2008) studied the mutagenic effectiveness and efficiency in two little millet varieties Co3 and Co4 using γ-rays. The mutagen dose of 500 Gray registered the highest mutation rates both on M_1 panicle-family basis and on M_2 seedlings basis in both varieties. They also observed that the effectiveness decreased with the increase in dose of the mutagen in both genotypes.

6.5 Critical Research Gaps

1) A good number of little millet germplasm is being conserved at AICSMIP, Bangalore, and ICRISAT gene banks. Limited attempts were made to evaluate them for various traits of economic importance.
2) Basic studies on floral biology and breeding behaviour are lacking in all small millets, including little millet.
3) The majority of the present-released varieties are selections made from germplasm/local landraces without much hybridisation efforts, and this is one of the reasons for less genetic progress in yield compared to sorghum and pearl millet.
4) Small millets including little millet are known for their drought-tolerance ability and as less-water-demanding crops. Few isolated studies are available on the aspects.
5) Although millets are grown under limited moisture conditions, performance of genotypes is limited to specific regions/soil types. Such studies are widespread in sorghum and are not done in small millets.
6) Although the crop is known for its high nutritional value, few studies are available on grain proximate and nutritional composition and the data available are analyzed from few genotypes/germplasm which is not representative of the variability existing in the crop.
7) These crops are also excellent sources of dry fodder and sustain fodder requirement for cattle population in the dry tracts of India. Genetic improvement on fodder yield and quality improvement should receive priority.

6.6 Strategies for Genetic Improvement

1) Systematic evaluation for different yield, agronomic and nutritional traits is required for unlocking the genetic potential in the crop and should be the primary objective for genetic improvement.
2) Knowledge on floral structure and crossing techniques are not well understood. Moreover, the small-sized florets hinder the recombination breeding in this crop. Efforts to develop suitable emasculation and crossing techniques needs attention.
3) Grain yield has always been an important trait for genetic improvement. Efforts towards yield per se have led to marginal improvement. In addition to per se yield, selection for component traits such as compact panicle types and large seed size should be done.
4) Although millets are grown on poor soils under dry conditions, genotypes/cultivars responsive to high-input conditions should also be identified.
5) Little millet is one of the least water-demanding crops. A few studies isolated have indicated less loss in yield under water stress compared to *P. Miliaceum*, *S. Italica* and *S. glauca*. Varieties with drought tolerance potential and better regenerative capacity on reversal of dry spell for harsh conditions in drought-prone areas should be the focus.
6) There are many superior nutritional properties such as high fibre content and mineral content in the grains which in-turn have numerous health-benefitting properties. Improved cultivars possessing high nutritional value would make a great way in increasing the demand for the crop.
7) The stover after harvest of the crop is a source of fodder. Genetic improvement in this area of research has received less attention.

8) Few pests and diseases are known to infect this crop. Among them shootfly and grain smut as are the major ones. Host-plant resistance should be tried for the development of disease/insect resistance.
9) Stem lodging and grain shattering are the other important agronomic traits which should receive due attention while improving grain yield.
10) Breeding for specific end-uses should receive priority as this attracts the private-sector industries to invest in millets.
11) Little millet is known to mature in 60–80 days. However, early-maturing genotypes with substantial high yield and photo-insensitive genotypes suiting different cropping systems should be developed.

References

Abinash, Y. and Srivastava, D.P. (1976) Path analysis in *Panicum miliare*. *Indian J Genet*, **36** (1), 64–68.

Ajithkumar, I.P. and Panneerselvam, R. (2013) ROS scavenging system, osmotic maintenance, pigment and growth status of *Panicum sumatrense* Roth. under drought stress. *Cell Biochem Biophys*, **68** (3), 587–595.

Arunachalam, V., Rengalakshmi, R. and Kubera Raj, M. (2005) Ecological stability of genetic diversity among landraces of little millet (*Panicum sumatrense*) in South India. *Genet Res Crop Evol*, **52**, 15–19.

Backer, C.A. (1960) *Beknopte Flora van Java. Gramineae*, Rijksherbarium, Leiden.

Bhaskaran, J. and Panneerselvam, R. (2013) Accelerated reactive oxygen scavenging system and membrane integrity of two Panicum species varying in salt tolerance. *Cell Biochem Biophys*, **67** (3), 885–892.

Channappagoudar, B.B., Hiremath, N.S.M., Biradar, R. *et al.* (2007) Morpho-physiological traits influencing the grain yield potential in little millet. *Karnataka J Agric Sci*, **20** (3), 473–476.

Chaturvedi, V.K., Mishra, Y., Singh, C.B. and Kharche, S.K. (1990) Genetic variability, correlated response and association analysis in little millet (*Panicum miliare* L.). *Mysore J Agric Sci*, **24**, 163–167.

Chennaveeraiah, M.S. and Hiremath, S.C. (1990) *Cytogenetics of minor millets, in Chromosome Engineering in Plants Genetics, Breeding and Evolution. Vol. II*. Chapter 32 (eds T. Tsuchiya and P.K. Gupta), Elsevier Sci. Publ., Amsterdam, The Netherlands.

Clayton, W.D., Vorontsova, M.S., Harman, K.T. and Williamson, H. (2006) *GrassBase – The Online World Grass Flora*. http://www.kew.org/data/grasses-db.html

de Wet, J.M.J., Rao, K.E.P. and Brink, D.E. (1983) Systematics and domestication of *Panicum sumatrense* Gramineae. *J Agric Trad Bot Appl*, **30** (2), 159–168.

Ganapathy, S., Nirmalakumari, A., Senthil, N. *et al.* (2008) Isolation of macromutations and mutagenic effectiveness and efficiency in little millet varieties. *World J Agric Sci*, **4**, 483–486.

Girish, G., Bharathi, S., Jayalakshmi, S.K. *et al.* (2013) Improved varieties of little millet for dryland, in *Compendium of Paper & Abstracts*, Global Consultation on Millets Promotion for Health and Nutritional Security, December 18–20, 2013 (eds S. Rakshit, I.K. Das, G. Shyamprasad *et al.*), Society for Millets Research & Directorate of Sorghum Research, Rajendranagar, Hyderabad, p. 108.

Gollagi, S.G., Chetti, M.B. and Ashvathama, V.H. (2013) Biophysical basis of productivity in little millet (*Panicum miliare* L). *Int J Agric Sci*, **9** (1), 117–120.

Hiremath, S.C., Patil, G.N.V. and Salimath, S.S. (1990) Genome homology and origin of *Panicum sumatrense* (Gramineae). *Cytologia (Tokyo)*, **55**, 315–319. doi: 10.1508/cytologia.55.315

Jain, A.K. and Tripathi, S.K. (2007) Management of grain smut (*Macarpinomyces sharmae*) in little millet. *Indian Phytopath*, **60** (4), 467–471.

Nambi, V.A., Eganathan, P. and Philip, P.I.M. (2012) Proximate and mineral composition analysis of little millet collected from some millet growing areas in Tamil Nadu. *Indian J Plant Genet Res*, **25** (2), 189–191.

Nirmalakumari, A., Arulselvi, S., Ganapathy, S. *et al.* (2007) Gamma ray induced variation for lodging resistance and its associated characters in little millet (*Panicum sumatrense* Roth Ex-roem and schult). *Madras Agric J*, **94** (7–12), 151–155.

Nirmalakumari, A., Salini, K. and Veerabadhiran, P. (2010) Morphological characterization and evaluation of little millet (*Panicum sumatrense* Roth. ex. Roem. and Schultz.) germplasm. *Electron J Plant Breed*, **1** (2), 148–155.

Nirmalakumari, A. and Ulaganathan, V. (2013) Selection of trait specific little millet genotypes involving farmer's participation, in *Compendium of Paper & Abstracts*, Global Consultation on Millets Promotion for Health and Nutritional Security, December 18–20,2013 (eds S. Rakshit, I.K. Das, G. Shyamprasad *et al.*), Society for Millets Research & Directorate of Sorghum Research, Rajendranagar, Hyderabad, p. 318.

Patel, R.H., Desai, K.B., Desai, M.S. and Modi, N.D. (1990) study on stability analysis in little millet (*Panicum miliare* L.). *Madras Agric J*, **77** (5–6), 252–254.

Salini, K., Nirmalakumari, A. and Senthil, N. (2014) Genetic analysis of yield and its components in little millet (*Panicum sumatrense* Roth ex Roem. and Schultz). *2nd International Conference on Agricultural & Horticultural Sciences Hyderabad, India, February 3–5, 2014*, **2** (4), 177.

Sasamala, A.C., Sahoo, L.P. and Mahapatra, K.C. (2012) Classificatory analysis in little millet germplasm collections of Odisha. *Indian J Plant Genet Res*, **25** (3), 294–297.

Selvi, V.M., Nirmalakumari, A. and Subramanian, A. (2014) Genetics and interrelationships of yield traits for enhancing productivity of little millet. *Electron J Plant Breed*, **5** (1), 82–86.

Status paper on Millets (2010) *Directorate of Millets Development*, Ministry of Agriculture, Department of Agriculture and Cooperation, Jaipur.

Upadhyaya, H.D., Dwivedi, S.L., Singh, S.K. *et al.* (2014) Forming core collections in barnyard, kodo, and little millets using morpho agronomic descriptors. *Crop Science*, **54** (6), 2673–2682.

Usha, R., Madhuprasad, V.L., Suresha, S.V. and Jagadeeshwara, K. (2011) Little millet (*Panicum miliare* L.) – A source of functional food for sustainable nutrition security, in *7th Asia Pacific Conference on Clinical Nutrition, June 5–8, 2011*, Bangkok, Thailand, p. 449.

7

Barnyard Millet: Present Status and Future Thrust Areas

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7.1 Introduction

Barnyard millet has two major cultivated species, *Echinochloa frumentacea* (Indian barnyard millet, sawa millet or billion dollar grass) and *E. utilis* (Japanese barnyard millet), which are widely grown as a minor cereal in India, China, Japan, Pakistan, Africa and Nepal. Major cereals such as rice and wheat are preferably cultivated on resource-rich fertile soils, whereas, for the small millets, least care is taken to select lands for cultivation, as they are generally grown on resource-poor marginal lands. Here also, small millets score high to give sustainable yields, as they have exceptional potential to withstand drought and other abnormal fluctuations in weather conditions. In India, barnyard millet is grown up to 2300 m from mean sea level (MSL) predominantly in kharif season in the hilly tracts of Uttarakhand and Tamil Nadu states (Kumar *et al.*, 2007; Joshi, 2013). Like other small millets, barnyard millet also is gaining attention as a health food. Traditionally it was used as a substitute for rice in Northern India. Traditional foods prepared from barnyard millet such as *idli*, *dosa* and *muruku* are very popular in Southern India. Recently, it is being used for developing various value-added products such as biscuits, sweets, vermicelli, ready mixes, multi-grain *atta* (flour), etc. (Sood, Khulbe, Gupta *et al.*, 2015). As a health food, it is highly suitable and recommended for infants, pregnant women and people with diabetes. In addition, it has important use as cattle feed due to the high palatability of its fodder, which can be used for making hay or silage.

7.2 Nutritional Composition and Food Value

Barnyard millet has nutritional merits which make it the most suitable food for the patients suffering from *celiac* disease in which the patients are intolerant to gluten and exhibit allergies after consuming wheat-based food products. This is true with the other small millets also, as these are not closely related to wheat. Barnyard millet is nutritionally very superior (Table 7.1) and contains substantial amount of iron (Fe) in the grain (Anonymous, 2014).

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Table 7.1 Nutrient composition of barnyard millet and cereals (per 100 g).

Food grain	Protein (g)	Carbohydrates (g)	Fat (g)	Crude fibre (g)	Mineral matter (g)	Calcium (mg)	Phosphorous (mg)	Fe (mg)
Barnyard millet	6.2	65.5	2.2	9.8	4.4	11	280	15.0
Wheat	11.8	71.2	1.5	1.2	1.5	41	306	5.3
Rice	6.8	78.2	0.5	0.2	0.6	45	160	—

Table 7.2 Wild species of barnyard millet.

Wild species	Chromosome no.	Characteristics
E. crus-galli	$2n = 48$	Annual tufted grass grown as fodder
E. stagnina	$2n = 54$	Perennial weed, grown as fodder, made into hay
E. pyramidalis	$2n = 54, 72$	A weed-like perennial, excellent fodder and pasture
E. colona	$2n = 36, 48, 54, 72$	Jungle rice, a good fodder at all stages.

Source: Joel *et al.* (2006).

7.3 Origin and Taxonomy

The majority of the species (total 35) in the genus *Echinochloa* are spread over the warmer regions of the world. Most of them are aggressive weeds of cultivated farms. Out of the 35 *Echinochloa* species, *E. frumentacea* Link and *E. Utilis* Ohwi and Yabuno are the cultivated species. Indian barnyard millet (*E. frumentacea* Link) revealed a simultaneous evolutionary path both in India and Africa and its wild progenitor is the *E. colona* (L.) Link which is the tropical grass popularly called 'Jungle rice' (Table 7.2). The exact information about the domestication is not available (Sood, Khulbe, Gupta *et al.*, 2015). Japanese barnyard millet (*E. esculenta* (A. Braun) H. Scholz; syn *E. utilis* Ohwi et Yabuno) is a habitant of the temperate regions (De Wet *et al.*, 1983) of East Asian countries. Doggett (1989) reported *E. crus-galli* (L.) Beauv. (barnyard grass) as its wild ancestor domesticated about 4000 years ago in Japan. Based on the inflorescence morphology, the species *E. frumentacea* was classified into four races, and *E. utilis* into two races (Table 7.3).

Table 7.3 Barnyard millet species, sub-species and races.

Cultivated species	Sub-species	Races
Indian barnyard millet [*E. colona* (L.) Link]	*Colona*	—
	Frumentacea	*Stolonifera, intermedia, robusta and laxa*
Japanese barnyard millet [*E. crus-galli* (L.) Beauv]	*Crus-galli*	*Crus-galli and macrocarpa*
	Utilis	*Utilis and intermedia*

7.4. Reproductive Biology

There is a considerable variation of traits such as panicle type, glumes and lower lemma texture to differentiate the two cultivated Indian (smaller awnless spikelets, with membranous glumes) and Japanese (awned spikelets and papery upper glumes and lower lemma) barnyard millet species (Yabuno, 1987; De Wet *et al.*, 1983; Sood, Khulbe, Gupta *et al.*, 2015).

7.4.1 Roots

The barnyard millet plant has two sets of roots, viz., (i) the seminal roots, and (ii) the adventitious or secondary roots. The seminal roots emerge from the germ and help the seedlings become established. These are produced by the young plants. They may remain functional for the life of the plant but form only small fraction of the total root system. The adventitious roots arise from the basal node which forms near the soil surface and eventually become the permanent root system.

7.4.2 Stem/Culm

This is usually hollow, jointed cylindrical, simple or sparingly branched, glabrous to variously hairy, with nodes and internodes. Tillers and lateral branches arise from the axillary buds at the lower internodes.

7.4.3 Leaves

Leaves are simple, flat, wide, glabrous or slightly hairy without ligule. The leaves are arranged alternately on the culm, consist of the sheath and blade. The uppermost leaf on the plant is called as the flag leaf.

7.4.4 Panicle

The plant produces inflorescence of 10–25 cm-long terminal panicles that are usually erect with different shapes, viz., cylindrical, pyramidal and globose to elliptic. The panicle consists of few to numerous dense racemes with 4–6 mm-long spikelets arranged in four irregular rows on the triquetrous rachis (Napper, 1965; Joel *et al.*, 2006; Sood, Khulbe, Gupta *et al.*, 2015). The colour of spikelets varies from green, brown to purple, and mostly crowded on one side of the rachis. Forms with spikelets arranged around the rachis also reported. Spikelets can be awned or awnless, depending on the species. Pedicilate spikelets are enfolded by unequal glumes; the upper glume is as long as the spikelet, is many-veined (Mitich, 1990) and consists of two florets – lower sterile (with lemma and small palea), and the upper fertile bisexual floret which has thick broad lemma (~2 mm) and palea, two lodicules, three stamens and superior ovary with two plumose stigmas (Sundararaj and Thulasidas, 1976; Gupta *et al.*, 2010) (Plate 7.1).

7.4.5 Seed

It is very small, smooth, rounded at base and pointed at apex, botanically called *caryopsis*, usually 2–3 mm long and 1–2 mm wide. The seeds are enclosed in shining white-coloured hard and firm lemma and palea (Sood, Khulbe, Gupta *et al.*, 2015).

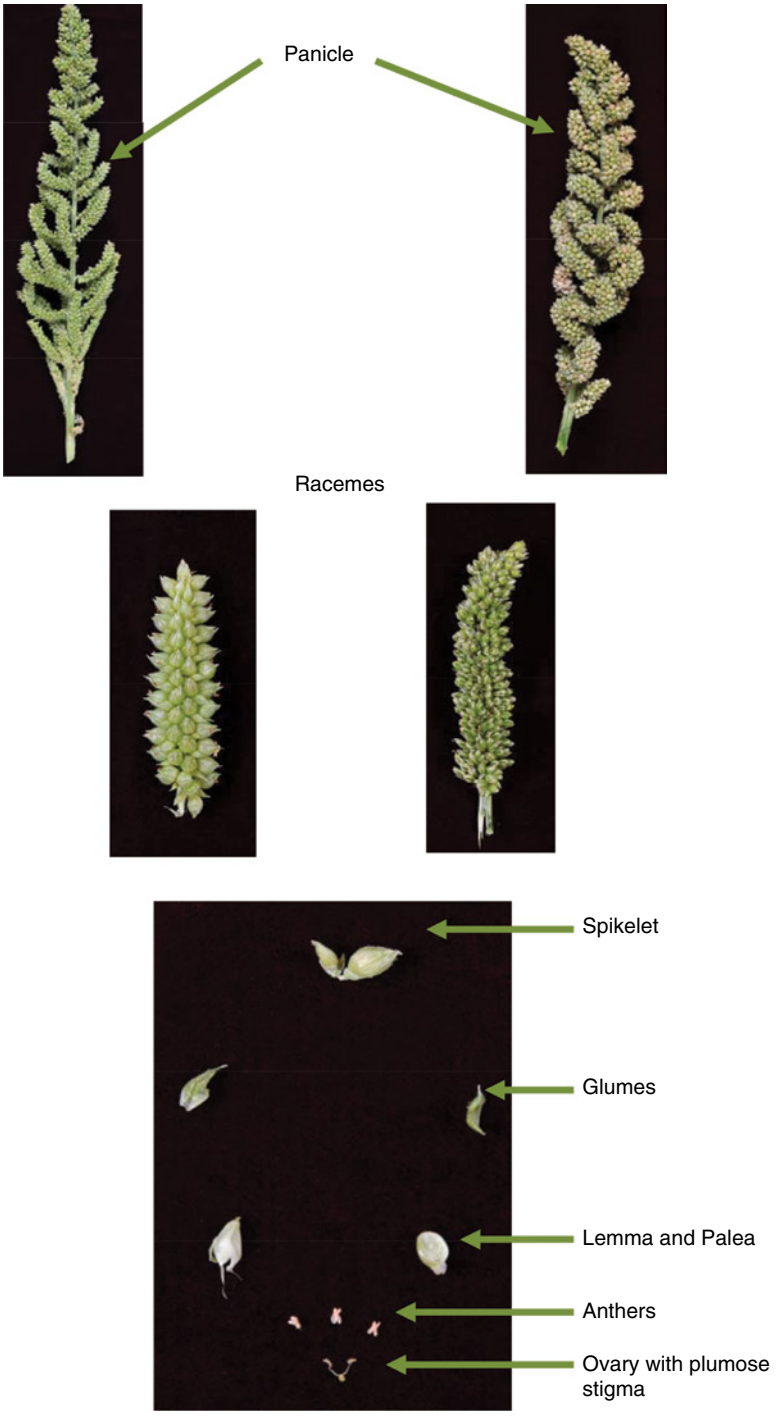

Plate 7.1 Barnyard millet inflorescence and floral parts. (Photo credit: H.S. Gawali) (*See color plate section for the color representation of this figure.*)

7.4.6 Floral Biology

The flowering occurs from tip of the inflorescence to base. It takes about 10–15 days for complete flowering; in some cases, it may extend up to 22 days, and in compact panicles it requires 3–4 days more. Opening of individual flowers happens between 0500 and 1000 hours with the maximum opening during 0600–0700 hours (Sundararaj and Thulasidas, 1976; Jayaraman *et al.*, 1997; Sood, Khulbe, Gupta *et al.*, 2015). In the individual spikes, the spikelets along the two margins open earlier than those at the middle raceme. The whole process for the opening of the glumes to their complete closing takes about 24 minutes. The flowers open out gradually with the stigmatic branches spreading out followed by the anthers and then the dehiscence of the anthers. It is basically an autogamous crop (Maun and Barrett, 1986; Potvin, 1986; 1991), but some percentage of cross-pollination is also reported mainly via wind. All these make artificial hybridisation difficult, and hand emasculation is very hard to perform with the very tiny florets. The hot-water method can be successfully used to emasculate the florets. Sood, Khulbe, Gupta *et al.* (2015) effectively used this method at 48°C for 4–5 min to induce male sterility in the hilly areas in both species of barnyard millet. Progress has been made in crossing by using contact method where the desirable male parent with distinct morphology is planted adjacent to female parent (emasculated), and the panicles of both plants are tied together. After pollination and fertilisation, they are separated. Here, identification of the true hybrid is very crucial as it can be done only by critically observing the dominant characters like plant height, open panicles, glume pigmentation, etc. Another method of pollination is by hand. Artificial pollination is practised by selecting the suitable male and by shaking its flowering panicle over the emasculated female panicle and covering the panicle with butter paper to avoid further pollination from other pollen sources.

7.5 Cytogenetics

Genus *Echinochloa* comprises more than 25 annual or perennial species and many of them are paddy-field weeds. The basic chromosome number in this genus is $x = 9$, polyploidy series include diploid *E. obtusiflora* Stapf ($2n = 2x = 18$), tetraploid *E. oryzicola* Vasing ($2n = 4x = 36$) and hexaploid *E. untilis* ohwi. ($2n = 6x = 54$). Yabuno (1962) reported inter-specific polyploidy in several cytotypes ($2n = 4x = 36$, $6x = 54$, $7x = 63$, $12x = 108$, $14x = 126$). The Japanese barnyard millet (*E. esculenta*) and Indian barnyard millet (*E. frumentacea*) exhibit close relationship with their wild relatives, *E. crus-galli* and *E. colona*. These species, like their cultivated forms, are hexaploids with basic chromosome number $x = 9$ ($2n = 6x = 54$). The inter-specific crosses among cultivated species and their wild counterparts (*E. crus-galli* × *E. esculenta* and *E. colona* × *E. frumentacea*) showed normal meiotic behaviour with formation of 27 bivalents. However, crosses among cultivated species and between their ancestors exhibited meiotic irregularities (formation univalents, laggards and micronuclei). Cytogenetic evidences revealed that the wild species *E. crus-galli* and *E. colona* are probable progenitors of *E. esculenta* and *E. frumentacea*. The wild species *E. crus-galli* is allohexaploid which shares two of the three genomes with *E. oryzoides* as the crosses between them showed 18 bivalents and 9 univalents. This suggests that *E. crus-galli* generated through natural hybridisation between the tetraploid *E. oryzoides* with the still unknown species of *Echinochloa* (Yabuno, 1966; 1984; Sood, Khulbe, Gupta *et al.*, 2015). These findings were also confirmed using internal transcribed spacer and chloroplast DNA sequences (Aoki and Yamaguchi, 2008).

7.6 Genetic Resources and Utilisation

The worldwide germplasm collection (Table 7.4) of barnyard millet is about 8600 accessions. The largest collection is held by Japan (about 3700 accessions), followed by India (about 3200 accessions), China (700 accessions) and the United States (300). In India, the largest collection is held at the National Bureau of Plant Genetic Resources (1677), All India Coordinated Research Project (AICRP) on Small Millets (868) and ICRISAT holds 743 accessions.

Table 7.4 Worldwide barnyard millet germplasm collections.

Country	Institute	Accessions
Australia	Australian Tropical Crops & Forages Genetic Resources Centre	60
Austria	AGES Linz – Austrian Agency for Health and Food Safety/Seed Collection	01
	Office of the Styrian Regional Government, Department for Plant Health and Special Crops	01
Brazil	Empresa Catarinense de Pesquisa Agropecuaria	09
	Instituto de Zootecnia	04
Bulgaria	Institute for Plant Genetic Resources 'K.Malkov'	01
Canada	Plant Gene Resources of Canada, Saskatoon Research Centre, Agriculture and Agri-Food Canada	02
China	Institute of Crop Science, Chinese Academy of Agricultural Sciences	717
Colombia	Centro Internacional de Agricultura Tropical	20
Czech Republic	Genebank Department, Division of Genetics and Plant Breeding, Crop Research Institute	03
Ethiopia	International Livestock Research Institute	92
Germany	Genebank, Leibniz Institute of Plant Genetics and Crop Plant Research	36
Guyana	National Agricultural Research and Extension Institute	01
Hungary	Institute for Agrobotany	08
India	AICRP on Small Millets	868
	International Crop Research Institute for the Semi-Arid Tropics	743
	National Bureau of Plant Genetic Resources	1677
Iran, Islamic Rep. of	National Plant Gene Bank of Iran, Seed and Plant Improvement Institute	13
Japan	Department of Genetic Resources I, National Institute of Agrobiological Sciences	3671
	Plant Germplasm Institute, Faculty of Agriculture, Kyoto University	65
Kenya	National Genebank of Kenya, Crop Plant Genetic Resources Centre – Muguga	208
Malawi	Chitedze Agricultural Research Station	01
Mexico	Banco Nacional de Germoplasma Vegetal, Departamento de Fitotecnia, Universidad Autónoma de Chapingo	02

(*Continued*)

Table 7.4 (Continued)

Country	Institute	Accessions
Namibia	National Plant Genetic Resources Centre, National Botanical Research Institute	01
Nepal	Central Plant Breeding and Biotechnology Division, Nepal Agricultural Research Council	02
Oman	Sultan Qaboos University	01
Pakistan	Plant Genetic Resources Program	50
Philippines	International Rice Research Institute	02
Poland	Plant Breeding and Acclimatization Institute	01
Slovakia	Botanical Garden, University of Agriculture	02
South Africa	Grassland Research Centre, Department of Agricultural Development	04
	RSA Plant Genetic Resources Centre	01
Spain	Comunidad de Madrid. Universidad Politécnica de Madrid. Escuela Técnica Superior de Ingenieros Agrónomos. Banco de Germoplasma	08
United Kingdom	Millennium Seed Bank Project, Seed Conservation Department, Royal Botanic Gardens, Kew, Wakehurst Place	44
United States of America	National Plant Material Center USDA/SCS, NPMC	01
	North Central Regional Plant Introduction Station, USDA-ARS, NCRPIS	304
	Total accessions	**8624**

Source: http://apps3.fao.org/wiews/germplasm_report.jsp?

Core collections in crops provide an opportunity to explore the entire variability for different traits at one go. It also helps in the better utilisation of this existing variation for improving the crop agronomically and nutritionally. In proso millet, core collections comprising 50 (Gowda *et al.*, 2009) and 89 (Upadhyaya *et al.*, 2014) genotypes have been developed. These are being widely distributed and used for increasing its utilisation.

Characterisation and evaluation of germplasm gives precise information about each significantly distinct trait. Gupta, Mahajan, Gupta *et al.* (2009) identified an easy dehulling accession (B29) within the germplasm collected from Uttarakhand hills. This accession has recovery of 40% over the national check VL 172 and about 140% over PRJ 1, a variety selected from *E. esculenta* accessions. Few new lines have been identified with abundant pollen production with protruding stigma which allows easy accessibility for emasculation and pollination. These lines (IEC 566 and IEC 566/2) exhibit differences for various characters when compared to cultivated varieties (Nirmalakumari and Vetriventhan, 2009). Halaswamy *et al.* (2001) in characterisation experiment comprising national collection identified several accessions for superior agronomic traits, viz., plant height, basal tillers, early flowering and longer inflorescence. The existing adapted material in major growing areas in India belongs to *E. frumentacea.* When PRJ 1 was selected and introduced for cultivation, it gave higher (45.4%) yield than the existing ruling checks varieties (Upadhyaya *et al.*, 2008).

Lal and Maloo (2006) recorded maximum direct effect of main panicle weight on seed yield followed by plant height and primaries per panicle. Gupta, Mahajan, Kumar

et al. (2009) confirmed that flag leaf width, number of racemes along with internode length are the desirable traits to be looked for while performing selection in segregating generations. Similarly, Mehta *et al.* (2007) found that heat units at maturity (HUM), photo-thermal units at 50% flowering (PTUF), plant height, days to 50% flowering and weight of panicle had high direct effect on grain yield. Joshi (2013) observed considerable variability among the evaluated germplasm for days to maturity (73–90 days), number of productive tillers (2–15), number of leaves on the main tiller (2–18), ear length (9–21 cm), finger length (21–55 mm), number of grains/finger (26–117), grain yield/ear (0.13–18 g) and grain yield/plant (0.35–26 g). Prakash and Vanniarajan (2013), in an experiment over four locations comprising 65 barnyard germplasm of indigenous and exotic origin, observed wide range of variability both at genotypic and phenotypic levels with little influence of environment on the expression of the most of the agronomic traits. High heritability coupled with high genetic advance observed for ear head width, grain weight per ear head, single ear head weight, ear head length and grain yield per plant.

Barnyard millet is grown in India in two different agro-climatic zones – the Himalayan region in the North and the Deccan plateau in South India specifically in Tamil Nadu. In hilly areas with steep slopes and undulating topography where very limited scope remains for crop diversification, the barnyard millet occupies an important place and in the North Western Himalayan region as it is very easy for cultivation, gives voluminous fodder and assured crop harvest (Sood, Khulbe, Arun Kumar *et al.*, 2015). Cultivation of this crop in a substantial area is recorded in the North-eastern states of Arunachal Pradesh and Sikkim (Anonymous, 2010). It is also cultivated in Uttarakhand, Madhya Pradesh, Maharashtra and Tamil Nadu. Although being an important crop for food and nutritional security, very little improvement work has been carried out in barnyard millet. Most of the varieties (Table 7.5) developed and released are selections from local germplasm of *E. frumentacea* and are susceptible to various diseases with low yield levels. As mentioned earlier, exotic introductions of different barnyard species (PRJ 1) has opened new avenues for increasing productivity and resistance levels for various pests and diseases (Yadav *et al.*, 2010). More such efforts are required to further enhance its competence in changing climatic conditions.

7.7 Breeding Objectives

In India, the cultivation of barnyard millet is mainly confined to Tamil Nadu, Andhra Pradesh, Karnataka and Uttarakhand. The yield level of barnyard millet is as high as 10 t/ha in Japan, where as in India it is 1.5–2 t/ha. Hence, there is great scope for exploiting its potential in Indian conditions (Channappagoudar *et al.*, 2008). Yield potential of the popular released barnyard millet variety (PRJ-1) is more than 2500 kg/ha, but the present maximum state average yields are very low, around 1138 kg/ha (maximum state-average yield of Uttarakhand). The crop and variety-wise yield potential and state-average yield reveals a larger yield gap which could be exploited for making these nutritious crops more profitable. Front-line demonstrations (FLDs) conducted over 5 years (2007–2008 to 2012–2013) in major growing states revealed yield gaps of 52 and 27% in Uttarakhand and Tamil Nadu, respectively, in control plots. This suggests wide scope for genetic improvement of this crop in India (Anonymous, 2014).

Table 7.5 Barnyard millet – released varieties at national level in India.

S. No.	Name of variety	Pedigree	Institute where developed	Year	Maturity (days)	Average yield (kg/ha)	Area of adaptation	Special features
1	K-1	A pure-line selection from Tenkasi local	TNAU	1970	90–110	1000	Tamil Nadu	Panicles loose and spear-shaped. Grains dull white in colour
2	Kudiraivali K2 (Kovilpatty-2)	A pure-line selection from a local cultivated type	TNAU	1978	90	2300–3000	Tamil Nadu	—
3	VL Madira-8	Isolated from local collection	VPKAS, Almora	1978	90–120	1800	Uttar Pradesh	Grains light grey, smooth with white endosperm
4	Anurag	Selection from genetic collection of Gorakhpur	ARS	1983	75	1700–2000	Uttar Pradesh	Resistant to pink borer and shoot fly
5	Gujarat banti-1	F-2 is a selection from the segregating material of Banti	AICSIP, GAU, Surat	1984	85–90	2000	Gujarat	Grain colour is yellowish white
6	Rau-3	Pure-line selection	IDRO-minor millets improvement project, RAU, Dholi, Muzaffarpur (Bihar)	1985	80–50	1800	Bihar	Moderately resistant to *Helminthosporium frumentace*
7	VL Madira-21	Local collection from Garhwal region of Uttar Pradesh	VPKAS, Almora	1988	85–100	2500–2600	Central	Very low incidence of smut and leaf spot diseases
8	VL Madira-29	Location collection (vhc 5360-1) from the Kumaon region of Uttar Pradesh	VPKAS, Almora	1988	88	2500	Central except Tamil Nadu	Very low incidence of smut disease
9	Chandan	Selection from genetic collections of Ballia district	—	1989	75–85	1200–1600	Central	Plants remain erect with thick and strong stem synchrony in tillering spike

10	Kanchan	Selection from germplasm	CSAUAT, Kanpur	1993	85–90	1500–1800	Uttar Pradesh	
11	VL Madira 172	EF 2 × VHC 5205	VPKAS, Almora	2000	90–95	2100–2300	Uttar Pradesh, Gujarat and Karnataka	Tolerant to grain smut
12	Sushrutha (RAU 11)	Introduction	RAU, Pusa and UAS, Dharwad	2000	90–95	2000–2200	Karnataka	
13	VL Madira 181	ECC 27 × VL 60	VPKAS, Almora	2001	90–95	1600–1700	Bihar, Karnataka, Madhya Pradesh, Tamil Nadu	
14	PRJ-1	Selection from germplasm accession IEc 542 obtained from ICRISAT, India	GBPUA&T, Uttaranchal	2003	118	2500	Uttarakhand	Resistant to grain smut disease
15	Praptap sanwa-1(ER-64)	Selection from local germplasm of Agro-climatic zone IVa (Udaipur)	MPUA&T, Udaipur, Rajasthan	2004	85–91	1500–1700	Rajasthan	Moderately resistant to the diseases like grain smut and brown spot
16	VL Madira 207	Vl Madira 172 × GECH 506	VPKAS, Almora	2008	85–100	1800–1900	All the states except Gujarat and Tamil Nadu	Tolerant to grain smut
17	Co(KV)2	Pure-line selection from a genetic accession ef 79	TNAU, Coimbatore	2009		2100		
18	Co 1	A selection from the germplasm collection from Palladam area in Coimbatore district	TNAU, Coimbatore	2009	105–110	1600	Tamil Nadu	

7.7.1 Development and Evaluation of Core Collections

Core collections comprising about 10% of the available accessions represent nearly all the available diversity within the germplasm. Core collections comprising 50 (Gowda *et al.*, 2009) and 89 (Upadhyaya *et al.*, 2014) genotypes have been developed in barnyard millet. These core collections can be evaluated in different locations to identify location-specific desirable genotypes and to isolate other trait-specific stable genotypes which can be of great value for the overall genetic improvement of this crop (Table 7.6).

7.7.2 Exploitation of the Wild Relative Gene Pool

Introgression of desirable traits from wild relatives and progenitors can open new avenues for genetic improvement. Inter-specific hybridisation between Indian and Japanese barnyard millets can bring mutual genetic improvement of the two species. There is also need to evaluate the existing variability to identify genetic resources for better agronomic performance, disease resistance and nutritional qualities.

Table 7.6 Trait-specific barnyard millet germplasm identified in the Indian programme.

Traits	Promising genotypes	Reference
Grain smut, head smut, sheath blight	HCBM 1016, HCBM 1018, HCBM 1019, HCBM 1020	NBPGR Annual Report (2012)
Grain smut	TNAU 25, TNAU 63, VL 10, PRJ 1, PRB 903, DHBMV 56-6, DHBMV93-3, RBM 82, RBM 45, RBM 78, RBM 85	NBPGR Annual Report (2012; 2013)
Shoot fly	VL 207, VL 172, TNAU 151, TNAU 155, KOPBM 46	NBPGR Annual Report (2012)
Days to 50% flowering	IEC 336, IEC 343, IEC 344, IEC 330, IEC 217, JEC 340 and JEC 338, IC257799	NBPGR Annual Report (1986; 1987)
Days to maturity	IEC I57, IEC 159, lEC 71, IEC 78, lEC 257, IEC 271, IEC 158, IEC 156, IEC 282, IC426595, IC436926, IC426594, IC257799	NBPGR Annual Report (1986; 1987)
Basal tillers	IC257799, IC24848, VL 29, IC52701, IC338896	NBPGR Annual Report (2011–2012)
Length of inflorescence	IC426595, IC97034, VL 29, IC97031	NBPGR Annual Report (2011)
Width of inflorescence	IC426594	NBPGR Annual Report (2011)
1000-seed weight	IC326725, KL I	NBPGR Annual Report (2011)
Yield per plant	IC97034 , VL 29 IC338960, IC97031	NBPGR Annual Report (2011)
Ear head length	IC548696, IC548635, IC548697	NBPGR Annual Report (2011)
Plant height	IC548681, IC548696, IC548658	NBPGR Annual Report (2011)
100-seed weight	IC548641, IC538089, IC548697	NBPGR Annual Report (2011)

7.7.3 Breeding for Waxy Endosperm Genotypes

Recently, demand for barnyard millet has increased due to its nutritious grains with high levels of anti-oxidative compounds. Most of the released cultivars are non-waxy (non-glutinous), which give a poor texture to the food products. In Asian countries, including India and Japan, a glutinous texture as in rice is preferred, and so incorporating the waxy trait into the elite cultivars, thereby imparting the glutinous texture to the food preparations, would be highly beneficial to making barnyard millet popular. Fully waxy stable mutant lines have been developed using γ-irradiation treatment to low amylase land race 'Nogehie' (Hoshino *et al.*, 2010).

7.7.4 Breeding for Pests and Diseases

Grain smut is the most important disease in barnyard millet. It is caused by *Ustilago panici-frumentacei* Brefeld fungus. Head smut is caused by *Ustilago crus-galli* Tracy and Earle (Nagaraja *et al.*, 2007). Phenotypic screening is the most important method to identify the sources for resistance. Two accessions of barnyard millet from species *E. esculenta*, PRB 9402 and PRB 9602 were observed to be immune for the grain smut (AICSMIP, 2001). Pink stem borer (*Sesamia inferens*) and shoot fly (*Atherigona falcata*) are the major pests damaging this crop. The accessions identified can be used to develop cultivars with increased resistance levels.

7.7.5 Breeding for Dual-Purpose Genotypes (Grain and Stover)

Barnyard millet stover is as important as the grain. It is considered superior to rice and oat straws because of the high protein and calcium contents (Yabuno, 1987). While breeding for increasing grain yield, there is need to look for the high straw yield as well. Thus, the genotypic selection of barnyard millet could be practised on the basis of its performance on both grain and fodder yield while, selection of genotypes on the basis of grain yield alone might not be suitable for the promotion of dual-purpose cultivars at higher elevation of hills as in this region fodder has great value. In Uttarakhand, barnyard millet contributes 11.5% of the total fodder consumption in the state (Singh and Singh, 2005).

7.7.6 Breeding for Genotypes Suitable for Mechanical Harvesting and Post-Harvest Processing

Breeding for optimum plant type is required to develop genotypes for mechanical harvesting. Genotypes with plant height of about 120–130 cm could also minimise the problem of lodging and will give required strength to the culm (Sood, Khulbe, Gupta *et al.*, 2015). The reduction in the fodder yield due to reduced height can be compensated by increasing the number of basal tillers. Breeding genotypes for easy dehulling is much needed to reduce the drudgery involved in the post-harvest processing. An easy dehulling genotype 'B29' was selected from the diverse germplasm available at Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora (VPKAS), in Uttarakhand, India. It has recorded advantage in reducing the total processing time (Gupta *et al.*, 2010; 2015). This characteristic is mainly contributed by its extended lemma over the kernel, which exerts pressure and gets split easily with impact of force when processed in the dehulling machine '*Vivek* Thresher 1'. It significantly recorded faster dehulling (42 and 146.4%) when compared to the processing of two other promising varieties VL *Madhira* 172 and PRJ1.

7.8 Future Prospects

Barnyard millet is gaining recognition as a health food due to its high protein, minerals and fibre content. This makes it suitable for the preparation of commercial foods, especially for diabetic patients, patients with gluten intolerance, infants and pregnant women. Despite this, the pace of the genetic improvement in this crop is very low. There are several reasons which hinder the breeding programmes. Presently, the genetic base in this crop is very narrow specifically for characters (disease, pest resistance, seed size, etc.) due to its autogamous nature. The genetic base can be effectively broadened with the use of its wild ancestors. The desired genes from these species can be introgressed in to the released high-yielding cultivars. Molecular markers can make it easier and help in accelerating the pace. As of now, the two cultivated species, Indian and Japanese barnyard millets, showed some reproductive barriers to give viable hybrids. If this can be made possible by using various biotechnological tools such as embryo rescue and protoplast fusion, then this would provide new avenues for the mutual improvement of these two species. Technology development and its dissemination are of immense importance as this crop is mainly cultivated on marginal lands with minimum inputs. Major interventions are required to minimise drudgery associated with the harvesting and processing of this crop. Barnyard millet fits very well in cropping systems, especially in the hilly regions where it is highly valued for its grain as well as fodder. The early-maturity duration and its climate-resilient attributes give it an added advantage for sustaining the agriculture production and livelihood of the farmers in these areas.

References

AICSMIP (2001) Annual Report 2000–2001, in *All India Coordinated Small Millet Improvement Project (ICAR)*, Bengaluru, India, p. 6.

Anonymous (2010) *Status Paper on Millets*, Directorate of Millets Development, Department of Agriculture and Cooperation, Ministry of Agriculture, Government of India.

Anonymous (2014) *Status Paper on Coarse Cereals*, Directorate of Millets Development, Department of Agriculture and Cooperation, Ministry of Agriculture, Government of India.

Aoki, D. and Yamaguchi, H. (2008) Genetic relationship between *Echinochloa crus-galli* and *Echinochloa oryzicola* accessions inferred from internal transcribed spacer and chloroplast DNA sequences. *Weed Biology and Management*, **8**, 233–242.

Channappagoudar, B.B., Hiremath, S.M., Biradar, N.R. *et al.* (2008) Influence of morpho-physiological and biochemical traits on the productivity of barnyard millet. *Karnataka Journal of Agricultural Sciences*, **20** (3), 477–480.

De Wet, J.M.J., Rao, K.E.P., Mangesha, M.H. and Brink, D.E. (1983) Domestication of sawa millet *Echinochloa colona*). *Economic Botany*, **37**, 283–291.

Doggett, H. (1989) Small millets – a selective overview, in *Small Millets in Global Agriculture* (eds A. Seetharam, K.W. Riley and G. Harinarayana), Oxford & IBH, New Delhi, pp. 3–18.

Gowda, J., Bharathi, S., Somu, G. *et al.* (2009) Formation of core set in barnyard millet [*Echinochloa frumentacea* S. (Roxb.) Link] germplasm using data on twenty four morpho-agronomic traits. *International Journal of Plant Science*, **4**, 1–5.

Gupta, A., Mahajan, V. and Gupta, H.S. (2010) Genetic resources and varietal improvement of small millets for Indian Himalaya, in *Biodiversity Potentials of the Himalaya* (eds L.M. Tewari, Y.P.S. Pangtey and G. Tewari), Gyanodaya Prakashan, Nainital, India, pp. 305–316.

Gupta, A., Mahajan, V., Gupta, H.S. *et al.* (2009) Kagazi madira (B 29) (IC568707; INGR09023), a Barnyard millet (*Echinochloa frumentacea*) germplasm, easy de-hulling type. *Indian Journal of Plant Genetic Resources*, **22**, 281–317.

Gupta, A., Mahajan, V., Kumar, M. and Gupta, H.S. (2009) Biodiversity in the barnyard millet (*Echinochloa frumentacea* Link, Poaceae) germplasm in India. *Genetic Resources and Crop Evolution*, **56**, 883–889.

Gupta, A., Sood, S., Agrawal, P.K. and Bhatt, J.C. (2015) B 29: An easy dehulling barnyard millet (*Echinochloa frumentacea* Link) genotype. *National Academy Science Letters*, **38** (1), 21–24.

Halaswamy, B.H., Srinivas, G.V., Ramakrishna, B.M. *et al.* (2001) Characterization and preliminary evaluation of national collections of Barnyard millet (*Echinochloa spp*.) germplasm. *Indian Journal of Plant Genetic Resources*, **14**, 213–216.

Hoshino, T., Nakamura, T., Seimiya, Y. *et al.* (2010) Production of a full waxy line and analysis of waxy genes in the allohexaploid crop, Japanese barnyard millet. *Plant Breeding*, **129**, 349–355.

Jayaraman, N., Suresh, S., Nirmala, A. and Ganeshan, N. M. (1997) Genetic enhancement and breeding strategies in small millets. In *National Seminar on Small Millets*, April 23–24, Coimbatore, India, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India, pp. 19–21 (Extended summaries).

Joel, J.A., Raveedran, T.S., Vanniarajan, C. and Gopalan, A. (2006) *Fundamentals of Crop Botany.* Directorate of open and distance learning, Tamil Nadu Agricultural University (TNAU), Coimbatore. ISBN 81-902081-9-5

Joshi, V. (2013) Assessment of genetic variability and identification of genotypes for different traits in barnyard millet (*Echinochola spp*.). *International Journal of Agriculture and Food Science Technology*, **4** (2), 65–67.

Kumar, J., Kumar, B. and Yadav, V.K. (2007) *Small Millets Research at GB Pant University*, G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, India, pp. 3–17.

Lal, M. and Maloo, S.R. (2006) Path coefficient analysis for seed yield in barnyard millet (*Echnichloa frumentacea* (roxb.) link). *Agriculture Science Digest*, **26** (2), 151–152.

Maun, M.A. and Barrett, S.C. (1986) The biology of Canadian weeds. 77. *Echinochloa crus- galli* (L.) Beauv. *Canadian Journal of Plant Sciences*, **66**, 739–759.

Mehta, H., Tyagi, P.C. and Mohapatra, K.P. (2007) Genetic analysis of morpho-physiological and yield component traits in barnyard millet (I). *Crop Improvement*, **34** (1), 82–85.

Mitich, L.W. (1990) Intriguing world of weeds. Barnyard grass. *Weed Technology*, **4**, 918–920.

Nagaraja, A., Kumar, J., Jain, A.K. *et al.* (2007) *Compendium of Small Millets Diseases, All India Coordinated Small Millets Improvement Project*, GKVK, Bangalore, p. 80.

Napper, D.M. (1965) *Grasses of Tanganyaika: With Keys for Identification, Bulletin 18, Ministry of Agriculture Forest and*, Widlife, Tanzania, p. 146.

NBPGR (1986) National Bureau of Plant Genetic Resources, India. *Annual Report*, **1986**, 132.

NBPGR (1987) National Bureau of Plant Genetic Resources, India. *Annual Report*, **1987**, 82.
NBPGR (2011) National Bureau of Plant Genetic Resources, India. *Annual Report*, 2011–2012.
NBPGR (2012) National Bureau of Plant Genetic Resources. *India. Annual Report*, 2012–2013.
NBPGR (2013) National Bureau of Plant Genetic Resources, India. *Annual Report*, 2013–2014.
Nirmalakumari, A. and Vetriventhan, M. (2009) Phenotypic analysis of anther and pollen in diversified genotype of barnyard millet (*Echinochloa frumentacea*) floral characters. *ICFAI Univ. Journal of Genetic and Evolution*, **2**, 12–16.
Potvin, C. (1986) Biomass allocation and phenological differences among southern and northern populations of the C4 grass *Echinochloa crusgalli*. *Journal of Ecology*, **74**, 915–923.
Potvin, C. (1991) Temperature-induced variation in reproductive success: field and control experiments with the C4 grass *Echinochloa crus-galli*. *Canadian Journal of Botany*, **69**, 1577–1582.
Prakash, R. and Vanniarajan, C. (2013) Genetic variability for panicle characters in indigenous and exotic barnyard millet (*Echinochloa frumentacea* [Roxb.] Link) germplasm over environment. *Vegetos*, **26** (2), 297–306.
Singh, H.S. and Singh, K. (2005) Status and needs of pasture and fodder management in Uttaranchal, in *Road Map for Pasture and Fodder Development in NWHR for Livestock Sustenance* (eds J.K. Bisht and A.K. Srivastava), Vivekananda Parvatiya Krishi Anusandhan Sansthan (Indian Council of Agriculture Research), Almora, Uttarakhand, India, pp. 39–64.
Sood, S., Khulbe, R.K., Arun Kumar, R. *et al.* (2015) Barnyard millet global core collection evaluation in the submontane Himalayan region of India using multivariate analysis. *The Crop Journal*, **3** (6), 517–525.
Sood, S., Khulbe, R.K., Gupta, A.K. *et al.* (2015) Barnyard millet – a potential food and feed crop of future. *Plant Breeding*, **134**, 135–147.
Sundararaj, D.P. and Thulasidas, G. (1976) *Botany of Field Crops*, Macmillan Publisher, India, p. 509.
Upadhyaya, H.D., Dwivedi, S.L., Singh, S.K. *et al.* (2014) Forming core collections in barnyard, kodo, and little millets using morphoagronomic descriptors. *Crop Science*, **54**, 2673–2682.
Upadhyaya, H.D., Gowda, C.L.L. and Sastry, D.V.S.S.R. (2008) Plant genetic resources management: collection, characterization, conservation and utilization. *Journal of SAT Agricultural Research*, **6**, 1–15.
Yabuno, T. (1962) Cytotaxonomic studies on the two cultivated species and the wild relatives in the genus Echinochloa. *Cytologia*, **27**, 296–305.
Yabuno, T. (1966) Biosystematic study of the genus Echinochloa. *Journal of Japanese Botany*, **19**, 277–323.
Yabuno, T. (1984) A biosystematic study on *Echinochloa oryzoides* (Ard.) Fritsch. *Cytologia*, **49**, 673–678.
Yabuno, T. (1987) Japanese barnyard millet (*Echinochloa utilis*, Poaceae) in Japan. *Economic Botany*, **41**, 484–493.
Yadav, V.K., Kumar, B., Yadav, R. *et al.* (2010) *All India Coordinated Small Millet Improvement Project*, Ranichauri, GB Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, India, p. 79.

8

Kodo Millet, *Paspalum scrobiculatum* L.

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8.1 Introduction

Kodo millet is one of the hardiest crops among the small millets, and it is grown primarily in India. It is common in upland rice regions in India, Indonesia, Philippines, Thailand and Vietnam, and present in Bangladesh and Myanmar (Galinato *et al.*, 1999). It is harvested as a wild annual cereal grain in West Africa and India. It is grown as a minor food crop in most of these areas, with the exception of the Deccan plateau in India, where it is grown as a major food source. It is known by different names around the world, as Scrobic, kodo millet, koda millet, kodra, mijo koda, ditch millet, creeping paspalum, Indian paspalum, water couch, herbe à épée, ricegrass, etc. (Heuzé *et al.*, 2012). It is grown as a single crop or as the major cereal in mixed cultures. The seeds are ground into flour/meal and used to make puddings (Quattrocchi, 2006; Heuzé *et al.*, 2012). The crop possesses a number of valuable characteristics such as more herbage, branched inflorescence, more number of seeds per spike, high fertility and unique storage ability (Yadava and Jain, 2006). Kodo millet is also grown in the hot arid regions of Asia, New Zealand and United States as a pasture crop.

Kodo millet is a self-pollinating grass belonging to the family *Poaceae* and sub-family *Panicoideae*. It grows wild as a perennial in the west of Africa, where it is consumed as a famine food (FAO and ICRISAT, 1996; NRC, 1996). Often it grows as a weed in rice fields, and farmers do not weed it out as it can be harvested as an alternative crop if their primary crop fails. In the Southern United States and Hawaii, it is considered to be a noxious weed. Kodo millet varies considerably: light red grains are said to be sweet tasting and dark grey ones to be bitter (Galinato *et al.*, 1999). It is a very hardy crop, drought tolerant and can survive on marginal soils where other crops may not survive, and can yield 450–900 kg/ha (Stephen and Eisendrath, 1986; Heuzé *et al.*, 2012). The crop matures in 3–4 months, with the average yield varying from 250 to 1000 kg/ha (Hulse *et al.*, 1980), and a potential yield of 2000 kg/ha (Harinarayana, 1989). Kodo millet prefers full light for optimal growth, but can tolerate some partial shading (Heuzé *et al.*, 2012).

In the Indian sub-continent and on Socotra (Miller and Morris, 2004) it is used as secondary cereal. In India, kodo millet is widespread in the states of Madhya Pradesh, Uttar Pradesh, Chhattisgarh, Tamil Nadu, Gujarat, Maharashtra, Karnataka and various other parts, and is grown in about 2.44 lakh ha (2005–2006) in south, west, central and

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north of the country, producing about 0.73 lakh tonnes, with a productivity of about 312 kg/ha. Madhya Pradesh (0.50 lakh t) and Chhattisgarh (0.17 lakh t) account for nearly 80% area under this crop, and other important states are Tamil Nadu (0.12 lakh t), Maharashtra (0.08 lakh t), Uttar Pradesh (0.07 lakh t) and Gujarat (based on mean production during 2001–2006). The production potential under marginal, low-fertility soils and under chronic moisture deficiency is responsible for its existence and survival in many parts of the country in spite of the modernisation in agricultural system (Yadava and Jain, 2006). The productivity is the highest in Tamil Nadu followed by Uttar Pradesh, whereas it is the lowest in Andhra Pradesh followed by Karnataka and Madhya Pradesh (Yadava and Jain, 2006). Its cultivation is mostly confined to the tribal areas and it is grown under poor environment. It is also used as fodder and forage for livestock. The leaves are antiseptic, and it is used externally as paste on cutaneous afflictions. On the basis of ethno-botanical records, this species is also used for carbuncle, diabetes, intoxication, narcotics, ophthalmia, parturition and sores (Knees and Gupta, 2013). Kodo millet grains possess excellent storage properties and can be stored for several years without pest damage even under ordinary storage conditions. Because of this reason, kodo millet is known as the famine grain in many parts of the country (Yadava and Jain, 2006).

Kodo millet is a balanced and staple food grain of tribal and poor populations, and is the main source of protein and minerals in the daily diets of these people living in remote rural areas (Ahmad and Yadava, 1996). It contains a high proportion of complex carbohydrate and dietary fibre which helps in the prevention of constipation and for the slow release of glucose to the blood stream. Kodo millet contains water-soluble fibre, and this property may be utilised for maintaining or lowering blood glucose response among diabetic and cardiovascular disease patients (Yadav *et al.*, 2013). The grain varies in colour from light red to dark grey and is enclosed in a tough husk that is difficult to remove. The seed coat is multiple layered. Kodo millet has high protein, low fat and very high fibre content. The nutritional value of the protein has been found to be slightly better than that of foxtail millet but comparable to that of other small millets. It is however deficient in the amino acid tryptophan. It is also reasonably low in fat with high fibre content. Due to high antioxidant content, it is beneficial in protecting against oxidative stress and maintaining glucose levels in type-2 diabetes (Taylor, 2004). As with other food grains, the nutritive value of kodo millet protein could be improved by supplementation with legume protein.

In India, a lot of breakfast food and snacks made out of kodo millet are available. In Africa, it is cooked as rice. It is also a good choice for fodder for cattle, goats, pigs, sheep and poultry. The grains are larger than foxtail and little millet grains. When cooked as rice, the grains keep their shape and can be used to make 'lime rice', 'coconut rice' or any other such dish where the grain integrity is to be maintained. Kodo millet is very easy to digest; it contains a high amount of lecithin and is excellent for strengthening the nervous system. Kodo millets are rich in B vitamins, especially niacin, B6 and folic acid, as well as the minerals such as calcium, iron, potassium, magnesium and zinc (Table 8.1). Kodo millet contains no gluten and is good for people who are gluten-intolerant. Regular consumption of kodo millet is very beneficial for post-menopausal women suffering from signs of cardiovascular disease, such as high blood pressure and high cholesterol levels (Malathi *et al.*, 2012). Kodo millet has the highest total phenolic content for whole grain and hulls among the different types of millets (Chandrasekara *et al.*, 2012). It has been reported that the 1,1-diphenyl-2-picrylhydrazyl (DPPH) radical scavenging activity was also high in kodo millet hulls compared to whole or dehulled or cooked grains vs. other millets. The roasting or boiling of kodo millet reduces the free

Table 8.1 Nutritive value of kodo millet vs. rice and wheat (per 100 g).

Item	Kodo millet	Wheat (whole)	Rice (raw, milled)
Carbohydrates (g)	65.9	71.2	78.2
Protein (g)	8.3	11.8	6.8
Fat (g)	1.4	1.5	0.5
Energy (KCal)	309	346	345
Crude fibre (g)	9	1.2	0.2
Mineral matter (g)	2.6	1.5	0.6
Amylose (%)	24	25	12–19
Amylopectin (%)	76	75	88–81
Ca (mg)	27	41	10
P (mg)	188	306	160
Vitamins (mg/100 g)			
Thiamin	0.15	0.41	0.41
Niacin	2.0	5.1	4.3
Riboflavin	0.09	0.1	0.04
Folic acid	23.1	36.6	8.0
Micronutrients (mg/100 g)			
Fe	0.5	5.3	0.7
Zn	0.7	2.7	1.4
Mg	147	138	90
Na	4.6	17.1	—
K	144	284	—
Cu	1.6	0.68	0.14
Mn	1.1	2.29	0.59
Cr	0.02	0.012	0.004
S	136	128	—
Cl	11	47	—

Source: Nutritive value of Indian foods (2007), National Institute of Nutrition, India.

radical quenching activity (Hegde and Chandra, 2005), thereby resulting in a reduction in anti-oxidant activity. Insoluble bound fraction phenolic compounds of kodo millet showed the highest phenolic content as well as anti-oxidant activity in the *in vitro* test systems (Chandrasekara and Shahidi, 2011).

8.2 Origin and Taxonomy

8.2.1 Origin and Distribution

Kodo millet is indigenous to Indian subcontinent and known to be in cultivation since time immemorial, and is mentioned in *Brihad Sanhita*. The tolerance of kodo millet to

drought stress is known since ancient past. It has originated in tropical Africa, and was first introduced and domesticated in India (Malleshi and Hadimani, 1994). The crop is believed to be domesticated in southern Rajasthan and Maharashtra states of India some 3000 years ago (Kajale, 1977; Vishnu-Mittre, 1977). The greater diversity in *Paspalum* species is found in Indian (Hindustan) centre, which is also supposed to be the centre of origin according to some researchers. Being indigenous to India, the crop is widely distributed in damp or humid habitats of tropics and subtropics across the Old World. Kodo millet was introduced to Australia from Zimbabwe in 1931 (FAO, 2010). It is commonly found on disturbed sites or as a weed in cropping land (Galinato *et al.*, 1999). It is found from sea level up to 1500 m above mean sea level altitude. It has no particular climatic preference provided that the average day temperatures are comprised between 25 and 27 °C and no frost occurs. Regions where annual rainfall ranges from 800 to 1600 mm and soil remains wet throughout the season, the crop comes up well. It is well adapted to waterlogged or flooded soils. Kodo millet thrives in cultivated fields, pastures and marshes, and along roadsides, dikes, bunds and canals and can sustain drier conditions. Wild kodo millet has only limited drought tolerance as it has relatively shallow roots (Galinato *et al.*, 1999; Ecoport, 2010; FAO, 2010).

Kodo millet occurs throughout the Old World tropics (Clayton, 1975). It is variable but lacks racial differentiation (de Wet *et al.*, 1983). Hybridisation with wild *P. scrobiculatum* obscures racial differentiation. Weedy kodo millet often invades kodo millet fields and hybridises with it making it difficult to distinguish wild and cultivated complexes in the field, and is harvested with the crop (de Wet *et al.*, 1983). The wild form is common across tropical Africa (as well as across wetter parts of the Asian tropics from Indonesia to Japan). In West Africa, it is a weed of rice and is harvested as a wild cereal. It is often abundant along paths, ditches, and low spots. Kodo millet prefers very fertile and very clayey soils, and responds well to fertilisation (Baki and Ipor, 1992; Galinato *et al.*, 1999) but also tolerates poor soil fertility. It prefers full sunlight but, as it can tolerate and flourish with only 30–50% sunlight, it is found in young plantations or orchards (Baki and Ipor, 1992). As *Paspalum* is an aggressive coloniser of disturbed areas and commonly invades agricultural fields, it is considered as a noxious weed in the United States and is potentially invasive in the Pacific (Baki and Ipor, 1992; Galinato *et al.*, 1999; GISD, 2010; USDA, 2010).

8.2.2 Taxonomy

The genus *Paspalum* includes about 350 species, widely distributed in the tropics and subtropics of both the hemispheres (Irene *et al.*, 1968). Among these, *Paspalum scrobiculatum* L., *P. notatum* Fluegge, *P. conjugatum* Bergius, *P. compactum* Roth and *P. dilatatum* Poir. are in cultivation, as grain or fodder crop. The wild progenitor of *Paspalum* species is *P. sanguinale* Lamk. As early as 1772–1786, the four species of *Paspalum*, namely *P. compactum*, *P. conjugatum*, *P. orbiculare* Forster. and *P. scrobiculatum*, were reported from Hassan district of Karnataka (Saldanha and Nicolson, 1978). There are two forms of *Paspalum*: kodo millet, *P. scrobiculatum* var. *scrobiculatum*, grown in India as an important annual crop. It is grown as a single crop or as the major cereal in mixed cultures. Wild *Paspalum*, *P.* scr*obiculatum* var. *commersonii*, is the wild variety indigenous to Africa, perennial and mostly found in damp places (Heuzé *et al.*, 2012). It is used for pasture and hay or as stand-over. It is also sometimes used for compost or mulch (Baki and Ipor, 1992; Galinato *et al.*, 1999; FAO, 2010). It withstands

moderate grazing and requires rest periods to permit sufficient seeding for regeneration. Wild *Paspalum* yields 3–10 t/ha dry matter forage (Ecocrop, 2010; FAO, 2010).

The species is recognised, as demonstrated by Clayton (1975), to include the African *P. orbiculare* Forst. f., *P. polystachyum* R. Br. and *P. cartilagineum* Presl, with usually smaller spikelets (1.8–2.5 mm long) than those of Indian wild specimens (2.5–3.5 mm). These taxa merge completely not only spikelet morphology, but also in overall inflorescence morphology and vegetative traits (de Wet *et al.*, 1983). Cultivated plants are grown as annuals, but many cultivars root at the lower nodes and under favourable conditions continue to produce culms after the older shoots have flowered and matured. Wild *P. scrobiculatum* is perennial.

Three races of *P. scrobiculatum*, viz., *regularis*, *irregularis* and *variabilis*, have been recognised based on the arrangement of spikelets on the rachis (Prasad Rao *et al.*, 1993). The kodo millet is characterised by racemes with the spikelets arranged in two rows on one side of flattened rachis in the race *regularis*. The plant with spikelets arranged along the rachis in two to four irregular rows forms the race *irregularis*. In some of the kodo plants, the lower part of each raceme possesses irregularly arranged spikelets, while the upper part has two regular rows of spikelet arrangement on the rachis. These plants are known as *variabilis* race.

8.2.3 Chromosome Number

Kodo millet is predominantly a self-pollinated plant having chromosome number $2n = 4x = 40$. The chromosome number varies from $2n = 20$ to $2n = 60$ in genus *Paspalum* (Bashaw and Forbes, 1958). The chromosome number in knot grass (*P. gigantium*) is reported to be $2n = 120$ (Chandrasekharan and Parthasarathy, 1975). The chromosome numbers of some *Paspalum* species are given in Table 8.2.

Table 8.2 Chromosome numbers of *Paspalum* species.

Species	Chromosome no. (2n)	Common name
P. commersonii	40	—
P. conjugatum	40	Sour grass
P. dilatatum	40, 50	Dallis grass
P. distichum	40, 48, 60	Water couch grass
P. gigantium	120	Knot grass
P. lanceolatum	40	—
P. longifolium	40	—
P. muchlenbergii	18, 20, 22	—
P. notatum	20, 40	Bahia grass
P. quandreferium	20, 30, 60	—
P. scrobiculatum	40	Kodo millet
P. setaceum	40	—
P. virgatum	40, 80	—

Source: Chandrasekharan and Parthasarathy (1975); adopted from Yadava and Jain (2006).

8.3 Germplasm Resources and Utilisation

Genetic resources are the basic building blocks for genetic improvement in any crop, and conservation of the germplasm is of paramount importance. About 5457 accessions of kodo millet have been conserved in main *ex situ* genebanks around the world (Padulosi *et al.*, 2009). At the Consultative Group for International Agricultural Research (CGIAR) genebanks, around 2418 accessions have been conserved, while at International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), 656 accessions of kodo millet have been conserved. At the Svalbard genebank in Norway, 654 accessions have been conserved. The US Department of Agriculture has 336 accessions in their National Plant Germplasm System (GRIN) (Table 8.3). While the seed of African origin does exist in some of these sources, it is rare. Better coverage and ecological exploration of the African continent is required to reveal and preserve the diversity of valuable traits in kodo millet (Goron and Raizada, 2015).

Realising the importance of genetic resources in kodo millet improvement, the first attempt to collect the available germplasm in India was made in 1961 under the PL 480 project on storage, maintenance and distribution of millet germplasm (Yadava and Jain, 2006). A total of 584 germplasm of kodo millet were collected in this programme. After that attempts were made to collect the range of gene pool of kodo millet including landraces and improved varieties from different parts of the country. As a result, at the National Genebank at National Bureau of Plant Genetic Resources (NBPGR), New Delhi, a total of 2273 accessions, including three exotic accessions, have been conserved and the catalogue on characterisations has been published (Umesh Chandra *et al.*, 1987). At the University of Agricultural Sciences (UAS), Bangalore, India, National Active Germplasm Site (NAGS) was established for small millets in 1992. Presently, a total of 1537 accessions of kodo millet, comprising landraces from eight Indian states and the United States, are being conserved at UAS, Bangalore. Of these, catalogue on evaluation of 1038 accessions for 16 and 11 qualitative and quantitative descriptors, respectively, has been published. At the Tamil Nadu Agricultural University

Table 8.3 Status of some of the significant kodo millet germplasm collections.

Organisation	Location	No. of accessions	Resource
National Bureau of Plant Genetic Resources (NBPGR)	New Delhi, India	2273	Umesh Chandra *et al.* (1987) http://www.nbpgr.ernet.in/
Project Coordinating Unit, AICSMIP	Bangalore, India	1537	http://www.smallmillets.res.in/
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)	Patancheru, India	656	Upadhyaya *et al.* (2014) http://www.icrisat.org/what-we-do/crops/kodomillet/Kodo_millet_Core_Collection.htm
Plant Genetic Resources Conservation Unit (PGRCU) of the USDA-ARS	Griffin, United States	336	http://www.ars-grin.gov/npgs/index.html
Tamil Nadu Agricultural University (TNAU)	Coimbatore, India	427	www.tnau.ac.in/

(TNAU), Coimbatore, India, 427 accessions of kodo millet have been conserved. Some of the promising germplasm accessions and elite sources of kodo millet are given in Table 8.4. These genotypes can be utilised in breeding programmes aimed at the development of new genetic variants and recombinants for selection for the target traits. The rate and accumulation of spontaneous mutants and slow release of hidden genetic variability through natural cross-pollination, recombination and segregation regulated by cytological homeostasis is major source of variation in kodo millet (Navale *et al.*, 1984). Therefore, all possible efforts should be made for collection, evaluation and cataloguing of these germplasms.

A core collection of the available germplasm at ICRISAT genebank has been developed recently (Upadhyaya *et al.*, 2014). The core subset of 75 accessions was selected

Table 8.4 Promising germplasm accessions and other genetic resources of kodo millet.

Trait	Promising accessions	References
High grain yield	IPs 149, IPs 147-1	—
Wider adaptability and yield stability	JK 41, JK 62, IPs 147-1	Mishra *et al.* (1987); Tickle and Yadava (1992)
	KMV 20, JNK 364	Yadava (1993); Rao and Srivastava (1997)
	KK 1, KMV 20, GPUK 3	Yadava *et al.* (1996); Singh *et al.* (1997)
Drought and salinity tolerance	IPs 583	Prasanthi Kumari and Vishnuvardhan (2013; 2014)
Early maturity	JK 76	Tickle and Yadava (1992)
Protogynous flowering	KM 32	Yadava (1997)
Protein stability	IPs 112, IPs 147, IPs 147-1	Koutu (1989)
	IPs 147, IPs 200, IPs 198, IPs 112, IPs 66, IPs 138, IPs 115	Koutu *et al.* (1993)
Carbohydrate stability	IPs 199, IPs 149, IPs 88, IPs 63, IPs 161, IPs 76	Koutu *et al.* (1993)
Tolerant to head smut	JK 41, JK 62, JNK 117, KMV 8, RPS 136-1	Verma (1989); Yadava (1993)
	GPLM 717, GPLM 779, GPLM 786	Jain *et al.* (1993)
	GPLM 78, GPLM 96, GPLM 176, GPLM 322, GPLM 364, GPLM 621, GPLM 641, GPLM 679, GPLM 720	Jain (2005)
	DPS 34, DPS 77, DPS 159, RPS 136-1, KMV 20	Jain (1995)
	KOPKM 1, KOPKM 10, RPS 973	—
Tolerant to shoot fly	IPs 6, IPs 32, IPs 110, IPs 131, IPs 142, IPs 178, RPS 40-1, RPS 40-2, RPS 62-3, RPS 72-2, RPS 120-1, Keharpur	Murthy and Harinarayana (1989)
	IPs 147-1, JK 41, RPS 140-1, RPS 136-1	Singh *et al.* (1990)
Other promising accessions	IPs 199, IPs 270, IPs 681, IPs 3417, IPs 669, IPs 585, IPs 79, IPs 346, IPs 570, IPs 325, IPs 135, IPs 663, IPs 679	Gautam *et al.* (2000)

from 53 distinct clusters. This core subset represents ~11% of the 656 kodo millet germplasm collection maintained at ICRISAT. In the core collection, 48 accessions are from *regularis*, 12 are from *irregularis* and 15 are from *variabilis* races. The differences between means of the core collection and the entire collection were not significant for any of the 12 quantitative traits, while the variances were also homogeneous. Comparison of statistical parameters apart from means and variances of quantitative traits, such as frequency distribution of qualitative traits, the species and racial diversity, the Shannon–Weaver diversity index and the similarity in correlation coefficients for quantitative traits in the entire collection and the core collection, indicated that genetic variation has been adequately preserved in the core collection. The core collection can be evaluated further to identify trait-specific diverse germplasm for genetic improvement.

8.5 Genetics and Cytogenetics

8.5.1 Genetic Studies

Information on the inheritance of important agronomic traits of kodo millet, including susceptibility to major diseases and insect pests, is limited. Some of the limited previous work has focused on estimating broad-sense heritability and genetic gains, with little attention directed to measuring levels of heterosis or to assessing the relative importance of different types of gene action because of difficulty in crossing. Some of the previous reports dealt with estimation of genetic variability, stability, correlation and path coefficient analysis, and selection indices (Yadava and Jain, 2006).

8.5.2 Genetic Diversity

Both multivariate analysis based on Mahalanobis D^2 statistics and non-hierarchical Euclidean cluster analysis for unreplicated data of huge germplasm have been used for quantification of genetically diverse germplasm in kodo millet. Dhagat (1978), who studied the genetic diversity among six exotic and 90 indigenous germplasm of kodo millet, observed no relation among genetic and geographic diversity. He also observed that vegetative characters such as days to 50% flowering and maturity, plant height and straw yield were the important factors in differentiation among the germplasm from different geographical regions. The relationship between geographic and genetic diversity was not evident in another study of 100 genotypes through D^2 analysis (Parihar, 1985). Among the quantitative traits, percentage contribution towards genetic divergence was maximum by plant height followed by tillers/plant, flag leaf length, peduncle length and ear length. The least contribution towards divergence was observed for harvest index.

8.5.3 Genetic Variability

Estimation of genetic parameters in the context of trait characterisation is an essential component for targeted trait-based crop improvement. Janoria (1963) was the first to study the variability in different cultures of kodo millet collected from Madhya Pradesh and classified them on the basis of leaf colour, spike structure and density along with grain yield. Amawate (1965), Satpute (1966), Tiwari and Janoria (1967), Amawate and Dabral (1970), Choudhary and Singh (1970) and Rao (1991) also observed a wide range of variability for morphological characters and grain yield in landraces of Madhya Pradesh.

Verma and Satpute (1969) and Ahluwalia *et al.* (1970) also recorded high heritable variability for days to flowering, ears/plant and tillers/plant in kodo millet. Dhagat *et al.* (1971), Dhagat (1978), Parihar (1985), Sharma (1988), Rao and Tiwari (1988), Yasin *et al.* (1988) and Kandaswamy *et al.* (1990) found maximum heritable variation for tillers/plant, ears/plant, ear weight, grains/ear, fodder yield and grain yield. Low amount of heritable variation was observed for plant height, days to ear emergence, days to flowering and period from flowering to maturity. High genotypic variance, phenotypic variance, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for dry fodder yield, plant height and grain yield per plant in a study of 188 accessions of kodo millet at TNAU, Coimbatore. Broad-sense heritability ranged from 97% for dry fodder yield to 57% for number of tillers. The highest genetic advance as percentage of mean was recorded by dry-fodder yield followed by grain yield per plant and plant height. High heritability coupled with high genetic advance observed for grain and dry-fodder yield indicates the influence of additive gene action (Subramanian *et al.*, 2010).

Leaf area index (LAI) at all stages, crop growth rate (CGR) at flowering and grain filling along with net assimilation rate (NAR) at flowering showed high heritability coupled with moderate to high genetic advance. For days to flowering, tillers/plant, and leaf area duration low heritability was observed (Nirmala Devi *et al.*, 1988). High heritability coupled with moderate to high genetic advance for LAI, NAR, dry matter production and CGR at flowering and grain filling along with days to flowering and maturity indicated that these physio-morphological and phenological characters are governed mainly by additive genes and can be improved through conventional breeding methods (Nirmala Devi *et al.*, 1988).

Genetic variability for protein and mineral constituents of the grains in kodo millet were determined by Koutu (1989) by evaluating the genotypes at four locations in different agro-climatic zones of Madhya Pradesh, India. The magnitude of PCV was higher than GCV with maximum estimate for protein followed by Cu, Zn, Fe and Mn, while low estimate of variability was observed for carbohydrate content. The magnitude of heritability and genetic advance were high for all the nutritional traits except carbohydrate, which showed high heritability coupled with low genetic advance. The results indicated that these traits are under additive genetic control and hence selection based on phenotypic performance would be effective.

8.5.4 Correlation Studies

Attempts have been made to determine the yield components through correlation and path coefficient analyses in kodo millet by Amawate (1965), Dhagat *et al.* (1971) and Dhagat (1978). Association analysis indicated that plant height was positively correlated with grain yield in early and medium maturing genotypes of kodo millet (Verma and Singh, 1982). In early genotypes, plant height also showed positive correlation with panicle length but it was negatively correlated with test weight. Path analysis revealed that only plant height had direct influence on grain yield in all maturity groups. The panicle length contributed indirectly via plant height towards grain yield. Parihar (1985) observed significant positive correlation between grain yield and days to flowering, days to maturity, plant height, grain–straw ratio, fodder yield, 1000-grain weight and grains/panicle. Path analysis revealed that fodder yield, grain–straw ratio, fingers/ear and days to flowering are the major grain yield components in kodo millet. Significant positive

association of grain yield with tillers/plant, finger/ear, biological yield and harvest index was reported by Rao and Tiwari (1988). Tillers/plant showed significant positive association with ears/plant and ear length. Fingers/ear, ear length, and days to flowering are also positively and significantly associated among themselves. Significant positive association between productive tillers/plant and grain yield was reported by Yasin *et al.* (1988). Nirmala Devi *et al.* (1988) reported significant positive association between grain yield and physiological parameters like NAR, CGR, biological yield and dry-matter production at flowering and grain filling stages. The relative selection efficiency was high for NAR at flowering followed by tillers/plant.

Yadava and Jain (2006) reported significant positive association between grain yield and plant height, tillers/plant and biological yield in early maturing (<100 days) genotypes, while plant height, tillers/plant, flag leaf length and biological yield exhibited significant positive association with grain yield in late-maturing (>100 days) genotypes. Path analysis indicated that ear length, biological yield and number of tillers/plant in early-maturing genotypes, while biological yield, harvest index, peduncle length and plant height in late-maturing genotypes, are the main components of grain yield in kodo millet. An overall assessment of yield factors based on correlation and path analyses revealed that number of tillers/plant, plant height, panicle length, and biological yield are the major yield components in kodo millet (Yadava and Jain, 2006). Verma and Singh (1982) had computed multiple regression equation and suggested that panicle length and 1000-grain weight accounts for substantial variation in grain yield of kodo millet.

8.5.5 Cytogenetics

The karyotype and meiotic behaviour of kodo millet was reported by Hiremath and Dandin (1975). The study confirmed the earlier reports of $2n = 40$ and $n = 20$ chromosomes. The somatic chromosomes are medium-sized, and the difference between longest and shortest chromosome in the complement is very small. Hence, the chromosomes cannot be categorised into long, medium and short. There are three types of chromosomes, a single satellited sub-median pair with SAT on long arm, eight pairs of median chromosomes, and 11 pairs of chromosomes with sub-median centromere. The satellite is small and measures about 0.5 micron. The chromosome length ranges from 1.9 to 3.5 microns with an absolute length of 103.9 microns. In the meiotic behaviour, 20 bivalents are observed at diakinesis and metaphase I. The bivalents are mostly ring-shaped, but approximately 10% of the pollen mother cells contain 1-2 quadrivalents. Anaphasic separation at first and second division is mostly normal. Sporadically 1-2 lagging chromosomes are found at anaphase I and II. The tetrad formation is regular. From the studies of Magoon and Manchanda (1961) and Hiremath and Dandin (1975), it could be concluded that *P. scrobiculatum* is a tetraploid with basic chromosome number of 10. Regular 20 bivalent formations at meiosis indicate the allotetraploid nature; however, the small percentage of quadrivalents possibly suggests the segmental allotetraploid nature of the species.

8.6 Reproductive Biology

8.6.1 Morphology and Floral Biology

Kodo millet is a vigorous, annual herb, tufted (up to 60 cm diameter) and slender grass (Plate 8.1). Plants are slender to stout, 60–90 cm tall, and often root from the lower

Plate 8.1 Kodo millet – field view. (*See color plate section for the color representation of this figure*.)

nodes. Adventitious roots arise from lower nodes with numerous thin roots, and roots are rather shallow. Branched roots spread laterally and profusely, remain functional throughout the life. The stem is erect, occasionally spreading or prostrate in habit, branched and somewhat succulent, tufted on a very short rhizome. Stem is glabrous with swollen nodes and fully sheathed internodes. Nodal bands become purple at later stage. First node is hairy and the other nodes are glabrous with solid internodes. The length of internodes increases gradually from bottom to top in any tillers. The number of tillers varies from five to 18 according to genotypes. Leaf blades are simple, alternate, bifarious, erect or sub-erect, finely acuminate, glabrous or sometimes soft hairy, up to 40 cm long, with the basal leaf sheaths glabrous or pilose. Leaf blades are 15–40 cm long, 5–12 mm wide, and pale green. Leaf-sheath and leaves are glabrous (Ayyangar and Panduranga Rao, 1934; Galinato *et al.*, 1999; Yadava and Jain, 2006; Ecoport, 2010).

Inflorescences are composed of spike or spike-like racemes, rarely more than five (three to seven), that are alternately arranged on a short to elongated primary axis (Plate 8.2). Spikes are sessile, usually distant and spreading; rachis is herbaceous, broad

Plate 8.2 Kodo millet – racemes. (*See color plate section for the color representation of this figure*.)

with ciliate margins. Racemes are up to 13 cm long, with the sub-sessile spikelets arranged in two to three rows along one side of a flattened rachis. Spikelets are glabrous, orbicular or broadly elliptic in outline, conspicuously plano-convex, 1.8–3.5 mm long, and never awned. Each spikelet consists of one or two flowers and bears at the base bracts or glumes, one placed a little above and opposite the other. The lower glume is absent, and the upper glume is as long as the spikelet. The lower lemma is almost flat, more or less membranaceous and without a palea or floret. The upper lemma is crustaceous and encloses a floret in its axil, often brown and shiny when grains are mature, and embraces the crustaceous palea. Stamens are three in number, filamentous, with three anthers, two locules, open by longitudinal sutures, versatile and pendulous. Gynoecium is monocarpellary, ovary is superior, one cell with one ovule, two stigmas, feathery with distinct style (de Wet *et al.*, 1983; Yadava and Jain, 2006). The early tillers set seeds well, while the later ones are more sterile (Ayyangar and Panduranga Rao, 1934).

The grain is elliptic–orbicular in outline and 1.5–2.5 mm long (de Wet *et al.*, 1983). The grains are convex in front, flat on back of palea, scutellum is up to half the length of the grain. The grain is enclosed in hard, corneous, persistent husks that are difficult to remove. Pericarp is usually attached to endosperm at only one point (Yadava and Jain, 2006). The grain may vary in colour from light red to dark grey. The 1000-grain weight ranges from 3 to 6.7 g.

8.6.2 Flowering Behaviour

Kodo millet is cleistogamous, but protogyny has been observed in some cultures like IPs 147, IPs 197, IPs 427, etc. Youngman and Roy (1923) observed opening of the flowers between 0730 and 0800 hours in Nagpur conditions. Only 5% flowers open, the remaining being cleistogamous. Ayyangar and Panduranga Rao (1934) reported that anthesis takes place between 0230 and 0335 hours in Coimbatore conditions, and glumes get completely closed at 0345 hours. They further observed that the anthers crowd at the orifice, non-emergent and undehisced, but emerged in rare cases. The dehiscence of anther occurred by a slit at one end and speed up gradually. Mostly the dehiscence of the anther begins from the middle and proceeds to both ends. The feathery stigma dries up in the evening. The anthers remain fresh and do not wither till next morning. The lodicules are fleshy and do not shrink immediately after the anthesis of flowers. They remain fleshy for 6–8 hours after opening of the glume and then dry up. The grains mature in 30–40 days after flowering and remain tightly enclosed by the hardened fourth glume and its palea and have various shades of brown colour (Ayyangar and Panduranga Rao, 1934).

Verma (1989) found that the best time of anthesis is between 0545 and 0730 hours at Rewa, in Madhya Pradesh. In this period, a single floret of panicle opens for 20–30 minutes. The stigma comes first during anthesis of flowers and anthers arise just after the emergence of stigma. Yadava (1997) studied the flowering behaviour of kodo millet with the help of a protogynous induced mutant (KM 32). In this mutant, the opening of flowers starts automatically on day 3 after complete panicle emergence. The flowering starts from middle of the panicle and proceed to both sides. The flowering in a panicle takes nearly a week to complete. The best time of blooming was from 0600 to 1130 hours. The dehiscence of anthers takes place after change in their colour from whitish to light yellow. In the Indian wild types, the stigmas protrude from the spikelets (Doggett, 1989).

8.7 Breeding Objectives

8.7.1 Agronomic Traits

Improvement in grain yield is the prime breeding objective in kodo millet like other crops. The breeding efforts have achieved only average genetic enhancement in kodo millet so far though many improved varieties have been released for cultivation. The average yield remains one-fifth to one-sixth of the yield levels observed in the advanced varietal trials of AICSMIP. Varieties with specific adaptation are needed in remote tribal areas. Hence, identification of genotypes promising for grain yield and yield-related traits with stable expression is an important breeding objective.

The kodo millet is prone to lodging at maturity, causing loss of grain (de Wet *et al.*, 1983). To prevent this, limited fertilisation is recommended. However, application of fertiliser dramatically improves yields through vigorous growth. Therefore, development of nutrient-use efficient cultivars to reduce the risk of lodging is another breeding objective. Identification of genotypes with special attributes such as synchronous maturity, stay green, easy threshing and dehulling, etc., are other areas requiring breeders' attention. The basic problem of milling for the grains in kodo millet needs to be addressed to lessen the milling drudgery associated with the upper husk sticking the endosperm tightly, which reduces the efficiency of grain recovery from each spikelet.

8.7.2 Biotic and Abiotic Factors

One of the important diseases of kodo millet which causes economic loss in grain yield is head smut incited by *Sorosporium paspalithunbergione* (Viswanath and Seetharam, 1989). In Madhya Pradesh, up to 32.9% loss in grain yield was reported (Jain and Yadava, 1997). Some resistant sources for head smut like RK31, RK65-18, RK87-9, RK162, RK106, DPS486, DPS516, DPS542, DPS672, DPS700, DPS727, ICK769 (Ramappa *et al.*, 2006), GPLM 78, GPLM 96, GPLM 176, GPLM 322, GPLM 364, GPLM 621, GPLM 641, GPLM 679 and GPLM 720 (Jain, 2005) have been identified recently. These have to be used in breeding programmes for introgression of the trait into high-yielding background.

Among the other diseases, kodo millet is susceptible to ergot. Hardened masses of this fungus will grow in place of the millet grain, called sclerotia. These compact fungi growths contain a chemical compound that is poisonous to humans and livestock if consumed, and potentially fatal. It causes damage to the central nervous system, causing excitability in animals and eventually loss of muscle control. Cleaning the seeds by winnowing them before storage may remove the fungal spores only partially. Hence, development of ergot-resistant cultivars is an important breeding objective. Kodo millet grains are frequently infested by *Aspergillus tamarii* Kita in humid environment or if crop moistened before harvesting and threshing. *Aspergillus* produces cyclopiazonic acid (CPA), a toxic indoletetramic acid – a mycotoxin producing acute hepato-toxicty in humans and animals (Antony *et al.*, 2003). Fungal growth in grains and fodder causes a decrease in nutritional value and also results in health hazards known as 'kodua poisoning' (Rao and Husain, 1985) or locally known as *Malona* in Madhya Pradesh and Chhattisgarh (Pall *et al.*, 1980; Ansari and Shrivastava, 1991). It produces unconsciousness, vomiting, tremors, giddiness, difficulty in swallowing and sometimes death of human beings and cattle after the use of infected grain as food and

feed (Jain and Singh, 2006). Hence, potential target for breeding may be resistance to the fungi *Aspergillus flavus* and *A. tamari* which produce cyclopiazonic acid.

Among the insect pests, as in many other small millets, shoot fly (*Atherigona simplex*) is a serious pest in kodo millet and can cause significant yield reduction in late-sown crops. Yield losses from 39% (Nagesh Chandra and Musthak Ali, 1983) up to 49% (Patel and Rawat, 1982) have been recorded due to shoot fly attack. Hence, development of shoot fly–tolerant cultivars is one of the important objectives for yield enhancement. At some isolated pockets, *Striga* spp., a phanerogamic semi-root parasite, are predominant in kodo millet (Kumar, 1940; Bharathalakshmi, 1983; Reddy and Dastagiraiha, 1987; Jain and Tripathi, 2002). These weed parasites are reported from all the kodo millet growing areas of the country, and the predominant ones are *Striga asiatica* and *S. densiflora*. Striga species causes stunting and weakening of the host plant. The infestation becomes visible only after its emergence from the soil. The roots of the parasite form haustoria, which penetrate the host root for absorption of water and nutrient. The loss in grain yield per plant is from 42.4 to 65.8% (Jain and Tripathi, 2002). Breeding for *Striga* tolerance, thus, assumes significance.

As kodo millet is cultivated in agro-ecologies frequently subjected to vagaries of nature like erratic rainfall, moisture and heat stress, drought tolerance is an important factor to sustain the yield levels in the cultivars. Upon receipt of precipitation during the crop season following a short spell of drought, the cultivars should be able to utilise the moisture available and put forth satisfactory growth and grain yield. Hence, identification of germplasm lines with ability to recover completely and sustain recurrent droughts, and utilisation in crop improvement is an important objective for the breeders working in the area of abiotic stress tolerance.

8.8 Breeding Methods

Like other small millets, kodo millet also received less priority in agricultural research, though the genetic improvement work started before the independence in the country. Some of the early efforts in crop improvement of kodo millet have resulted in the release of improved varieties as early as 1940s. The first improved variety PLR 1 was released in 1942 for the rainfed areas of Tamil Nadu. Another improved variety, T2, was released in 1949, and Co 1 was released from TNAU during 1953. Post-independence, the genetic improvement work was initiated in Madhya Pradesh during 1964 by the financial assistance from the state government. Niwas 1, another improved variety was released in 1971 as the outcome of this work for general cultivation in Madhya Pradesh (Yadava and Jain, 2006). Since 1978, the centre of excellence for the improvement of small millets established at Jawaharlal Nehru Krishi Vishwa Vidyalaya (JNKVV), Dindori, by Indian Council of Agricultural Research (ICAR) with the assistance of International Development Research Centre (IDRC), Canada, is devotedly working towards the improvement of kodo millet.

With the establishment of All India Coordinated Small Millets Improvement Project (AICSMIP) in 1986 at UAS, Bangalore, the IDRC centre became part of AICSMIP, and varietal development has gained momentum. The AICSMIP centres located at Tribal Agricultural Research Station, JNKVV, Dindori, and Agricultural College, JNKVV, Rewa, are exclusively working on kodo and little millets. Presently, emphasis is being given to (i) the development of high-yielding varieties with resistance to biotic and

abiotic stresses; (ii) enrichment of germplasm, their critical evaluation for morphological, physiological and biotic and abiotic resistance traits and (iii) enhancement in available genetic variability through hybridisation/mutagenesis for identification of ideotypes suitable for different farming situations (Yadava and Jain, 2006).

8.8.1 Introduction and Selection

The varieties released in kodo millet so far are mainly developed through selection from landraces or germplasm. Some of the kodo millet varieties, namely APK 1, GK 2 and KMV 20, were the products of selection from germplasm introduced in different agro-ecosystems. Still ample possibility exists for improvement in kodo millet through introduction and location-specific selection. The gene pools maintained at the NAGS (Bangalore), NBPGR (New Delhi) and ICRISAT (Patancheru) can be introduced anywhere in the country to know their potentiality under different agro-climatic zones. An early-maturing and high-yielding line (JK 155) has been developed at the JNKVV, Rewa, Madhya Pradesh, from the germplasm introduced from the Project Coordinating Unit of AICSMIP, Bangalore, in 1993 (Yadava and Jain, 2006).

8.8.2 Pure-Line Selection

The pure-line selection is the extensively practised breeding method for improving performance, particularly grain yield in kodo millet. Single plant selection from landraces and cultivated varieties, their evaluation for economic characters like earliness, resistance to biotic stresses and high yield have resulted in the development and release of many varieties in kodo millet. Breeding for high yield (Harinarayana, 1989), earliness (Singh *et al.*, 1993), resistance to head smut and shoot fly (Verma, 1989; Singh *et al.*, 1990; Yadava and Jain, 1996) have been achieved through pure-line selection to certain extent. Till date (1942–2015), about 33 varieties have been released, of which 11 were released before establishment of AICSMIP (1986) and 22 after 1986. Pure-line selection has resulted in the development and release of maximum number of kodo millet varieties; till 1986, 14 varieties were developed, and, between 1986 and 2015, 17 varieties were developed. Still, there is good scope for improvement of genetic yield potential through increase in growth rate, photosynthate translocation efficiency from source to sink and yield attributing characters along with tolerance of biotic and abiotic stresses (Yadava and Jain, 2006).

8.8.3 Recombination Breeding

The difficulties in artificial crossing due to small and delicate spikelets combined with brittleness of rachis have resulted in a slow progress in recombination breeding in kodo millet. Though, the methods of emasculation and pollination have been standardised and extensively used in the recent past for creation of variability and selection of transgressive segregants from advanced generations, the progress so far is very limited. However, recombination breeding has been achieving popularity in recent years.

8.8.3.1 Natural Hybridisation

Though kodo millet is a highly self-pollinated crop, it permits a certain degree of cross-pollination, nearly to the tune of 5% in protogynous types (Youngman and Roy, 1923). It may result in the development of natural hybrids in the germplasm. Protogynous types have been selected, and crosses have been made. The planting of protogynous

genotypes in germplasm or breeding nurseries, or together with selected parents may increase the prospects of natural hybrids (Yadava and Jain, 2006). Controlled pollination could also be effected in protogynous types.

8.8.3.2 Controlled Hybridisation

The methods of artificial hybridisation through emasculation and controlled pollination have been standardised to a certain extent. The hand emasculation technique developed by Verma (1989) and modified by Yadava (1997) has been found effective in kodo millet. The controlled pollination just after the emasculation helps in development of hybrids.

8.8.3.3 Contact Method of Hybridisation

The contact method suggested by Ayyangar and Warian Achuta (1934) for finger millet is being successfully used in kodo millet with slight modifications. In this method, the panicles of selected plants are tied to other panicle in which crossing is to be attempted before flowering to enhance the chances of natural cross-pollination. It results in the low frequency of true hybrids, which can be identified with the help of marker characteristics of the parents in the F_1 generation.

8.8.4 Mutation Breeding

Mutagenesis has been proved a powerful tool to generate polygenic variation in small millets. In kodo millet, Mishra *et al.* (1985) was the first to introduce quantitative variation through γ-irradiation. The sensitivity to γ-irradiation varied from genotype to genotype. Yadava (1997) found maximum mutation frequency and effectiveness at 25 Kr dose of γ-irradiation. Mutants having auricle pigmentation, late maturity, complete panicle emergence and dark brown seed have been developed (Yadava *et al.*, 2003). A protogynous mutant having two rows of spikelets on rachis was also identified from 5 Kr dose of γ-irradiation in JK 76. The development of protogynous mutant has opened new avenues in recombination breeding. Among the mutants identified, KM 86 and KM 99 have high yield potential coupled with early maturity. There is ample possibility for kodo millet improvement through physical and chemical mutagenesis.

8.8.5 Improved Varieties

A number of varieties with high yield potential have been released for different states (Table 8.5). Some of the recent varieties with yield potential, area of adaptation and special features are listed in Table 8.6. Some of the important varieties include RBK 155, DPS 48, GPUK 3, APK 1, JK 41, JK 48, JK 76, JK 106, JK 65, JK 98, GK 1, GK 2, DPS 9-1, JK155, K1, Co 2, Co 3, APK 1 and Vamban. Till date, 27 kodo millet varieties have been notified by the Government of India, of which 13 are central releases and rest are state releases. The list of notified varieties is given in Table 8.7.

Under AICSMIP, the kodo millet varietal evaluation trials are taken up at different testing centres, identified across the country based on kodo millet growing regions. Usually, the centres are located in Andhra Pradesh (Nandyal), Chhattisgarh (Jagdalpur and Ambikapur), Gujarat (Dahod, Waghai), Jharkhand (Ranchi), Karnataka (Bangalore), Madhya Pradesh (Dindori and Rewa) and Tamil Nadu (Coimbatore, Pudukottai and Aruppukottai). The latest national checks are GPUK 3 (selection from germplasm GPLM 826, Bangalore), RK 390-25 (Mutant of RK 390, Rewa) and TNAU 86 (selection from IPs 85, Coimbatore).

Table 8.5 State-wise high-yielding kodo millet varieties in India.

State	Kodo millet varieties
Andhra Pradesh	PSc 1, GPUK 3, DPS 48
Gujarat	GK 2, DPS 48
Karnataka	GPUK 3, RBK 155, DPS 48
Maharashtra	GPUK 3
Madhya Pradesh	JK 62, JK 76, JK 41, GPUK 3, RBK 155, DPS 48
Chhattisgarh	JK 62, JK 76, JK 41, GPUK 3, RBK 155, DPS 48
Tamil Nadu	GPUK 3, KMV 20, APK 1
Uttar Pradesh	GPUK 3, KK1, KK2

Source: http://smallmillets.res.in

8.9 New Tools for Genetic Improvement

Application of molecular tools such as molecular markers in kodo millet improvement is still in infancy. In one of the earliest reports, genetic diversity and patterns of geographic variation among collections of *P. scrobiculatum* and *P. polystachyum* were studied using molecular markers generated through the RAPD technique (M'Ribu and Hilu, 1996). A high level of polymorphism in RAPD markers was observed among the individual accessions, demonstrating the high genetic diversity of the crop. Through the study, three major groups were resolved: one representing the African accessions, and two for the Indian accessions. The accessions of the North African kodo millet and *P. polystachyum* (considered conspecific with *P. scrobiculatum*) were quite distinct. The Australian kodo millet showed higher affinity to the African types. The study demonstrated that the molecular markers can be applied to resolve degrees and patterns of genetic variation at the population and species levels, identifying cultivars, and defining gene pools of kodo millet.

In a more recent study by Cidade *et al.* (2013), molecular genetic approach using cross-species amplification was proven to be useful for distinguishing the different taxa of *Paspalum* and in evaluating the possibility of successful species hybridisation. So far, no genetic or molecular maps of the kodo millet genome are available (Dwivedi *et al.*, 2012), probably because of the problem of persistent cross-hybridisation with its wild relatives. Though molecular markers for kodo millet are a few, they have been utilised in characterising diversity and phylogeny (Kushwaha *et al.*, 2015). There has been some preliminary work in miRNA target-site prediction using ESTs from kodo millet (Babu *et al.*, 2013). For taking up transgene studies, the media conditions for callus regeneration have been investigated, and regenerated plantlets were successfully grown to maturity in soil (Ceasar and Ignacimuthu, 2010). With the availability of genomic resources in other related *Paspalum* species (Cidade *et al.*, 2013), as well as in other grass systems such as foxtail millet (Muthamilarasan and Prasad, 2015), it should be possible in the near future to develop detailed genetic maps and markers linked to traits of interest for enabling molecular breeding in kodo millet.

Table 8.6 Improved kodo millet varieties with characteristics.

Sl. No.	Name of variety	Pedigree	Institute where developed	Year of release	Maturity (days)	Average Yield (kg/ha)	Area of adaptation	Special features
1	JK 76	Selection from local germplasm	JNKVV, Rewa	1989	85–90	1600–1800	Madhya Pradesh and Chhattisgarh	Earliness
2	JK 62	Selection from local germplasm	JNKVV, Rewa	1989	100–105	1800–2000	Madhya Pradesh and Chhattisgarh	Earliness and high yield
3	GPUK 3	Selection from germplasm GPLM 826	PC Cell, Bangalore	1991	100–105	1800–2000	All states	Yield, earliness and resistance to head smut
4	APK 1	Selection from PSC 5	ARS, Aruppukotai	1993	100–102	1800–2000	Tamil Nadu	High seed yield
5	GK 2	Selection from GPUK 5	GAU, Gujarat	1993	110–112	1500–2000	Gujarat	
6	KMV 20 (Vamban 1) (Varugu 1)	Pure-line selection from entry Pali	TNAU, Coimbatore	1996	95–100	1000–1750	Tamil Nadu	Tolerant to sheath blight
7	Jawahar kodo-155 (RBK 155)	Selection from germplasm no. GPLM 251	JNKVV, Jabalpur	2000	105–110	2000–2200	Madhya Pradesh, Karnataka	Resistant to head smut and shoot fly
8	Jawahar kodo-48 (JK 48)	Pure-line selection from local germplasm 48	JNKVV, Jabalpur	2001	110–115	2600–2700	Andhra Pradesh, Madhya Pradesh, Chhattisgarh, Karnataka, Gujarat	Tolerance to head smut and high grain yield
9	KK 2	Selection from genetic collections of Ballia district	CSAUA&T, Kanpur	2002	110–115	2000–2300	Uttar Pradesh	Resistant to drought and lodging, suitable for saline condition

10	Jawahar kodo-439	Selection from germplasm RPS-123	JNKVV, Jabalpur	2002	89–110	2000–2200	Madhya Pradesh	Moderately resistant to smut and shoot fly
11	Jawahar kodo-13 (JK 13)	Mutant plant No. 13 of cv JK 76	JNKVV, Rewa	2006	79–129	2200–2300	All states	Moderately resistant to head smut, resistant to shoot fly
12	Jawahar kodo-65 (RK 65-18)	Selection from local germplasm of Rewa	JNKVV, Rewa	2008	104	2300	Madhya Pradesh, Gujarat, Uttar Pradesh	—
13	Jawahar kodo-106	Selection from local germplasm no. 106	JNKVV, Rewa	2008	100	1947	Madhya Pradesh	Resistant to head smut and shoot fly
14	JK 36	Pure line selection	JNKVV, Rewa	2009	75–80	1000–1200	Madhya Pradesh	Very early duration
15	JK 98	Pure line selection from 317	JNKVV, Rewa	2010	100–105	2500–3000	Madhya Pradesh	Early duration, high yielding
16	DPS 9-1	Pure line selection	JNKVV, Rewa	2011	105–110	2600–2800	Madhya Pradesh	Resistant to head smut
17	Indira kodo-1 (BK-1)	Selection from kodo genetic stock	IGAU, SGCA, Jagdalpur	2012	103–105	2200–2500	Chhattisgarh	Moderately susceptible to head smut
18	TNAU 86	Pure line selection from IPS 85	TNAU, Coimbatore	2012	95–110	2700–3000	Andhra Pradesh, Chhattisgarh, Gujarat, Karnataka, Madhya Pradesh, Tamil Nadu and Uttar Pradesh	Early duration, non lodging high yielding and milling
19	RK 390-25	Mutant of RK 390	JNKVV, Rewa	2012	100–105	2500–2800	Andhra Pradesh, Chhattisgarh, Gujarat, Karnataka and Madhya Pradesh	Moderately resistant to head smut

Source: Seed Division, DAC; http://smallmillets.res.in

Table 8.7 List of notified kodo millet varieties in India.

Sl. No.	Variety name	Year of release	Notification date	Notification number	State of release
1	PLR-1	1942	01/01/1944		Tamil Nadu
2	Co 1	1953	01/01/1955		Tamil Nadu
3	Co 2	1970	01/01/1972		Tamil Nadu
4	Niwas-1	1971	01/01/1973		Madhya Pradesh
5	JNK-101	1976	01/01/1978		Madhya Pradesh
6	JNK-364	1977	01/01/1979		Madhya Pradesh
7	K-1	1979	14/01/1982	19(E)	Tamil Nadu
8	Jawahar Kodo-2	1976	14/01/1982	19(E)	Madhya Pradesh
9	Jawahar Kodo-1	1976	14/01/1982	19(E)	Madhya Pradesh
10	Co 3	1980	14/01/1982	19(E)	Tamil Nadu
11	Gujarat Kodra-1	1977	09/04/1985	295(E)	Central
12	PSC-1	—	14/05/1986	258(E)	Central
13	Jawahar Kodo-62	—	14/05/1986	258(E)	Central
14	Jawahar Kodo-41	—	14/05/1986	258(E)	Central
15	Jawahar Kodo-76	—	16/08/1991	527(E)	Central
16	GPUK-3	—	16/08/1991	527(E)	Central
17	APK-1	—	17/08/1993	615(E)	Central
18	GK-2	—	04/05/1995	408(E)	Central
19	Vamban-1 (KMV-20)	1995	01/05/1997	360(E)	Tamil Nadu
20	KK-1	1998	08/06/1999	425(E)	Uttar Pradesh
21	Jawahar Kodo-155 (RBK-155)	—	13/09/2000	821(E)	Central
22	Jawahar Kodo-48 (JK-48)	2001	15/11/2001	1134(E)	Central
23	Jawarhar Kodo-439	2002	05/11/2005	1566(E)	Central
24	Jawahar Kodo-13 (JK-13)	—	06/02/2007	122(E)	Central
25	Jawahar Kodo-65 (RK 65-18)	—	11/02/2009	S.O. 449(E)	Central
26	Jawahar Kodo-106	2008	11/02/2009	S.O. 449(E)	Madhya Pradesh
27	Indira Kodo-1 (BK-1)	2012	10/09/2012	S.O. 2125(E)	Chhattisgarh

Source: http://seednet.gov.in/

8.10 Future Prospects

The creation and management of genetic variability assume prominence in a crop such as kodo millet, in which the available genetic variability is very limited, owing to complete self-pollination due to its cleistogamous nature (Harinarayana, 1989). Among the approaches to create genetic variability, induced mutation is an important approach (Yadava and Jain, 2006; Subramanian *et al.*, 2011). Many of the present-day entries tested under advanced yield trials of AICSMIP have resulted from mutagenesis. Recombination breeding efforts are still to make substantial gains because of difficulty in crossing due to flowering habit. Emasculation and crossing techniques have to be standardised for effective deployment of trait-specific germplasm available in genebanks for genetic enhancement following recombination breeding. Identification of trait-specific donors, especially for special traits like lodging tolerance, synchronous and early maturity, nutrient-response and nutrient-use efficiency, resistance to fungal colonisation and mycotoxin development, etc., need concerted research efforts. Development of molecular markers and association mapping, identification of markers linked to agronomic traits and marker-assisted breeding, and genomics are some of the areas that need to be addressed in future.

References

Ahluwalia, M., Singh, D., Solaman, C. and Naqvi, S. (1970) Studies on variability in kodo millet (*Paspalum scrobiculatum* L.). *Andhra Agric. J.*, **17**, 58–60.

Ahmad, M.S. and Yadava, H.S. (1996) Assessment of productivity and economics of small millets in Madhya Pradesh. *Crop Res.*, **12**, 391–393.

Amawate, J.S. (1965) Variability and correlation of important economic characters with yield in *Paspalum scrobiculatum* L. M.Sc. (Agric.) Thesis, JNKVV, Jabalpur, Madhya Pradesh, India.

Amawate, J.S. and Dabral, K.C. (1970) Variability in kodo millet (*Paspalum scrobiculatum* L.). *Indian J. Agric. Sci.*, **40**, 616–619.

Ansari, A.A. and Shrivastava, A.K. (1991) Susceptibility of minor millets to *Aspergillus flavus* for aflatoxin production. *Indian Phytopath.*, **44**, 533–534.

Antony, M., Shukla, Y. and Janardhanan, K.K. (2003) Potential risk of acute hepatotoxicity of kodo poisoning due to exposure to cyclopiazonic acid. *J. Ethnopharmacol.*, **87**, 211–214.

Ayyangar, G.N.R. and Panduranga Rao, V. (1934) Studies in *Paspalum scrobiculatum* L. – the kodra millet. *Madras Agric. J.*, **22**, 419–425.

Ayyangar, G.N.R. and Warian Achuta, V. (1934) Anthers and pollination in ragi. *Indian J. Agric. Sci.*, **4**, 386.

Babu, R.N., Jyothi, M.N., Sharadamma, N. *et al.* (2013) Computational identification of conserved microRNAs from kodo millet (*Paspalum scrobiculatum*). *Afr. Crop Sci. J.*, **21**, 75–83.

Baki, B.B. and Ipor, I.B. (1992) *Paspalum scrobiculatum* L, in *Plant Resources of South-East Asia (PROSEA),* No. 4: Forages (eds L.'t. Mannetje and R.M. Jones), Pudoc, Wageningen, The Netherlands, pp. 185–187.

Bashaw, E.C. and Forbes, S. (1958) Chromosome number and microsporogenesis in Dallis grass (*Paspalum dilatatum*). *Agron. J.*, **50**, 48.

Bharathalakshmi (1983) Studies on the root parasite *Striga asiatica* (L.) Kuntze, in Proceedings of the Second International Workshop of Striga (eds K.V. Ramaiah and M.J. Vasudeva Rao), Ouagadougou, ICRISAT, pp. 111–113.

Ceasar, S.A. and Ignacimuthu, S. (2010) Effects of cytokinins, carbohydrates and amino acids on induction and maturation of somatic embryos in kodo millet (*Paspalum scorbiculatum* Linn.). *Plant Cell Tissue Organ Cult.*, **102**, 153–162. doi:10.1007/s11240-010-9716-6

Chandra, U., Thomas, T.A., Ranjana, N. and Paroda, R.S. (1987) *Catalogue on Kodo Millet (Paspahum scrobiculatum L.)*, Germplasm, NBPGR, New Delhi, India, p. 66.

Chandrasekara, A., Naczk, M. and Shahidi, F. (2012) Effect of processing on the antioxidant activity of millet grains. *Food Chem.*, **133**, 1–9.

Chandrasekara, A. and Shahidi, F. (2011) Inhibitory activities of soluble and bound millet seed phenolics on free radicals and reactive oxygen species. *J. Agric. Food Chem.*, **59**, 428–436.

Chandrasekharan, S.N. and Parthasarathy (1975) *Cytogenetics and Plant Breeding*, 3rd edn, P. Vardachary & Co., Madras, India, p. 544.

Choudhary, L.B. and Singh, R. (1970) Variety × environment interaction in kodo millet under two levels of fertility. *Indian J. Agric. Sci.*, **40**, 977–983.

Cidade, F.W., Vigna, B.B.Z., de Souza, F.H.D. *et al.* (2013) Genetic variation in polyploid forage grass: Assessing the molecular genetic variability in the *Paspalum* genus. *BMC Genetics*, **14**, 50.

Clayton, W.D. (1975) The *Paspalum scrobiculatum* complex in Tropical Africa. *Kew Bull.*, **30**, 101–105.

de Wet, J.M.J., Prasada Rao, K.E., Mengesha, M.H. and Brink, D.E. (1983) Diversity in kodo millet, *Paspalum scrobiculatum*. *Econ. Bot.*, **37**, 159–163.

Dhagat, N.K. (1978) Variability in inter-relationship and genetic divergence, in *Paspalum scrobiculatum* L. PhD Thesis, JNKVV, Jabalpur, Madhya Pradesh, India.

Dhagat, N.K., Joshi, R.C. and Sharma, D. (1971) Correlation and heritability in kodo millet (*Paspalum scrobiculatum* L.). *Indian J. Agric. Sci.*, **41**, 682–684.

Doggett, H. (1989) Small millets – a selective overview, in *Small Millets in Global Agriculture* (eds A. Seetharam, K.W. Riley and G. Harinarayana), Proceedings of the First International Small Millets Workshop. October 29–November 2, 1986, Bangalore, Oxford and IBH Publishing Co. Pvt. Ltd., New Delhi, pp. 3–17.

Dwivedi, S.L., Upadhyaya, H. D., Senthilvel, S. *et al.* (2012) Millets: genetic and genomic resources, in *Plant Breeding Reviews,* Vol. 35 (ed J. Janick), John Wiley & Sons, Inc., Hoboken, NJ, USA, pp. 247–374. doi: 10.1002/9781118100509.ch5

Ecocrop (2010) Ecocrop database. FAO. http://ecocrop.fao.org/ecocrop/srv/en/home

Ecoport (2010) Ecoport database. Ecoport. http://www.ecoport.org

FAO (2010) *Grassland Index. A Searchable Catalogue of Grass and Forage Legumes. FAO*. http://www.fao.org/ag/AGP/AGPC/doc/GBASE/Default.htm

FAO and ICRISAT (1996) The World Sorghum and Millet Economies: Facts, Trends and Outlook. Basic Foodstuffs Service, FAO Commodities and Trade Division and the Socioeconomics and Policy Division, International Crops Research Institute for the Semi-Arid Tropics, ICRISAT, Andhra Pradesh, India & FAO, Rome, Italy, p. 68.

Galinato, M.I., Moody, K. and Piggin, C.M. (1999) *Upland Rice Weeds of South and Southeast Asia*, International Rice Research Institute, Manila, Philippines, p. 156.

Gautam, P.L., Sharma, G.D., Srivastava, U. *et al.* (eds) (2000) *20 Glorious Years of NBPGR (1976–1996)*, National Bureau of Plant Genetic Resources, New Delhi, p. 333.

GISD (2010) *Global Invasive Species Database.* Invasive Species Specialist Group of the IUCN. http://www.issg.org/database

Goron, T.L. and Raizada, M.N. (2015) Genetic diversity and genomic resources available for the small millet crops to accelerate a new Green Revolution. *Front. Plant Sci.*, **6**, 157. doi: 10.3389/fpls.2015.00157

Harinarayana, G. (1989) Breeding and varietal improvement of small millets in India, in *Small Millets in Global Agriculture* (eds A. Seetharam, K.W. Riley and G. Harinarayana), Proceedings of the First International Small Millets Workshop, October 29–November 2, 1986, Bangalore, Oxford and IBH Publishing Co. Pvt. Ltd., New D0elhi, pp. 59–70.

Hegde, P.S. and Chandra, T.S. (2005) ESR spectroscopic study reveals higher free radical quenching potential in kodo millet (*Paspalum scrobiculatum*) compared to other millets. *Food Chem.*, **92**, 177–182.

Heuzé, V., Tran, G. and Giger-Reverdin, S. (2012) Scrobic *(Paspalum scrobiculatum)* forage and grain. Feedipedia.org. A programme by INRA, CIRAD, AFZ and FAO. http://www.feedipedia.org/node/401

Hiremath, S.C. and Dandin, S.B. (1975) Cytology of *Paspalum scrobiculatum* Linn. *Curr. Sci.*, **44**, 20–21.

Hulse, J.M., Laing, E.M. and Pearson, O.E. (1980) *Sorghum and the Millets: Their Composition and Nutritive Value*, Academic Press, New York, p. 997.

Irene, M., De Moraes Fernandez, B., Barreto, I.L. and Salzano, F.M. (1968) Cytogenetic, ecologic and morphologic studies in Brazilian forms of *Paspalum dilatatum*. *Canad. J. Genet. Cytol.*, **10**, 131–138.

Jain, A.K. (1995) Management of head smut in kodo millet (*Paspalum scrobiculatum* L.). *Ann. Agric. Res.*, **16**, 172–178.

Jain, A.K. (2005) Stable sources of resistance for head smut in kodo millet. *Indian Phytopath.*, **58**, 117.

Jain, A.K., Gupta, J.C. and Yadava, H.S. (1993) Sources of resistance to head smut in kodo millet. *Agric. Sci. Dig.*, **13**, 9–12.

Jain, A.K. and Singh, R.P. (2006) Current status of biotic stresses of kodo millet production in Madhya Pradesh, in *Future Policy Options in India. Vol. III: Small Millets* (eds K.T. Krishnegowda, N. Seetharama, I.S. Khairwal, *et al*.), Proceedings of the Third National Seminar on Millets Research and Development, March 11–12, 2004, All India Coordinated Pearl Millet Improvement Project, Agricultural Research Station, Mandor, Jodhpur, Rajasthan, India, pp. 61–64.

Jain, A.K. and Tripathi, S.K. (2002) Occurrence of *Striga* and its influence on yield of kodo millet. *Crop Res.*, **23**, 532–535.

Jain, A.K. and Yadava, H.S. (1997) Recent approaches in disease management of Small millets, in *Feed and in Processing for Value Addition*, National Seminar on Small Millets: Current Research Trends and Future Priorities as Food, April 23–24, 1997, TNAU, Coimbatore, India.

Janoria, M.P. (1963) Variability and classification of *Paspalum scrobiculatum* L. of Madhya Pradesh. M.Sc. (Agric.) Thesis, JNKVV, Jabalpur, Madhya Pradesh, India.

Kajale, M.D. (1977) Ancient grains from excavations at Nevassa, Maharashtra. *Geophytology*, **7**, 98–106.

Kandaswamy, G., Ramamoorthy, N. and Manoharan, V. (1990) Genetic variability in kodo millet (*Paspalum scrobiculatum* L.). *Madras Agric. J.*, **77**, 9–12.

Knees, S.G. and Gupta, A.K. (2013) *Paspalum scrobiculatum*. The IUCN Red List of Threatened Species. Version 2014.2. www.iucnredlist.org. Downloaded on 30 July, 2014.

Koutu, G.K. (1989) Productivity and stability analysis of biomass, yield and quality of kodo millet. PhD Thesis, JNKVV, Jabalpur, Madhya Pradesh, India.

Koutu, G.K., Singh, S.P. and Singh, C.B. (1993) Breeding for nutritional stability in kodo millet. *Indian J. Genet.*, **53**, 182–186.

Kumar, L.S.S. (1940) *Striga* research in Bombay. *Indian Farming*, **1**, 609–610.

Kushwaha, H., Jillo, K.W., Singh, V.K. *et al.* (2015) Assessment of genetic diversity among cereals and millets based on PCR amplification using Dof (DNA binding with One Finger) transcription factor gene-specific primers. *Plant Syst. Evol.*, **301**, 833–840. doi: 10.1007/s00606-014-1095-8

Magoon, M.L. and Manchanda, P.L. (1961) A cytological study of some species in the genus *Paspalum*. *Indian J. Genet.*, **21**, 212–221.

Malathi, D., Thilagavathi, T. and Sindhumathi, G. (2012) *Traditional Recipes from Kodo Millet*, Tamil Nadu Agricultural University, Coimbatore, India, p. 14.

Malleshi, N.G. and Hadimani, N.A. (1994) Nutritional and technological characteristics of small millets and preparation of value-added products from them, in *Advances in Small Millets* (eds K.W. Riley, S.C. Gupta, A. Seetharam and J.N. Mushonga), International Science Publisher, New York, pp. 271–287.

Miller, A. and Morris, M. (2004) *Ethnoflora of Soqotra Archipelago*, Royal Botanic Garden Edinburgh, Huddersfield, Scotland, p. 759.

Mishra, D.K., Verma, S.N.P. and Yadava, H.S. (1987) Stability analysis for grain yield in kodo millet. *Indian J. Agric. Sci.*, **57**, 613–616.

Mishra, P.C., Singh, C.B., Sahi, B.G. *et al.* (1985) Study of induced variability in *Paspalum*. *JNKVV Res. J.*, **9**, 30–31.

M'Ribu, H.K. and Hilu, K.W. (1996) Application of random amplified polymorphic DNA to study genetic diversity in *Paspalum scrobiculatum* L. (kodo millet, Poaceae). *Genet. Resour. Crop Evol.*, **43**, 203–210.

Murthy, T.K. and Harinarayana, G. (1989) Insect-pests of small millets and their management in India, in *Small Millets in Global Agriculture* (eds A. Seetharam, K.W. Riley, and G. Harinarayana), Proceedings of the First International Small Millets Workshop. October 29–November 2, 1986, Bangalore, Oxford and IBH Publishing Co. Pvt. Ltd., New Delhi, pp. 255–270.

Muthamilarasan, M. and Prasad, M. (2015) Advances in Setaria genomics for genetic improvement of cereals and bioenergy grasses. *Theor. Appl. Genet.*, **128**, 1–14. doi: 10.1007/s00122-014-2399-3

Nagesh Chandra, B.K. and Musthak Ali, T.M. (1983) Losses due to shoot fly on minor millets. *MILWAI Newsl.*, **2**, 16.

Navale, P.A., Harinarayana, G. and Mungse, H.B. (1984) Intra population improvement in a variety of kodo millet. *J. Maharashtra Agric. Univ.*, **9**, 354.

Devi, N., Yadava, H.S. and Verma, S.N.P. (1988) Physiological parameters and their association with grain yield in kodo millet. *Bhartiya Krishi Anusandhan Patrika*, **3**, 97–102.

NRC (1996) *Lost Crops of Africa. Volume I: Grains*, National Research Council, USA, p. 249.

Padulosi, S., Mal, B., Bala Ravi, S. *et al.* (2009) Food security and climate change: role of plant genetic resources of minor millets. *Indian J. Plant Genet. Resour.*, **22**, 1–16.

Pall, B.S., Jain, A.C. and Singh, S.P. (1980) *Diseases of Lesser Millets*, JNKVV, Jabalpur, Madhya Pradesh, India, p. 66.

Parihar, S.S. (1985) Genetic variability, association analysis and genetic divergence in kodo millet (*Paspalum scrobiculatum* L.), in M.Sc. (Agric.) Thesis, JNKVV, Jabalpur, Madhya Pradesh, India.

Patel, R.K. and Rawat, R.R. (1982) Note on estimation of loss in yield of kodo millet caused by the attack of shoot fly. *Indian J. Agric. Sci.*, **52**, 880.

Prasada Rao, K.E., de Wet, J.M.J., Gopal Reddy, V. and Mengesha, M.H. (1993) Diversity in small millets collection at ICRISAT, in *Advances in Small Millets* (eds K.W. Riley, S.C. Gupta, A. Seetharam and J.N. Mushonga), Oxford & IBH Pub. Co. Pvt. Ltd., New Delhi, pp. 331–346.

Prasanthi Kumari, R. and Vishnuvardhan, Z. (2013) The negative effects of calcium chloride on kodo millet (*Paspalum scrobiculatum*) germplasm during germination. *IOSR J. Agri. Vet. Sci.*, **6**, 63–74.

Prasanthi Kumari, R. and Vishnuvardhan, Z. (2014) A hydroponic approach to evaluate responses of kodo millet (*Paspalum scrobiculatum*) germplasm against NaCl stress. *Int. J. Adv. Res.*, **2**, 156–163.

Quattrocchi, U. (2006) *CRC World Dictionary of Grasses: Common Names, Scientific Names, Eponyms, Synonyms, and Etymology*, CRC Press, Taylor and Francis Group, Boca Raton, USA, p. 2408.

Ramappa, H.K., Ravishankar, C.R. and Prakash, P. (2006) Reaction of kodo millet and barn yard millet entries to smut disease, in *Future Policy Options in India. Vol. III: Small Millets*, Proceedings of the Third National Seminar on Millets Research and Development, March 11–12, 2004 (eds K.T. Krishnegowda, N. Seetharama, I.S. Khairwal *et al.*), All India Coordinated Pearl Millet Improvement Project, Agricultural Research Station, Mandor, Jodhpur, Rajasthan, India, pp. 73–74.

Rao, B.L. and Husain, A. (1985) Presence of cyclopiazonic acid in kodo millet (*Paspalum scrobiculatum*) causing 'kodua poisoning' in man and its production by associated fungi. *Mycopathologia*, **89**, 177–180. doi: 10.1007/BF004 47028

Rao, S.S. (1991) Genetic variability in minor millets. *Indian J. Agric. Sci.*, **61**, 322–323.

Rao, S.S. and Srivastava, M.N. (1997) Phenotypic stability in kodo millet (*Paspalum scrobiculatum* L.). *Indian J. Genet.*, **57**, 200–203.

Rao, S.S. and Tiwari, R.D. (1988) Variability and correlation studies in kodo millet. *Millets Newsl.*, **7**, 53–54.

Reddy, P.L. and Dastagiraiha, P. (1987) Preliminary screening of kodo millet varieties against witch weed. *Millets Newsl.*, **6**, 57.

Saldanha, C.J. and Nicolson, D.H. (1978) *Flora of Hassan District, Karnataka, India,* Amerind Pub, Co. Pvt. Ltd., New Delhi, pp. 746–747.

Satpute, R.G. (1966) Correlation studies on yield attributes in *Paspalum scrobiculatum* L. M.Sc. (Agric.) Thesis, JNKVV, Jabalpur, Madhya Pradesh, India.

Sharma, S.K. (1988) Assessment of genetic variability for some quantitative and physiological traits in kodo millet. M.Sc. (Agric.) Thesis, JNKVV, Jabalpur, Madhya Pradesh, India.

Singh, O., Jain, A.K., Gupta, J.C. and Yadava, H.S. (1993) *Status Report on Small Millets,* JNKVV, Rewa campus, Madhya Pradesh, India, pp. 19–24.

Singh, O., Shrivastava, O.S., Verma, S.N.P. and Rathore, J.S. (1990) Field evaluation of some kodo selections for resistance to shoot fly (*Atherigona* sp.). *Indian J. Ent.*, **52**, 191–194.

Singh, S.B., Yadava, H.S. and Singh, O. (1997) Phenotypic stability for grain yield and shoot fly incidence in kodo millet (Paspalum scrobiculatum). *Adv. Pl. Sci.*, **9**(II, Suppl.), 67–70.

Stephen, R.M. and Eisendrath, B. (1986) Koda millet, in *Understanding Cereal Crops II: Maize, Sorghum, Rice and Millet*, Technical Paper 55, Volunteers in Technical Assistance, Arlington, USA.

Subramanian, A., Nirmalakumari, A. and Veerabadhiran, P. (2010) Trait based selection of superior Kodo millet (*Paspalum scrobiculatum* L.) genotypes. *Electronic J. Plant Breed.*, **1**, 852–855.

Subramanian, A., Nirmalakumari, A. and Veerabadhiran, P. (2011) Mutagenic efficiency and effectiveness in kodo millet (*Paspalum scrobiculatum* L.). *Madras Agric. J.*, **98**, 22–25.

Taylor, R. (2004) Causation of type 2 diabetes – the Gordian knot unravels. *N. Engl. J. Med.*, **350**, 639–641.

Tickle, A.N. and Yadava, H.S. (1992) Stability assessment of grain yield in kodo millet. *Asv. Pl. Sci.*, **6** (I, Suppl.), 34–38.

Tiwari, D.K. and Janoria, M.P. (1967) Breeding potentialities of *Paspalum scrobiculatum* L. *JNKVV Res. J.*, **1**, 88–89.

Upadhyaya, H.D., Dwivedi, S.L., Singh, S.K. *et al.* (2014) Forming core collections in barnyard, kodo, and little millets using morpho-agronomic descriptors. *Crop Sci.*, **54**, 2673–2682.

USDA (2010) *GRIN – Germplasm Resources Information Network*. National Germplasm Resources Laboratory, Beltsville, Maryland. http://www.ars-grin.gov/cgi-bin/npgs/html/index.pl?language=en

Verma, S.N.P. (1989) *Researches on Small Millets at JNKVV*, College of Agriculture, JNKVV, Rewa, Madhya Pradesh, India, p. 126.

Verma, S.N.P. and Satpute, R.G. (1969) Heritability studies in kodo millet (*Paspalum scrobiculatum* L.). *JNKVV Res. J.*, **3**, 77–79.

Verma, S.N.P. and Singh, R.P. (1982) Association analysis in three maturing groups of kodo millet. *Indian J. Agric. Sci.*, **52**, 488–491.

Vishnu-Mittre (1977) Changing economy in ancient India, in *Origins of Agriculture* (ed. C.A. Reed), Mouton Press, The Hague, pp. 569–588.

Viswanath, S. and Seetharam, A. (1989) Diseases of small millets and their management in India, in *Small Millets in Global Agriculture*, Proceedings of the First International Small Millets Workshop, October 29–November 2, 1986 (eds A. Seetharam, K.W. Riley and G. Harinarayana), Bangalore. Oxford and IBH Publishing Co. Pvt. Ltd, New Delhi, pp. 237–253.

Yadav, N., Chaudhary, K., Singh, A. and Gupta, A. (2013) Evaluation of hypoglycemic properties of kodo millet based food products in healthy subjects. *IOSR J. Pharm.*, **3**, 14–20.

Yadava, H.S. (1993) Plant genetic resources: Conservation, management and prospective in small millets, in Proceedings of the National Seminar on Biodiversity; Strategies for Conservation and Future Challenges, October 16–17, 1993, Bharathiar University, Coimbatore, India.

Yadava, H.S. (1997) Gamma rays induced variation in kodo millet. *Adv. Pl. Sci.*, **9** (II Suppl.), 165–169.

Yadava, H.S., Ahnad, M.S. and Singh, S.B. (1996) Phenotypic stability for grain yield and fodder yield in kodo millet. *Crop Res.*, **12**, 343–348.

Yadava, H.S. and Jain, A.K. (1996) An overview of small millets research at Rewa, AICRP on Small millets, ZARS, JNKVV, Rewa, Madhya Pradesh, India.

Yadava, H.S. and Jain, A.K. (2006) *Advances in Kodo Millet Research*, DIPA, ICAR, New Delhi, India, p. 95.

Yadava, H.S., Tikle, A.N. and Bhagat, D.V. (2003) Effect of induced mutation through gamma rays on growth and yield parameters of kodo millet. *J. Soils Crops.*, **13**, 25–28.

Yasin, M., Verma, S.N.P., Jain, A.K. and Gupta, J.C. (1988) Variability and correlation studies in kodo millet. *Millets Newsl.*, **7**, 52.

Youngman, W. and Roy, S.C. (1923) Pollination methods among the lesser millets. *Agric. J. India*, **18**, 580–583.

9

Tef, *Eragrostis tef* (Zucc.) Trotter

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9.1 Introduction

Tef, *Eragrostis tef* (Zucc.) Trotter, is the most important cereal of Ethiopia, accounting for about one-third of the total acreage and one-fifth of the gross grain production of all cereals cultivated in the country (CSA, 2014). In Ethiopia, tef is annually cultivated by over 6 million smallholder farmers, and it is the staple food for about 50 million people. The cultivation of tef as a cereal grain has so far been restricted to Ethiopia, except that it appears in small quantities in Eritrea, and recently in the United States, Israel, the Netherlands and Spain. However, it grows as pasture or forage grass in the United States, South Africa, India, Australia and Kenya. In Ethiopia, the cultivation of tef predates historical records, existing before the introduction of wheat and barley in the country. In spite of its low productivity (the current national average yield of 1.5 t ha^{-1}), the Ethiopian farmers who engineered domesticating the crop have continued growing it over the millennia with its acreage increasing through time. The continued extensive cultivation of tef is attributed to its relative merits compared to the other cereals with respect to both husbandry and utilisation (Ketema, 1997; Tefera and Ketema, 2001; Assefa, Aliye *et al.*, 2011; Assefa, Yu *et al.*, 2011).

The major relative merits of tef over the other crops in terms of husbandry include:

i) Broad agro-ecological adaptation from below sea level up to 3000 meters above sea level under varied climatic, edaphic and socio-economic conditions;
ii) Reasonable tolerance to both low (drought) and high (water-logging) moisture stresses;
iii) Importance as a reliable and low-risk catch crop at times when other particularly long-season crops (such as maize and sorghum) due to natural calamities such as drought and pests (diseases and insect pests);
iv) Suitability to various cropping systems and crop rotation schemes;
v) Relative resilience to serious epidemics of pests and diseases in at least the major tef production regions of the country; and
vi) Minimal post-harvest losses since the grains suffer less from damage by storage pests such as weevils and diseases. Normally, tef grains can be stored for 3–5 years without considerable loss of viability even under traditional storage conditions.

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In addition to its aforementioned beneficial features in husbandry, the long-sustained extensive cultivation of tef in Ethiopia has been due to a number of its peculiar beneficial features with respect to utilisation. Among others, these include the following:

i) The grains of tef give the best quality and most consumer-preferred bread (known as *injera*) in terms of high water-holding capacity, long shelf-life, unique flavour (slightly sour but pleasant), pliability, smooth and glossy texture.
ii) The grains offer high returns in flour of 99% compared to the 60–80% from wheat (Ebba, 1969) and in injera.
iii) Minimal post-harvest losses and high storage longevity of the grains even under traditional storage conditions.
iv) Importance of the straw mainly as fodder for cattle, as a binder of mud used for plastering walls of local houses, and as bedding and mulch material.
v) Cash-crop value for farmers owing to the high market prices of both the grains and the straw.

Tef is a very nutritious cereal grain. Its nutritional content is generally comparable to that of the major world cereals like wheat, rice, barley and millets (Table 9.1) (USDA, 2015). Tef is superior in many aspects particularly in minerals such as calcium, iron, magnesium, phosphorus and potassium. The grains of tef are also rich in essential amino acids particularly in alanine, methionine, threonine and tyrosine (USDA, 2015).

In recent years, tef has become popular as a health and performance food in the global market. Since the grains are gluten-free, it is useful as food for humans suffering from gluten protein allergy ailments known as celiac disease (Spaenij-Dekking *et al.*, 2005). Its low glycemic index characterised by slow release type starches, makes it particularly suitable for diabetic people (Baye, 2014). Moreover, its high iron content is associated with the low prevalence of hookworm (ENS, 1959) and pregnancy-related anaemia in people consuming tef as staple food.

9.2 Origin and Taxonomy

9.2.1 Origin

Ethiopia is the centre of both the origin and diversity of tef (Vavilov, 1951), and over the years the crop species has co-evolved with Ethiopians. This is because Ethiopia harbours not only a wealth of diversity in the crop species but also it is believed to be the centre of origin for its domestication, including the existence of the possible wild progenitors. As one of the biggest genus in the grass family, the genus *Eragrostis* contains over 350 species (Watson and Dallwitz, 1992). Of these species, about 43% are considered to have originated in Africa, 18% in South America, 12% in Asia, 10% in Australia, 9% in Central America, 6% in North America and 2% in Europe (Costanza *et al.*, 1979). Among the 54 species found in Ethiopia, 14 are endemic to the country (Cufodontis, 1974).

Globally, the fact that tef originated in Ethiopia is not debatable; however, the exact location where it was first domesticated in Ethiopia yet remains unknown. Many maintain that tef originated in the northern highlands of Ethiopia, particularly in Tigray, where it is still an important crop. Based on the archaeological remains from northern Ethiopia, D'Andrea (D'Andrea, 2008) suggested that the earliest-known cultivation of

Table 9.1 Nutritional composition of raw and cooked tef grains (per 100 g) compared to those in wheat, rice, barley and millet.

		Tef		Wheat		Rice		Barely		Millet	
Item	**Unit**	**Raw**	**Cooked**	**Raw**	**Cooked**	**Raw**	**Cooked**	**Raw**	**Cooked**	**Raw**	**Cooked**
Proximates											
Energy	Kcal	367	101	337	132	370	97	352	123	378	119
Protein	g	13.30	3.87	14.54	5.71	6.81	2.02	9.91	2.26	11.02	3.51
Fat	g	2.38	0.69	2.13	0.83	0.55	0.19	1.16	0.44	4.22	1
Carbohydrate	g	73.13	19.86	70.11	27.60	81.68	21.09	77.72	28.22	72.85	23.67
Fiber	g	8	2.80	11.10	4.30	2.80	1	15.60	3.80	8.50	1.30
Minerals											
Calcium	mg	180	49	22	9	11	2	29	11	8	3
Iron	mg	7.63	2	3.77	1.76	1.60	0.14	2.50	1.33	3.01	0.63
Magnesium	mg	184	50	130	48	23	5	79	22	114	44
Phosphorus	mg	429	120	364	147	71	8	221	54	285	100
Potassium	mg	427	107	403	164	77	10	280	93	195	62
Sodium	mg	12	8	5	8	7	5	9	3	5	2
Amino acids											
Alanine	g	0.75	0.22	0.54	0.21	0.40	0.12	0.39	0.09	0.99	0.31
Arginine	g	0.52	0.15	0.70	0.27	0.57	0.17	0.50	0.11	0.38	0.12
Aspartic acid	g	0.82	0.24	0.80	0.31	0.64	0.19	0.62	0.14	0.73	0.23
Cysteine	g	0.24	0.07	0.31	0.12	0.14	0.04	0.22	0.05	0.21	0.07
Glutamic acid	g	3.35	0.98	4.84	1.88	1.33	0.39	2.59	0.59	2.40	0.76
Glycine	g	0.48	0.14	0.58	0.23	0.31	0.09	0.36	0.08	0.29	0.09

Histidine	g	0.30	0.09	0.38	0.15	0.16	0.05	0.22	0.05	0.24	0.08
Isoleucine	g	0.50	0.15	0.57	0.22	0.29	0.09	0.36	0.08	0.47	0.15
Leucine	g	1.07	0.31	1.11	0.43	0.56	0.17	0.67	0.15	1.40	0.45
Lysine	g	0.38	0.11	0.42	0.16	0.25	0.07	0.37	0.08	0.21	0.07
Methionine	g	0.43	0.13	0.25	0.10	0.16	0.05	0.19	0.04	0.22	0.07
Phenylalanine	g	0.70	0.20	0.77	0.30	0.36	0.11	0.56	0.13	0.58	0.19
Proline	g	0.66	0.19	1.59	0.62	0.32	0.10	1.18	0.27	0.88	0.28
Serine	g	0.62	0.18	0.76	0.30	0.36	0.11	0.42	0.10	0.64	0.21
Threonine	g	0.51	0.15	0.44	0.17	0.24	0.07	0.34	0.08	0.35	0.11
Tryptophan	g	0.14	0.04	0.13	0.05	0.08	0.02	0.17	0.04	0.12	0.04
Tyrosine	g	0.46	0.13	0.35	0.14	0.23	0.07	0.28	0.07	0.34	0.11
Valine	g	0.69	0.20	0.69	0.27	0.42	0.12	0.49	0.11	0.58	0.18
Vitamins											
Thiamin	mg	0.39	0.18	0.57	0.10	0.18	0.02	0.19	0.08	0.42	0.11
Riboflavin	mg	0.27	0.03	0.18	0.03	0.06	0.01	0.11	0.06	0.29	0.08
Niacin	mg	3.36	0.91	6.38	2.31	2.15	0.29	4.60	2.06	4.72	1.33
Vitamin B6	mg	0.48	0.10	0.26	0.07	0.11	0.03	0.26	0.12	0.38	0.11

Source: Adapted from USDA (2015).

tef was during the pre-Axumite period from 800 to 400 BC in the northern part of the country. According to the author, Ona Nagast, a location near Axum showed the first indication of tef cultivation.

Over the years, several techniques involving morphological and cytogenetic methods (Jones *et al.*, 1978), biochemical methods (Bekele and Lester, 1981) and phylogenetic analysis using ribosomal DNA and transcription factor genes (Espelund *et al.*, 2000) or nuclear and plastid genes were used in order to decipher the putative ancestral species for tef. Using morphological and cytological evidence, Ponti (Ponti, 1978) and Tavassoli (Tavassoli, 1986) suggested *Eragrostis aethopica*, (2*x*), *E. pilosa* (4*x*), *E. mexicana* (6*x*), *E. barrelieri* (6*x*), *E. minor* (2*x*, 4*x*) and *E. cilianensis* (2*x*, 4*x*, 6*x*) to be closely related to tef. Analysis of genetic relationships among accessions of *E. tef*, *E. pilosa* and *E. curvula* which were collected from Ethiopia and the United States based on amplified fragment length polymorphism (AFLP) (Ayele *et al.*, 1999; Bai, Ayele *et al.*, 1999; Ayele and Nguyen, 2000) and random amplified polymorphic DNA (RAPD) markers (Bai *et al.*, 2000) depicted relatively low levels (18%) of polymorphism within *E. tef*, and high similarity between *E. tef* and *E. pilosa*. Using two molecular markers, *E. pilosa* was found to be closely related to tef while *E. heteromera* and *E. cilianesis* are distantly related (Ingram and Doyle, 2003). While similar conclusions were reached using biochemical methods (Bekele and Lester, 1981), the close relationship between tef and *E. pilosa* was also evidenced by successful hybridisation between the two (Tefera *et al.*, 2003). This hybridisation generated viable offspring and ultimately resulted in the release of a variety called *Simada* (DZ-Cr-285 RIL295) from the inter-specific hybrid of tef [DZ-01-2785 × *E. pilosa* (line 30-5) (MoA, 2014). The compatibility between tef and *E. pilosa* was also observed in the F_1-hybrid between the two species in which regular meiotic division and significantly high pollen or seed fertility was observed (Admas and Dagne, 2008). This suggests closeness of tef to *E. pilosa*. However, since the present *E. pilosa* is a tetraploid plant like tef, the diploid ancestor of tef has yet remained unknown.

9.2.2 Taxonomy

Various nomenclatures names given to tef by various authorities at different times are summarised in Table 9.2. However, presently the most accepted binomial nomenclature is *Eragrostis tef* (Zucc.) Trotter. This name which is based on the specific epithet 'tef' previously used by Zuccagni was proposed by Trotter in 1918.

Tef belongs to the Grass or Poaceae Family (formerly Gramineae), sub-family Chloridoideae, tribe Eragrostideae and genus *Eragrostis*. Together with finger millet (*Eleusine coracana* Gaertn.), tef constitute the sole species in the sub-family Chloridoideae cultivated as a cereal crop. At a molecular level, the relationship of tef to other millets and major cereal crops is shown in Figure 9.1. Most millets are grouped under the subfamily Panicoideae, except for finger millet and tef, which belong to the subfamily Chloridoideae. Due to the absence of a waxy gene sequence in the NCBI database, three millets from the subfamily Panicoideae, namely kodo millet (*Paspalum scrobiculatum* L.), barnyard millet (*Echinochloa frumentacea* Link) and Fonio or Acha (*Digitaria exilis* Stpf and *D. iburua* Stapf), are not shown and the related species from the same genera are included for the first two in Figure 9.1. The binomial names and NCBI accession numbers of the plants used in Figure 9.1 are: little millet (*Panicum sumatrense* Roth ex Roem. & Schult., KC477404.1); proso millet (*Panicum miliaceum* L., GU199266); foxtail millet (*Setaria italica* (L.) P. Beauvois, AB089143); Japanese

Table 9.2 Binomial nomenclatures given to tef by various authorities at different times.

Suggested name	Year
Poa tef Zuccagni	1775
Poa abyssinica Jacquin	1781
Poa cerealis Salisb	1796
Cynodon abyssinicus (Jacq.) Rasp.	1825
Eragrostis abyssinica (Jacq.) Link	1827
Eragrostis pilosa (L.) P. Beauv. subsp. *abyssinica* (Jacq.) Aschers and Graben	1900
Eragrostis tef (Zucc.) Trotter	1918

Source: Updated from Ebba (1975) and Ketema (1997).

millet (*Echinochloa esculenta*, AB668987.1); pearl millet (*Pennisetum glaucum* (L.) R.Br., AF488414); *Paspalum simplex* (AF318770); maize (*Zea mays* L., EU041692); sorghum (*Sorghum bicolor* (L.) Moench, EF089839); tef (*Eragrostis tef* (Zucc.) Trotter, AY136939); finger millet (*Eleusine coracana* Gaertn., AY508652); bread wheat (*Triticum aestivum* L., KF861808); barley (*Hordeum vulgare* L., X07931) and rice (*Oryza sativa* L., FJ235770.1). The maximum likelihood tree was inferred using PhyML and the default model of HKY85 + G. The scale bar reflects evolutionary distance, measured in units of

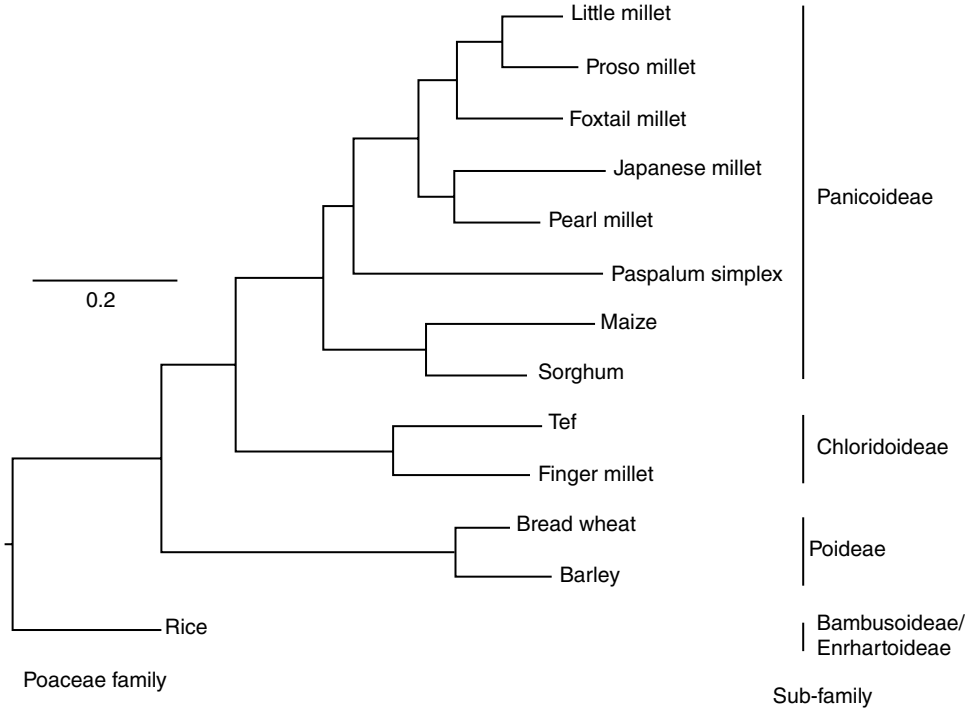

Figure 9.1 Phylogenetic tree showing the relationship among different millets and major cereal crops of the world using the waxy gene. *Source*: Gina Cannarozzi.

substitution per nucleotide site. Peterson and colleagues used six plastid DNA sequences (namely, ndhA intron, ndhF, rps16-trnk, rps16 intron, rps3 and rpl32-trnL) and one nuclear ITS DNA sequence to construct diverse phylogenetic trees which indicate the relationships among 246 species in the sub-family Chloridoideae (Peterson *et al.*, 2010).

Ebba distinguished, characterised and described 35 distinct tef cultivars based mainly on phenology, plant vigour, panicle form and ramification pattern, spikelet size, and lemma and caryopsis colour (Table 9.3) (Ebba, 1975). This was the first attempt to classify or group tef genotypes based on the morphological parameters. Since then, these ecotypes have been extensively used in many studies (Assefa, Tefera *et al.*, 2001; Assefa *et al.*, 2003; Chanyalew *et al.*, 2013; Plaza-Wüthrich *et al.*, 2013).

9.3 Genetic Resources and Utilisation

9.3.1 Genetic Resources of Tef

The Ethiopian gene-bank at the Ethiopian Biodiversity Institute (EBI) holds a total of 5169 accessions under both short-term at 4 °C and long-term at −10 °C *ex-situ* reserves of dried seeds at 3–7% moisture content (Tesema, 2013). Of the total accession in the EBI gene-bank, 3315 of them collected directly by EBI, while the remaining 1854 accessions were acquired through donations and repatriations.

Frankel and Brown distinguished three phases of genetic resources related activities in the world: the first phase emphasising bio-geography, taxonomy and evolution; the second conservation and the third utilisation of diverse germplasm (Frankel and Brown, 1984). But none of these three phases has been satisfactorily accomplished with regard to tef genetic resources. Although commendable efforts have been made in Ethiopia, neither the collection and conservation nor the evaluation and utilisation of the tef genetic resources has been done systematically and comprehensively. To this effect, several duplications of accessions are to be expected in the Ethiopian gene-bank holdings. There has been increasing risk of genetic erosion threats due both to natural calamities such as drought as well as replacement of landraces by recent expansion of improved varieties.

9.3.2 Utilisation of Tef Genetic Resources

The tef germplasm has been studied by the national research programme in Ethiopia and to the limited extent outside the country. In terms of phenology, tef generally takes 25–81 days to grow the panicle tips, 60–140 days to mature and 29–75 days for the grain filling period (Assefa, Tefera *et al.*, 2001; Chanyalew *et al.*, 2013) (Table 9.4). Tef plants grow to a total height ranging from about 20 to 155 cm, of which the culm (11–82 cm) and the panicle (10–65 cm) comprise 47–65% and 35–156%, respectively (Table 9.4). The existence of variability in tef germplasm for culm internode diameter (1.2–4.5 mm) is one key factor among others to possibly identify tef lines with improved lodging resistance.

The wealth of diversity in the species offers ample opportunities for genetic improvement of the crop to develop varieties suitable for different agro-ecologies, cropping systems and purposes. Besides, in the absence of possibilities for introductions of breeding materials from abroad, the genetic improvement of the crop relies heavily upon the indigenous genetic resources. Genetic diversity analysis of the tef germplasm

Table 9.3 Brief description of 35 tef ecotypes or cultivars characterized by Ebba (1975).

No.	Ecotype (cultivar) name	Plant height (cm)	Culm diameter (cm)	Panicle form*	Lemma colour**	Anther colour***	Number of		Seed colour****	Days to	
							Spikelets/ panicle	Florets/ spikelet		Heading	Maturing
1	Ada	80	1.8	S-comp	PY-green	D-purple	320	8.3	yWh	45–50	95–115
2	Addisie	80	1.9	V-comp	PY-green	D-purple	310	6	yWh	45–50	95–110
3	Adoensis	70	1.6	V-loose	PY-green	D-purple	440	6.5	mBr	45–50	90–95
4	Alba	85	2.2	F-loose	PY-green	D-purple	525	10	yWh	45–50	95–120
5	Balami	88	1.8	V-loose	D-purple	D-purple	424	8	yWh	40–45	90–110
6	Beten	70	1.6	V-loose	PY-green	D-purple	220	7	yWh	40–45	85–95
7	Bunniye	34	1	V-loose	PY-green	D- purple	90	6	mBr	35–40	75–85
8	Burssa	58	1.5	S-comp	G-green	Y-white	210	7.4	yWh	45–50	85–90
9	Curati	88	2.3	S-comp	PY-green	LG-red	600	6.5	poW	50–60	95–120
10	Dabbi	70	1.6	V-loose	G-purple	L-purple	295	6.5	mBr	40–45	80–95
11	Denkeye	60	1.5	S-comp	G-green	L-purple	165	9.6	mBr	45–50	90–115
12	Dschanger	75	1.8	F-loose	G-green	Y-white	210	6	mBr	40–65	90–110
13	Enatite	70	1.5	V-loose	PY-green	L-purple	270	6.2	yWh	40–45	90–100
14	Fesho	50	1.2	V-loose	D-purple	D-purple	135	6.2	Br	38–45	75–85
15	Gea Lamie	30	0.9	V-loose	G-green	D-purple	60	6.8	Br	25–30	60–70
16	Gofarie	78	1.8	S-comp	PY-green	Purple	285	7	yWh	45–50	90–100
17	Gommadie	75	2	S-comp	PY-green	L-purple	290	8.9	yWh	45–50	90–100
18	Gorradie	90	2.2	V-comp	PY-green	D-red	356	6.8	yWh	50–55	95–120
19	Hamrawe Murri	75	1.8	V-comp	D-purple	D-purple	310	6.9	yWh	50–55	90–100

(*Continued*)

Table 9.3 (Continued)

No.	Ecotype (cultivar) name	Plant height (cm)	Culm diameter (cm)	Panicle form*	Lemma colour**	Anther colour***	Number of		Seed colour****	Days to	
							Spikelets/ panicle	Florets/ spikelet		Heading	Maturing
20	Hatalla	90	2.1	V-loose	G-purple	D-purple	420	6.7	yWh	50–55	90–115
21	Janno	75	2	F-loose	G-red	D-red	325	8.5	yWh	45–50	85–105
22	Karadebi	55	1.1	V-loose	Brown	D-purple	160	6.7	Br	40–45	85–90
23	Kaye Agachem	77	1.8	V-comp	PY-green	D-purple	300	6.8	lBr	65–50	90–110
24	Kaye Murri	80	2	V-comp	D-red	D-red	289	6.5	yWh	45–50	90–105
25	Manya	75	2	F-loose	PY-green	D-red	550	9	yWh	40–45	90–110
26	Murri	95	2.3	V-comp	G-green	D-red	330	5	yWh	50–55	105–120
27	Purpurea	85	1.9	F-loose	D-red	D-purple	285	7.7	Br	45–50	90–100
28	Rosea	75	2	F-loose	P-green	D-purple	215	10.7	yWh	45–50	90–100
29	Rubicunda	85	2.4	F-loose	D-purple	D-purple	290	8.4	yWh	45–50	90–115
30	Shawa-Gemerra	35	0.9	F-loose	PY-green	D-purple	60	12	Br	30–35	60–75
31	Trotteriana	70	1.6	V-comp	PY-green	D-purple	210	8	Br	50–55	90–95
32	Tullu Nasy	42	1.1	V-loose	PY-green	D-purple	115	6.3	poW	35–40	60–70
33	Variegata	70	1.8	F-loose	PY-green	D-purple	160	10.9	lBr	45–50	90–100
34	Viridis	75	2.2	F-loose	G-green	Y-white	275	6.7	poW	45–50	85–95
35	Zuccagniana	65	1.3	V-comp	G-green	D-purple	200	6.4	Br	45–50	90–100

* *Panicle form*: F-loose: fairly loose; S-comp: semi-compact; V-comp: very compact; V-loose: very loose; ** *lemma colour*: D-purple: dark or deep purple; D-red: dark or deep red; G-Green: greyish, orange or olive green; G-purple: greyish, orange or olive purple; G-red: greyish red; PY-green: pale yellow green; *** *anther colour*: D-purple: dark, black or deep reddish purple; D-red: dark or deep red; L-purple: pale or light reddish purple; L-red: light greyish red; Y-white: yellowish or greyish white; **** *seed colour*: Br: brown; mBr: medium brown; lBr: light brown; poW: purple orange white; yWh: yellow white.

Table 9.4 Ranges of important traits of tef.

Traits	Minimum	Maximum
Time-related		
Days to heading	25	81
Days to maturity	60	140
Grain filling period (days)	29	75
Length-related		
Plant height (cm)	20	156
Culm length (cm)	11	82
Panicle length (cm)	10	65
Peduncle length (cm)	5.8	42.3
Diameter-related		
First culm internode length (cm)	2.7	8.1
Second culm internode length (cm)	4.1	11.5
First and second culm internode diameter (mm)	1.2	4.5
Grain diameter (mm)	0.5	1
Number-related		
No. of tillers/plant (total)	4	22
No. of tillers/plant (fertile)	1	17
No. of primary panicle branches	10	40
No. of spikelet/panicle	30	1070
No. of florets/spikelet	3	17
Mass- and yield-related		
100-kernel mass (mg)	18.9	33.9
Grain yield/panicle (g)	0.1	2.5
Grain yield/plant (g)	0.5	21.9
Grain yield (kg/ha)	1058	4599
Total phytomass/plant (g)	4	105
Shoot phytomass (kg/ha)	6355	19630
Other-properties		
Harvest index (%)	5	39
Lodging index	20	100

Source: Updated from Assefa, Tefera *et al.* (2001); Chanyalew *et al.* (2013).

accessions facilitates the development of improved varieties to achieve high productivity and yield stability. In view of this fact, efforts have been made in the past to assess and quantify the genetic diversity in the tef germplasm collections using different approaches. Assefa and colleagues made the first comprehensive review paper on tef genetic diversity (Assefa, Ketema *et al.*, 1999).

Trait variances in tef were estimated using genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) in different genotypes. Since the magnitude

of genetic variation is better assessed from GCV, breeders usually focus on traits with high GCV estimates. Accordingly, higher GCV values were reported for tiller number, panicle weight, grain yield per panicle, plant weight and grain yield (Tefera *et al.*, 1990; Hundera *et al.*, 1999; Assefa *et al.*, 2000; Chanyalew *et al.*, 2009) (Table 9.5). The reported wide genetic variation presents the scope for improving the crop through direct selection and/or hybridisation.

9.4 Genetics and Cytogenetics

9.4.1 Genetics of Qualitative Traits

The inheritance of lemma colour, seed colour and panicle form in tef was studied to determine the gene actions and interactions, the number of genes involved, the presence or absence of maternal effects and linkages and the kind of tetraploidy in the crop species (Berhe *et al.*, 2001). Four tef cultivars (viz. Fesho, Bursa, Kaye Murri and Trotteriana) having differing and contrasting phenotypic characteristics for the three traits were used, and six crosses and their reciprocals were made among the four cultivars. Data collected on individually transplanted plants and their progenies in the F_1, F_2 and F_3 as well as in backcross generations were used to determine the inheritance patterns.

9.4.1.1 Lemma Colour

Four genes controlled lemma colour inheritance (Table 9.6) as demonstrated by F_2 segregation ratios of 3:1, 12:13:1, 15:1, 45:3:16 and 180:12:48:16 (Berhe *et al.*, 1989a). Dominance, complementary and epistatic gene actions and interactions were found.

9.4.1.2 Seed Colour

Duplicate pairs of genes were involved in seed colour inheritance, and the gene action between the genes and their alleles was simple dominance with additive effects (Table 9.6) (Berhe *et al.*, 1989b). The cultivar Fesho (dark brown seed) produced an F_2 ratio of 15 brown:1 white when crossed with Kaye Murri (yellowish white seed), and 3 brown:1 white for the cross between Trotteriana (medium brown seed).

9.4.1.3 Panicle Form

This was controlled by duplicate pairs of genes for the degree of looseness and another pair of genes for branching pattern (Table 9.6) (Berhe *et al.*, 1989c). Segregation ratios in the F_2 of 15 loose:1 compact in the loose × compact crosses showed duplicate dominance gene action. Loose × loose crosses were all loose and compact × compact crosses were all compact in the F_2. On the other hand, an F_2 segregation ratio of 13 multilateral:3 unilateral for branching pattern suggested a recessive-suppressor type gene action.

Generally, the inheritance studies of all the three qualitative traits depicted no maternal effects, and all of them showed disomic inheritance patterns indicating that tef is an allotetraploid. This, in turn, indicates that quantitative genetic theories developed for diploids can be applied for the genetic improvement of the crop through breeding.

9.4.2 Genetics of Quantitative Traits

Quantitative traits, so called metric or biometric traits, are traits for which the observed variation is due to the segregation of several to many naturally occurring polymorphic

Table 9.5 Diversity levels for important traits as reported in different tef germplasm diversity evaluation studies.

	PCV (%)				GCV (%)			
Trait	**Ref. 1 (*n* = 35)**	**Ref. 2 (*n* = 20)**	**Ref. 3 (*n* = 320)**	**Ref 4 (*n* = 196)**	**Ref. 1 (*n* = 35)**	**Ref. 2 (*n* = 20)**	**Ref. 3 (*n* = 320)**	**Ref. 4 (*n* = 196)**
Days to heading	12.3	4.3	28.1	8.7	12.2	3.8	19.4	6.1
Days to maturity	8.4	4.7	7.1	10.5	8.4	4.1	2.3	4.2
Grain filling period (days)	—	7.1	—	—	—	6.4	—	—
Plant height (cm)	13.5	2.8	—	15.5	13.4	1.9	—	9.1
Culm length (cm)	—	—	44.3	—	—	—	13.5	—
Peduncle length (cm)	23.3	—	23.6	—	—	—	0.1	—
Panicle length (cm)	18.8	10.8	38.5	16.8	18.7	8.6	35.3	10.4
Grain yield/panicle (g)	29.4	18.9	2.4	—	28.1	8.9	0.9	—
Grain yield/plant (g)	22.4	—	21.8	36.7	18.7	—	5.5	29.8
Shoot biomass/plant (g)	—	—	48	22.5	—	—	10.4	23.7
Lodging index	—	9.9	—	17.9	—	—	—	15.3
Grain yield (kg/ha)	—	16	—	—	—	11	—	—
Harvest index (%)	—	15.7	71.8	16.3	—	10.2	27.1	25.8

Abbreviations: GCV: genotypic coefficient of variation; PCV: phenotypic coefficient of variation; Ref.: reference. Ref. 1: (Tefera *et al.*, 1990); Ref. 2: (Hundera *et al.*, 1999); Ref 3: (Assefa *et al.*, 2000); Ref. 4: (Chanyalew *et al.*, 2009).

Table 9.6 Proposed genotypes for tef cultivars used in inheritance studies of three qualitative traits (lemma colour, seed colour and panicle form).

		Tef cultivars			
Trait		**Fesho**	**Bursa**	**Kaye Murri**	**Trotteriana**
Lemma colour*		Purple	Grey	Red	Yellowish white
		$CCP_1P_1P_2P_2GG$	$ccP_1P_1P_2P_2GG$	$CCp_1p_1p_2p_2gg$	$ccP_1P_1P_2P_2gg$
Seed colour**		Dark brown	Greyish white	Yellowish white	Medium brown
		$B_1B_2B_2B_2$	$b_1b_1b_2^{gy}b_2^{gy}$	$b_1b_1b_2b_2$	$B_1B_1b_2^{gy}b_2^{gy}$
Panicle form***	Looseness	Effusum	Contractum	Compactum	Compactum
		Very loose	Fairly loose	Compact	Compact
		$Pa_1Pa_1Pa_2Pa_2$	$Pa_1Pa_1Pa_2Pa_2$	$pa_1Pa_1pa_2pa_2$	$pa_1pa_1pa_2pa_2$
	Branching	Multilateral	Unilateral	Multilateral	Multilateral
		MbMbsusu	mbmbSuSu	MbMbsusu	MbMbsusu

* *Lemma colour:* C = gene for basic anthocyanin colour; P_1 and P_2 = duplicate genes for purple lemma in the presence of dominant C such that either P_1 or P_2 alone can produce purple lemma in complementary action with C; p_1 and p_2 = genes responsible for red lemma in the presence of dominant C; G = gene for grey lemma visible only when dominant C is absent; g = gene for yellowish white lemma in the absence of C and G; ** *seed colour:* B = brown; b = white; gy = greyish; B_1 and B_2 = duplicate genes responsible for brown pigment; b_1 and b_2 = duplicate genes for yellowish white; b^{gy} = gene for greyish white; order of dominance $B_1 = B_2 > b_2^{gy} > b_1 = b_2$; *** *panicle form:* Pa_1 and Pa_2 = duplicate genes controlling loose panicle form; pa_1 and pa_2 = compact form; Mb = multilateral orientation of panicle branches; mb = unilateral branching; su = recessive suppressor of mutant gene mb; Su = inactive allele.

Source: Updated from Berhe *et al.* (1989a; 1989b; 1989c; 2001).

genes, for which the effects of the allelic difference on the phenotypes are generally small compared with the effects of the environment (Kearsey and Pooni, 1996). Generally, quantitative traits show continuous variations from one extreme to the other, their inheritance pattern is complex, and apart from genotype they are highly affected by environment and genotype × environment interaction.

Most agronomic traits of importance in crops are quantitative in nature manifested in terms of degree rather than kind. Knowledge on how to identify superior genotypes efficiently is crucial for plant breeders to select them and concentrate the underlying genes in a commercially acceptable line or variety. In order to do this, it is essential first whether the trait is heritable and then to understand the kind and extent of genetic components of the variation. The standard procedure for analysing major gene traits using the Mendelian F_2 phenotype segregation ratio such as 3:1 for one gene and 9:3:3:1 for two genes cannot be adopted for quantitative traits. This is associated with the problems of following the segregation patterns of polygenes that control quantitative traits. Instead, various statistics such as means, variances, covariances, regressions and correlations are employed to look at the degree of similarity or difference among related individuals and families.

Tefera made a comprehensive review on the genetics of quantitative traits in tef (Tefera, 2001). Analyses of generation means in different crosses of tef revealed that additive (a) and epistatic gene effects controlled the inheritance of grain yield while triple-test cross methods also indicated epistatic gene interactions on this trait (Tefera

and Peat, 1996; Tefera and Peat, 1997a; 1997b). Likewise, epistatis was also indicated for other quantitative traits, including grain yield/panicle, panicle mass, tiller number, harvest index, plant height, panicle length, and days to heading or panicle emergence and to mature. The consistent presence of epistasis in different studies indicates that non-allelic gene interactions play a great role in the inheritance of important (quantitative) phenologic and other agronomic traits of tef.

Regarding the implications for breeding of the inheritance patterns of quantitative traits in tef, Tefera made the following recommendations. Since tef is an autogamous crop, the final product of the breeding activity is an inbred variety (Tefera, 2001). Hence, the additive and additive × additive genetic components detected for various characters would be useful for achieving the desired genetic improvement. Because grain yield and other related characters show epistatic gene action, imposing selection at early generation may not be advisable and delaying selection to later generations would be useful by increasing the frequency of homozygous individuals. Segregating tef populations could be handled by a combination of the modified bulk population method and modified pedigree method of breeding. The F_2 and F_3 generations may be advanced by the population method, and individual plant selection (the pedigree method) can start at F_4. Such a breeding method minimises the unfixable non-additive gene action, which is prevalent in early generations.

Estimates of heritability and expected genetic advance are useful for exploiting genetic variability through selection. Table 9.7 summarises results of narrow sense heritability (h^2) estimates from three different studies (Tefera *et al.*, 1992; Tefera and Peat, 1996; Tefera and Peat, 1997b). Generally, relatively high narrow sense heritability values were noted for days to panicle emergence (0.48–0.74), days to mature (0.32–0.69), and panicle length (0.40–0.68), whereas grain yield/panicle (0.23), panicle mass (0.31–0.39) and

Table 9.7 Estimates of narrow sense heritability (h^2) for different traits of tef in various crosses.

	Estimates of h^2 in various crosses		
Traits	**(Tefera *et al.*, 1992)**	**(Tefera and Peat, 1996)**	**(Tefera and Peat, 1997b)**
Days to heading	0.46	—	0.74
Days to maturity	0.44	0.32	0.69
Plant height	0.11	0.35	0.56
Culm length	0.38	—	—
Panicle length	0.40	0.45	0.68
Culm diameter	—	—	0.35
Tiller number	0.15	0.52	0.44
Grain yield/panicle	—	—	0.23
Grain yield	—	0.19	0.31
Plant phytomass	0.37	0.35	0.23
Panicle phytomass	0.31	0.39	0.32
100-kernel mass	—	—	0.09
Harvest index	—	—	0.25

plant mass (0.23–0.37) also depicted moderate levels of h^2 estimates with less variation across different studies. Hence, the foregoing traits could be used as reliable guides to selection.

9.4.3 Cytogenetics Studies

The species in the genus *Eragrostis* generally range from diploid ($2x = 2n = 20$) to hexaploid ($2x = 6x = 60$). Tef is an allotetraploid species ($2n = 4x = 40$) originating from the hybridisation of two distinct species followed by diploidisation. This has been hypothesised based on the following two evidences. Cytological examinations depicted the formation of 20 bivalents in the meiotic Metaphase I in both the inter- and intraspecific hybrids (Tavassoli, 1986). In support of this, genetic studies further showed disomic inheritance patterns for some qualitative characters including panicle form and branching pattern, and glume/lemma and caryopsis colour (Berhe *et al.*, 1989a; 1989b; 1989c; 2001).

Although, the putative ancestral diploid progenitor species for tef have not yet been fully known, based on morphological and cytological evidences, Ponti (Ponti, 1978) and Tavassoli (Tavassoli, 1986) suggested that *Eragrostis aethopica* (2*x*), *E. pilosa* (4*x*), *E. mexicana* (6*x*), *E. barrelieri* (6*x*), *E. minor* (2*x*, 4*x*) and *E. cilianensis* (2*x*, 4*x*, 6*x*) are closely related to tef. Recent DNA-based studies (Ayele *et al.*, 1999; Bai, Tefera *et al.*, 1999; Ayele and Nguyen, 2000; Bai *et al.*, 2000; Ingram and Doyle, 2003) confirmed that *E. pilosa* is the closest relative and presumably one of the intermediate wild progenitors of tef.

As revealed from the karyotype analyses of 15 *Eragrostis* species, the chromosomes of tef are minute even by the standards of the genus, with the largest and smallest chromosomes of tef measuring 1.6–2.9 and 0.8–1.1 μm, respectively. The range in each of these two size groups is due to differences in condensation (Tavassoli, 1986). This implies that the largest chromosome of tef is approximately three times smaller than the smallest (1D) wheat chromosome (Gugsa *et al.*, 2001). Unlike that of some of its related wild *Eragrostis* species, the presence of chromosomal races and aneuploidy is not known in tef (Gugsa *et al.*, 2001).

Two independent flow cytometry studies on natural accessions and improved varieties of tef revealed that the tetraploid nuclear genome size of tef ranges from 666 to 926 Mbp (Ayele *et al.*, 1996; Hundera *et al.*, 2000). This indicates that the genome size of tef is roughly 50% larger than the rice genome, and the equivalent diploid tef genome size is about 75% the size of the rice genome (Kantety *et al.*, 2001). Notably, of the three major world cereals (i.e. wheat, rice and maize) two of them are large genome size polyploids with wheat being an allopolyploid ($6x = 16000$ Mbp) and maize being an ancient tetraploid ($4x = 2500$ Mbp).

9.5 Reproductive Biology

9.5.1 Floral Morphology of Tef

The tef inflorescence is paniculate, ranging in form from very compact with the branches appearing fused to the rachis thereby forming a whip-like or rat-tail-like structure to very loose types of open and laterally spread branches (Figure 9.2a). Broadly, four major panicle forms are distinguished. These are, very compact, semi-compact, fairly loose

and very loose. The primary panicle branches (10–40 per panicle) may rarely start to ramify from near the panicle base or first they are bare for a some centimetres, and then they get divided above into secondary and tertiary branches. Both the quantity and size of ramification of branches is greatest at the first node and gradually decreases upward becoming single and shortened at the end. In addition, the internodes are longest for the lower panicle branch, but become scabrous or branched at the apical parts. The branching or ramification pattern along the nodes of the central axis (rachis) can be either unilateral (inequilateral or asymmetrical) or multilateral (equilateral or symmetrical).

The panicle branches ultimately bear numerous spikelets varying in number from 30–1070 per panicle (Assefa, Ketema *et al.*, 1999). The spikelets are laterally compressed with a flexuous rachilla (with 3–18 nodes and about 1 mm long internodes) borne on a pedicel up to 2 mm long (Ebba, 1975). The spikelets are generally linear, oblong to lanceolate in shape, and each individual spikelet measures 3–15 mm long and 1–3 mm wide at the broadest part (Figure 9.2b). Each spikelet has got two unequal-sized glumes at the base and a number of florets above. The colour of the young glumes can generally be greyish-olive green, dark red, purple, yellow-green or variegated getting flecked with dark purple or dark red on a greyish yellow-green or greyish olive-green background.

The tef florets (3–17 per spikelet) are characterised by asynchronous development and maturation which is basipetal commencing at the top of the panicle and proceeds downwards. While this is on panicle basis, the flowering on spikelet basis on the other hand is acropetal beginning at the bottom of each spikelet and proceeding upwards. Each floret comprises a tri-nerved lemma, a two-nerved, bow-shaped palea, three stamens arising from near the ovary base and having very fine slender filaments apically bearing two-celled, length-wise-opening anthers, and a pistil or an ovary (Ebba, 1975) (Figure 9.2c). The ovary has often got two or in a few exceptional cases three styles each ending in a plumose (feathery) yellowish white stigma. In addition to genotype differences, the number of florets or kernels per spikelet and the size of the spikelet vary depending on the particular position along the panicle being highest and largest at the top and dismissing to the base of the panicle.

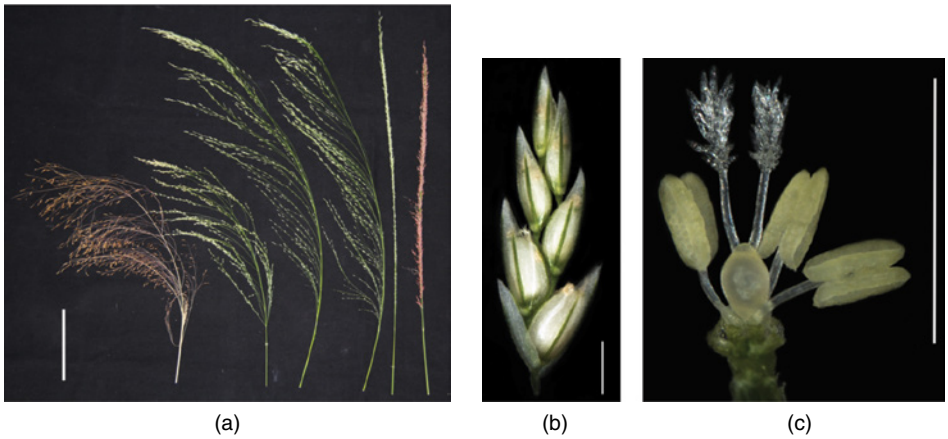

Figure 9.2 The inflorescence and flower of tef. (a) Panicles of tef differ in form, colour and size (scale bar = 10 cm); (b) spike of tef showing individual spikelet (scale bar = 1 mm); (c) structure of tef flower indicating three stamens and a pair of hairy stigmas (scale bar = 1 mm). *Source*: Regula Blösch.

9.5.2 Breeding Behaviour

As described earlier, the tef floret is a hermaphrodite with three stamens and two stigmas. As a result, it is an autogamous species. Until the discovery by Berhe, tef was thought to be entirely cleistogamous (closed flowers) with no options for out-crossing of its chasmogamous nature that deciphered the opening of the florets early in the morning at about 0645–0745 hours (Berhe, 1975). The rate of natural out-crossing in tef is 0.2% in the field and 0.05–1.37% in the greenhouse (Kedir *et al.*, 1992). Hence, due to this very low level of out-crossing, tef is considered as a strictly self-pollinated crop.

Based on the breakthrough discovery of the chasmogamous nature of tef florets, Berhe developed the artificial surgical hybridisation method for tef which is still in use in the tef hybridisation programme (Berhe, 1975). Accordingly, the conventional binocular-aided tef crossing involves emasculation of the maternal parent (by removal of the three stamens) a day before at about 1600–1900 hours, storage of the paternal parent under dark and cold conditions in a refrigerator (4 °C) overnight, collection of pollen from the paternal parent and subsequent brushing of the pollens over the stigma of the previously emasculated florets of the maternal parent.

Other methods for inducing male sterility using male-selective gametocidal chemicals treatments such as ethephon (ethrel) at flag leaf stage, although phytotoxic at high concentration, have shown some promise (Berhe and Miller, 1978; Ketema, 1983, 1993). The recent study in which four gametocides were investigated, suggested E4FO at 1000–1500 ppm due to low phytotoxicity and high female fertility (Ghebrehiwot *et al.*, 2015). Dark and hot water treatments were found to have also induced male sterility, but they produced other undesirable effects (Ketema, 1983, 1993). In spite of the attempts made to find alternative methods of emasculation, however, the most practicable method for tef hybridisation has still remained to be the surgical binocular-aided hand emasculation and pollination technique.

9.6 Constraints in Tef Production

The major tef production constraints and challenges can be grouped into two major categories as: (i) technical constraints/challenges, and (ii) socio-economic-related constraints and challenges.

9.6.1 Technical Constraints

The major constraints and challenges in Ethiopia's tef husbandry are outlined in the following text.

9.6.1.1 Relatively Low Productivity of Tef Crop

The national average grain yield of tef is 1.5 t ha^{-1} in 2013 (CSA, 2014). This among others is due to the widespread use of low-yielding varieties by majority of the tef-growing farming community coupled with unimproved traditional practices. According to the Central Statistical Agency, only 2.4% of the total tef farmers in Ethiopia grew improved varieties on 17% of the total land area (2.6 million ha) allocated for tef in 2009 cropping season (CSA, 2010; Ferede, 2013).

Furthermore, most of the tef-growing farmers still use age-old traditional practices in all pre- and post-harvest husbandry operations coupled with minimal and utmost suboptimal inputs as indicated in a recent review (Ferede, 2013).

9.6.1.2 Susceptibility of the Crop to Lodging

Lodging is defined as an anomaly manifested as a displacement of the aerial parts of plants from the upright position, and it is induced by factors both extrinsic and intrinsic to the plant, and also by the interactions among the plant's external and internal factors (Ketema, 1983, 1993). The causes for lodging in cereals comprise complex of factors including high rates of nitrogen fertilisation, wind and heavy rain splashes, fungal crop damage, inadequate development of root system, high seeding rates, lack of phosphorus and potassium fertilisation and insufficient strengthening of sclerenchyma tissue in the culms (Hamilton, 1951; Pinthus, 1973).

The direct and indirect deleterious effects of lodging on crops can be summarised as follows (Pinthus, 1973; Ketema, 1983, 1993):

i) Inflicts losses in yield and quality of both grains and straw harvested;
ii) Creates favourable conditions for the development and spread of diseases and insect pests;
iii) Imposes restrictions on the use of growth and yield promoting high input husbandry technologies such as high rates of nitrogen fertilisers;
iv) Poses difficulties in manual and mechanical crop-harvesting operations.

While studying the lodging phenomenon with tef, Ketema identified the following major types of lodging (Ketema, 1983):

i) *Transient lodging* is a temporary situation occurring before heading with the plants often capable of recovering into the upright position.
ii) *Permanent lodging* is a permanent displacement from the upright position often manifested after heading. It comprises three sub-categories:

   a) *Root lodging* involves uprooting of the whole plant while the stems still appear intact.
   b) *Break lodging* involves breakage of the stem usually near the base of the peduncle.
   c) *Bend lodging* is characterised by loss of plant elasticity leading to bending of stems while the roots are still secure in the soil.

In practical husbandry, bend lodging is by far the commonest, most prevalent and economically most important type of lodging in tef (Ketema, 1983, 1993). While bend lodging is the most significant, break lodging is of minor concern, and root lodging is relatively unimportant. In contrast, Van Delden and co-workers (van Delden *et al.*, 2010), using biomechanical models with two tef cultivars in field trials in the Netherlands, reported that tef is most sensitive to root lodging and that given its current morphology, lodging of free-standing plants is inevitable in the tested environments. If the root lodging that the latter workers meant is similar to that described earlier, it may not be unexpected especially on the sandy soil conditions and particularly under low plant density. But under Ethiopian conditions, tef is predominantly a heavy clay soil crop, and even on light soils the crop is grown in densest and such that root lodging is not the most important type of lodging.

In tef, lodging reduces grain yield by 11–22% (average = 17%), 1000-kernel weight by 35%, grain yield per panicle by 51%, and percentage and rate of seed germination by 41 and 44%, respectively (Ketema, 1983). This, therefore, indicates the economic significance of the problem of lodging in tef, and the urgent need for finding means for combating the problem.

9.6.1.3 Labour-Intensive Nature of Tef Husbandry

All the cultural operations in tef husbandry including land preparation, planting, weeding and harvesting and threshing are both demanding and labour-requiring. This is mainly associated with the minute size of the tef seeds with the 100-kernel mass amounting to 19–34 mg (Assefa, Ketema *et al.*, 1999; Chanyalew *et al.*, 2013). This, in turn, necessitates the preparation of fine and smooth seed bed, poses difficulties in optimising planting method and plant population density, and imposes drudgery in harvesting and threshing. The other problem with the minute-sized tef seeds is mechanical mixing and contamination of the pure grain at all stages of operations, starting from sowing up to the final harvesting and threshing as well as storage.

Besides, tef crop are generally poor competitors with weeds particularly at the early stages, and country-wide yield losses in tef due to weeds varied from 23 to 65% (Fessehaie and Tadele, 2001; Zewdie and Damte, 2013), Hence, weed control has been one of the most labour-demanding and back-breaking activity in tef husbandry. On the other hand, the harvesting and threshing of tef has also remained as very cumbersome operation due mainly to the small size of the seeds as well as due to the problems of lodging shattering associated with tef crops.

9.6.1.4 Biotic and Abiotic Constraints

The foregoing technical constraints involving low yield potential, lodging, and culture-demanding and labour-intensive husbandry requirements are mainly associated with the nature of the tef crop. Apart from these, however, other factors constraining tef production and productivity in different parts of Ethiopia include biotic stresses such as weeds, diseases and insect pests, and abiotic stresses like drought, water-logging, soil acidity and salinity, and cold. However, significant variations were observed among tef accessions towards tolerance to soil acidity (Abate *et al.*, 2013) and salinity (Asfaw and Dano, 2011).

9.6.2 Socio-Economic Constraints

The principal constraints to tef production and productivity in Ethiopia with regard to socio-economic aspects include lack of attention to the research and development of the crop both at the global and local level, lack of adequate quality and quantity of planting seeds of improved varieties due to weakness in the seed system, and weak extension systems and research-extension linkages for dissemination of improved tef technologies.

9.6.2.1 Lack of Adequate Attention

Tef can be categorised as an orphan or a neglected crop because of its localised solitary importance in Ethiopia. Consequently, it has lacked the attention of the global scientific community as well as that of donors, and has, therefore, remained under-researched. Unlike that of the other major world crops, no Consultative Group on International Agricultural Research (CGIAR) centres or regional institutions have been established to deal with the improvement of such localised crops like tef. Furthermore, the national focus has remained very limited. Even though there have been trends for improvement in crop development, tef has for a long time been omitted from the national research and development priority commodities of the country, which does not seem to correspond to the significance of the crop in Ethiopia. Besides, the national tef improvement programme suffers due to a lack of basic information on the species, and capacity limitations in terms of required human, physical infrastructure and facility resources.

9.6.2.2 Weak Seed and Extension Systems

Presently, lack of adequate quality and quantity of planting seeds of improved varieties has become a constraint due to the limitation of the existing seed system. Although the government of Ethiopia has in recent years established the most robust public agricultural extension systems in Africa in terms of structure, this extension system hardware still suffers from serious drawbacks in terms of efficiently and effectively discharging the dissemination of improved agricultural technologies, innovations and knowledge to the farming communities.

Factors such as expensiveness and unavailability of seeds and lack of awareness have commonly been cited as the major constraints contributing to the low level of tef technology adoption (Tefera, Kelemework *et al.*, 2001). Lack of awareness was reported by 34% of the farmers as the most important factor for the non-adoption of improved tef varieties.

There has been a wider consensus that the weak seed system in Ethiopia is the major limiting factor for the slow dissemination of improved tef varieties. Since the formal seed sector which consists of both the private and public seed enterprises is driven by profit, it is virtually engaged in the production of seeds of hybrid maize and of the self-pollinated crops almost solely for wheat. In Ethiopia, the formal seed sector covers only 5% of the tef but 53% of the maize and 20% of the wheat seed requirement (Alemu *et al.*, 2007). In general, smallholder tef farmers in Ethiopia depend on the informal system involving farmer-to-farmer seed exchange and use of their own recycled seeds. About 50% of farmers in Lume and Minjar areas reported that seed exchange among farmers is the major source of tef seed (Ferede, 2012).

9.6.2.3 Unavailability of Agricultural Inputs

Improved seeds constitute only part of the agricultural inputs for boosting productivity and production of tef in Ethiopia since other components should also go in par as a package. Among others, availability of the required inputs such as fertilisers, required pesticides (when and where necessary) are crucial. To that end, provisions of adequate credit services would be important.

9.7 Genetic Improvement of Tef

9.7.1 Historical Milestones

Scientific research in tef improvement started in 1956 at the then Jima Technical and Agricultural High School, now College of Agriculture and Veterinary Medicine of Jima University. About 3 years later, the research was moved to the then Central Experiment Station, now the Debre Zeit Agricultural Research Center.

In the overall history of tef breeding, three inter-related phases can be distinguished as follows.

- *Phase I* (1956–1974) – This was characterised by: (i) germplasm enhancement (collection/acquisition, characterisation and evaluation, systematics and conservation); (ii) genetic improvement relying entirely upon mass and/or pure-line selection directly from the existing germplasm and (iii) initiation of induced mutation techniques.
- *Phase II* (1975–1995) – This phase featured: (i) the discovery of the chasmogamous floral opening behaviour of tef flowers (from about 0645–0745 hours) and thereby the

artificial crossing technique by Berhe (Berhe, 1975) and (ii) incorporation of intra-specific hybridisation in the genetic improvement program following the discovery of the crossing technique.

- *Phase III* (1995–to-date) – This phase is characterised by: (i) initiation of molecular/genomics approaches involving development of molecular markers and genetic linkage maps and analyses of molecular genetic diversity; (ii) incorporation of *in vitro* culture techniques and inter-specific hybridisation; (iii) re-appraisal of induced mutagenesis particularly for lodging and leaf rust disease resistance and (iv) strengthened use of participatory breeding approaches (Belay *et al.*, 2006; 2008).

9.7.2 Breeding Objectives

The overall objectives of the tef breeding program are: (i) to enrich and improve the germplasm resource base; (ii) to develop suitable varieties for different agro-ecologies and cropping systems and (iii) to generate basic scientific information on the crop species.

In order to achieve these objectives, attention has focused on: (i) high productivity in terms of both grain and straw yield; (ii) tolerance to low moisture stress; (iii) improved lodging resistance and (iv) desirable grain quality mainly in terms of farmer and consumer-preferred traits which at present concern mainly caryopsis colour (often white).

With these considered, the major strategies of the current tef-breeding focus include: (i) shift from wide to specific adaptation due mainly to high genotype × environment interaction while still looking for broad adaptation; (ii) market orientation with respect to quality, quantity and food security and (iii) expansion to non-conventional (new) tef-growing areas.

9.7.3 Breeding Methods

The process of the general breeding methodology employed in tef variety development is shown in Figure 9.3.

9.7.3.1 Conventional Approaches

Since genetic variation forms the fundamental basis for breeding, the first step in tef variety development anchors primarily upon germplasm enhancement through three complementary ways: (i) collection/acquisition, characterisation, evaluation and conservation of germplasm; (ii) hybridisation (intra- and inter-specific) among selected parents and (iii) other techniques.

i) *Indigenous germplasm*: The indigenous germplasm constitutes the major source of variability for tef breeding (Tefera, Assefa *et al.*, 2001) because, tef being a native and unique crop to Ethiopia, there have been no opportunities for introductions of germplasm and breeding materials from abroad.

ii) *Hybridisation*: This involves mainly intra-specific crosses and recently some inter-specific crossings especially with *E. pilosa*. A total of about 590 crosses have been made so far at Debre Zeit Agricultural Research Center. Subsequent segregating populations are handled using the modified bulk and modified pedigree methods of breeding. However, some varieties have been developed as recombinant inbred lines (RILs) through F_2-derived single-seed descent (SSD) method.

iii) *Other techniques*: This includes modern and novel techniques such as induced mutation and marker-assisted breeding. Artificial induction of mutation creates

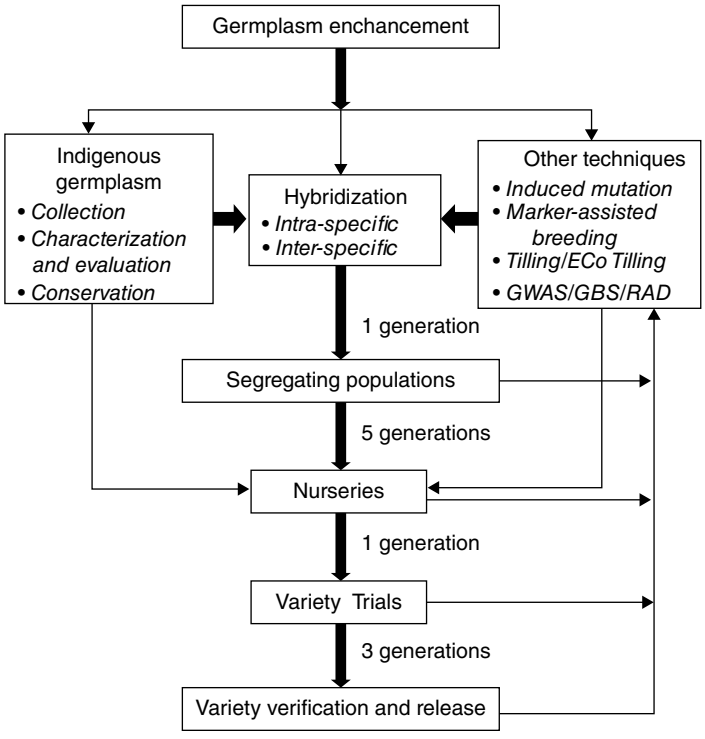

Figure 9.3 Schematic representation of the variety development process in the National Tef Improvement Program in Ethiopia indicating the numbers of generations required for each category of evaluation. Abbreviations: GBS: genotyping by sequencing; GWAS: genome-wide association study; RAD: restriction site associated DNA; TILLING: Targeting Induced Local Lesions in Genomes.

variability for some important traits such as lodging resistance since sufficient variability in the existing germplasm is lacking.

Following the pre-breeding germplasm-enhancement stage is the nursery for initial screening and evaluation of selected genotypes from the three germplasm-enhancement schemes. This, in turn, is followed by a series of yield trials including preliminary and national variety trials. In the variety testing, genotypes are categorised into early- and late-maturing sets depending on the period of maturity. The late types are mainly targeted for high potential or optimum environments, while the early sets are targeted for terminal moisture stress areas. At the last stage of the process, elite and promising genotypes selected as candidate varieties based on their performance in the various variety trials are entered into variety verification trials for evaluation by the National Variety Release Committee. At all stages, even after release as a variety, genotypes could be selected to be taken back to the earlier steps of hybridisation and induced mutation schemes of germplasm enhancement.

9.7.3.2 Modern and Novel Approaches

The research achievement in tef molecular breeding approaches can be categorised into six parts as (i) molecular marker development, (ii) molecular analysis of genetic diversity and relationships, (iii) development of molecular marker linkage maps; (iv) identification of quantitative trait loci (QTL); (v) comparative genomics; (vi) regeneration and

transformation techniques and (vii) high-throughput techniques such as Targeting Induced Local Lesion IN Genomes (TILLING) and eco-TILLING.

9.7.3.2.1 Marker Development

Molecular markers provide an invaluable tool for studying genetic diversity and relationships, classification of germplasm, construction of genetic linkage maps, and in marker-assisted selection or breeding. Recently, several marker systems have been developed in tef and used for various purposes. These include amplified fragment length polymorphism (AFLP) (Ayele *et al.*, 1999; Bai, Ayele *et al.*, 1999; Bai, Tefera *et al.*, 1999; Ayele and Nguyen, 2000), RAPD (Bai *et al.*, 2000) and restriction fragment length polymorphism (RFLP) (Zhang *et al.*, 2001) that were applied to various tef genetic and genomic studies (Yu, Kantety *et al.*, 2006; Yu, Sun *et al.*, 2006). Following generation of tef-expressed sequence tag (EST) sequences from four cDNA libraries, tef sequence-specific markers have been developed such as expressed sequence tag derived simple sequence repeat (EST-SSR), intron fragment length polymorphism (IFLP), and single-nucleotide polymorphism/insertion and deletion (SNP/INDEL) (Yu, Kantety *et al.*, 2006).

The fact that EST sequences are derived from the coding regions of genes renders EST-derived markers highly transferable to closely related species. To that end, testing of 812 EST-derived markers from other grass species on tef revealed successful amplification of approximately 30% of the markers, and markedly EST-SSRs developed from sorghum and pearl millet (both belonging to subfamily *Panicoideae* which is taxonomically close to the subfamily of tef, *Chloridoideae*, in the grass family; Figure 9.1) showed a transferability rate higher than 80% on tef (Zeid *et al.*, 2010).

More recently, tef genomic SSR markers (gSSRs) have been developed and thereby alleviated the problem of low rate of polymorphism of EST-SSRs (Zeid *et al.*, 2011). The genomic libraries were enriched for (AG) and (AC) dinucleotide repeats, and in tef the (AG) repeat occurs at much higher frequency (=20 repeats/Mbp) as compared to other grass species such as barley, rice and wheat (=9 repeats/Mbp). A total of 561 gSSRs were developed and 48% of the markers showed polymorphism on *E. tef* (Kaye Murri) and *E. pilosa* (Zeid *et al.*, 2011). This indicates that the rate of polymorphism of gSSRs is twice as high as the EST-derived markers in tef (24%) (Yu, Kantety *et al.*, 2006). Presently, there are more than 1500 locus-specific tef markers available for use in genetic studies (Table 9.8).

Table 9.8 Summary of validated locus-specific markers in tef.

Marker	Clones/sequences	No. of markers	Originating species	Reference
RFLP	cDNA	151	Tef	(Zhang *et al.*, 2001)
RFLP	cDNA	133	Barley, oat, rice	(Zhang *et al.*, 2001)
EST-SSR	EST	106	Tef	(Yu, Kantety *et al.*, 2006)
EST-SSR	EST	770	Rice, wheat, tall fescue, rye	(Zeid *et al.*, 2011)
SNP/INDEL	EST	18	Tef	(Zeid *et al.*, 2010)
gSSR	Genomic SSR	561	Tef	(Zeid *et al.*, 2011)
gSSR	Genomic SSR	47	Tall fescue	(Zeid *et al.*, 2011)

9.7.3.2.2 Molecular Genetic Diversity

Different types of markers have been used to study genetic diversity in tef and related wild *Eragrostis* species. Earlier works using AFLP generally showed low level of polymorphism (18%) in tef with Jaccard similarity coefficient ranging 84–96% for RAPD and 73–99% for AFLP (Ayele *et al.*, 1999; Bai, Tefera *et al.*, 1999; Ayele and Nguyen, 2000) and RAPD (Bai *et al.*, 2000). Later, using inter-simple sequence repeat (ISSR) markers, Assefa and colleagues noted relatively high diversity with the Jaccard similarity coefficient ranging from 26–86% (Assefa *et al.*, 2003).

Zeid and colleagues made a more prolific genetic-diversity study using molecular markers (Zeid *et al.*, 2012). In this study, assessments were made on the genetic diversity and relationships among 326 cultivated tef accessions, 13 wild relatives, and four commercial tef varieties from the United States using 39 SSR markers, 26 of which were flanking QTL intervals for yield, lodging index- and stem–strength-related traits. In addition, in this study the allelic diversity was estimated and markers associated with agronomic traits were identified in the tef germplasm collections. Forty-seven loci were sufficient to differentiate 80.8% of the tef accessions. In contrast to earlier studies, genetic similarity estimates ranged from 0.21 to 0.99, indicating a high level of genetic diversity. In the course of this investigation, it was discovered that seed admixture is a serious problem affecting the integrity of almost all released tef varieties. Association was observed between the marker CNLTs 540 and seed weight/plant. The majority of the alleles detected were present in tef breeding lines and varieties suggesting that tef breeders have been using a broad range of germplasm in their programmes. The markers documented in this study will be useful to identify and verify hybrids from crosses between promising lines that lack morphological differences, an approach that was never attempted before in the tef-breeding programmes. Overall, Assefa and colleagues reviewed genetic diversity studies in tef using molecular markers (Assefa, Yu *et al.*, 2011; Assefa *et al.*, 2013).

9.7.3.2.3 Genetic Linkage Map

In attempts to develop molecular marker for marker-assisted breeding, five linkage maps have so far been constructed using both intra- and inter-specific recombinant inbred lines as mapping populations.

i) The first linkage map was constructed using 211 AFLP loci with 85 F_8 recombinant inbred lines (RILs) of the intra-specific cross Kaye Murri × Fesho (Bai, Tefera *et al.*, 1999). This map consisted of 25 linkage groups as opposed to the gametic number for the species of 20 chromosomes, and covered 2149 cM of the genome while a polymorphism level of only 6.1% was detected between the parental lines.
ii) The second linkage map, which is a RFLP-based map, was constructed by Zhang and colleagues on the basis of 116 RILs from the inter-specific cross *E. tef* (cv. Kaye Murri) × *E. pilosa* (30-5) using tef cDNA probes and heterologous cDNA probes from rice, barley and oats (Zhang *et al.*, 2001). This map comprised 149 cM of the tef genome based on 149 RFLP loci distributed among 20 linkage groups. As such, the RFLP map showed better genome coverage of 88% compared with the previous AFLP map which had genome coverage of 81%.
iii) The third linkage map was developed by Chanyalew and colleagues based on 124 F_8 RILs from the inter-specific cross *E. tef* (DZ-01-2785) × *E. pilosa* (30-5) using a combination of different markers including AFLP, ISSR, rice EST-SSR and tef-specific

EST-SSR markers (Chanyalew *et al.*, 2005). This map spanned 78.8% of the tef genome.

iv) The fourth linkage map was developed by Yu and colleagues using 94 F_9 RILS from the cross Kaye Murri × *E. pilosa* (acc. 30-5)] (Yu, Kantety *et al.*, 2006; Yu *et al.*, 2007). Genetic markers applied were RFLP, IFLP, EST-SSR and ISSR. The map covered 2082 cM of the tef genome and consisted of 21 linkage groups.

v) The fifth linkage map was made by Zeid and colleagues using 151 F_9 RILS from Kaye Murri × *E. pilosa* (acc. 30-5) cross (Zeid *et al.*, 2010). The four genetic markers indicated above were used in this study. The map covered 1277 cM of the genome and comprised 30 linkage groups.

9.7.3.2.4 QTL Mapping

Some attempts have been made towards mapping of QTL for important agronomic traits especially lodging, yield and yield-related traits (Chanyalew *et al.*, 2005; Yu *et al.*, 2007; Zeid *et al.*, 2011). Using recombinant inbred lines from the inter-specific cross *E. tef* (cv. Kaye Murri) × *E. pilosa* (30-5), Yu and colleagues phenotyped 22 agronomic traits including eight yield-related and 14 morphological traits at eight locations for two growing seasons (Yu *et al.*, 2007). In the genotyping with 94 RILs using composite interval mapping and a linkage map incorporating 192 loci, a total of 99 QTL for 19 traits were identified on 15 of the 21 linkage groups with the phenotypic variances ranging from 11 to 34%. Clusters of more than five QTL for various traits were identified on seven linkage groups, and the largest cluster of 10 QTL was noted on LG8 and eight of these were for yield or yield-related traits suggesting linkage or pleiotropic effects of loci. A total of 12 QTL on nine linkage groups were identified for grain yield. Of the total QTL, 31% were observed in multiple environments, and two of the yield QTL were consistent across all agro-ecological zones. There were 25 two-way interactions of loci to detect potential epistasis identified and 75% of the interactions were derived from grain and shoot biomass yield. For about 29% of the QTL, the alleles from the wild relative *E. pilosa* had a beneficial effect indicating the potentials of introgressing beneficial genes from the wild *Eragrostis* species.

In general, for use in marker-assisted selection (MAS) tef breeding, the QTL mapping ventures so far indicated the need for further works, and validation and confirmation especially for those QTL that have multi-QTL regions, QTL identified across multiple environments, and QTL having high phenotypic variances.

Zhang and colleagues mapped 149 loci of which nearly 40% were derived from rice, barley and oat, and all were previously mapped in rice (Zhang *et al.*, 2001). The alignment of the RFLP tef map with that of the rice genome depicted a number of syntenic chromosomal fragments between tef and rice, and the gene orders between the two crops were mostly collinear.

9.7.3.2.5 In-vitro Regeneration

In vitro regeneration, or plant tissue culture, is an asexual method of propagation to produce clones in large quantities from a starting material called explant. An efficient *in vitro* regeneration system is necessary for the genetic improvement of the crop which includes mutation breeding, somatic hybridisation, double haploid development and genetic transformation. In the last two decades, diverse *in vitro* regeneration studies have been

investigated in tef using a variety of explants, tef cultivars and techniques (Bekele, 1995; Bekele *et al.*, 1995; Mekbib *et al.*, 1997; Kebebew *et al.*, 1998; Gugsa *et al.*, 2006, 2009; Ishikawa *et al.*, 2010; Plaza-Wüthrich and Tadele, 2012, 2013). Immature embryos were shown to be a very suitable explant for *in vitro* regeneration (Plaza-Wüthrich and Tadele, 2013). However, the efficiency regeneration is mainly dependent on the type of genotype. Using immature embryo technique, over 80% of explants from the natural tef accession *Manyi* formed somatic embryogenesis while only 10% from the improved variety called *Tsedey* (Plaza-Wüthrich and Tadele, 2013). The proportions of explants developing into plantlet were also significantly low for *Tsedey* compared to *Manyi*. Hence, it is important to first study regeneration efficiency of diverse tef ecotypes or varieties before embarking large-scale study on a single or limited numbers of germplasm.

9.7.3.2.6 Genetic Transformation

Plant transformation is commonly done using the *Agrobacterium* and the particle or microprojectile bombardment method. Mekbib and colleagues evaluated the ability of diverse *Agrobacterium* strains to attach to tef explants from mature embryos, mature seeds, seedlings, leaf base segment and callus tissues (Mekbib *et al.*, 2001). According to them, *Agrobacterium* was able to attach to the surface of all types of explants although the intensity of attachment was significantly different among the explants; the lowest being from mature seeds. Among three *Agrobacterium* strains investigated by Plaza-Wüthrich and Tadele, LBA4404 and EHA105 were more efficient or virulent in transient tef transformation compared to GV3101 (Plaza-Wüthrich and Tadele, 2013). Stable transformation in tef was recently reported using GA inactivating gene under the control of triple 35S promoter (Gebre *et al.*, 2013). According to the authors, despite inconsistencies in some results, semi-dwarf plants with reduced level of endogenous GA were obtained.

Particle bombardment using reporter gene under the control of different promoters was studied. Mengiste revealed transient expression of the reporter GUS gene using 35S promoter in suspension culture cells, callus tissues and zygotic embryos of tef (Mengiste, 1991). However, Plaza-Wüthrich and Tadele observed equal level of transient expression of GUS for three promoters (ubiquitin, actin and double 35S) in tef callus derived from immature embryos (Plaza-Wüthrich and Tadele, 2013).

9.7.3.2.7 High-Throughput Techniques

High-throughput techniques such as TILLING and eco-TILLING are attractive methods for tef improvement since the products from these techniques do not require biosafety regulations as they are free of transgene. TILLING is a reverse genetic technique which uses traditional mutagenesis followed by high-throughput mutation detection. While TILLING is applied to the induced mutagenized population, EcoTILLING is used in the natural population. The TILLING technique has been implemented on ethyl methane-sulfonate (EMS) mutagenized tef population at the University of Bern, Switzerland, mainly to develop semi-dwarf and lodging-tolerant cultivars (Tadele *et al.*, 2010; Esfeld, Plaza-Wüthrich *et al.*, 2013; Esfeld, Uauy *et al.*, 2013b). Since tef is a tetraploid, mutation in a single genome might not result in the expected phenotype, hence double crossing were made between candidate lines harbouring point mutation in the two copies of tef genome. The crossing and field-testing of the breeding materials are done at the experimental site of the Debre Zeit Agricultural Research Center in Ethiopia. Unlike the above technique, which uses a LiCOR machine to detect point

mutations, next-generation sequencing was also applied to validate six mutations in EMS mutagenized tef population (Zhu *et al.*, 2012).

9.7.3.2.8 Genome Sequencing of tef

The tef genome was made due to the following reasons:

i) The sequence information of any gene is elucidated; hence facilities in primer design and cloning of genes.
ii) It is useful in marker-assisted breeding especially in developing genetic markers such as simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs).
iii) Since tef has several desirable agronomic, nutritional and health-related properties, availability of sequence of the genes controlling these traits will shed light on their pathways and mechanisms and allow them to be isolated in the laboratory.
iv) Since the tef genome is the first to be sequenced from the sub-family Chloridoideae (Figure 9.1), information from the sequence is useful for researchers working on finger millet (Chloridoideae sub-family) or other closely related crops.

The first whole-genome sequence of tef which was recently published contains 672 Mbp representing 87% of the total tef genome size (Cannarozzi *et al.*, 2014).

9.7.4 Variety Development and Dissemination

9.7.4.1 Improved Tef Varieties

To date, a total of 35 varieties have been released in Ethiopia through the National Agricultural Research System (MoA, 2014) (Table 9.9). Of these, 21 varieties have been

Table 9.9 Improved tef varieties in Ethiopia developed through selection and hybridization techniques.

Name		Year of release	Releasing centre	Days to mature	Seed colour	On-farm yield ($t\,ha^{-1}$)
Common name	Variety name					
Using selection techniques						
Asgori	DZ-01-99	1970	Debre Zeit	80–130	Brown	1.8–2.2
Enatit	DZ-01-354	1970	Debre Zeit	85–100	Pale white	2–2.4
Magna	DZ-01-196	1978	Debre Zeit	80–113	Very white	1.6–2
Wellenkomi	DZ-01-787	1978	Debre Zeit	90–130	Pale white	2–2.4
Dukem	DZ-01-974	1995	Debre Zeit	75–137	White	2–2.7
Holetta Key	DZ-01-2053	1999	Holetta	84–112	Brown	1.2–2.2
Ambo Toke	DZ-01-1278	2000	Holetta	86–116	Brown	1.5–2.2
Gerado	DZ-01-1281	2002	Debre Zeit	73–95	White	1.6–2.2
Key Tena	DZ-01-1681	2002	Debre Zeit	84–93	Brown	1.6–2.2
Koye	DZ-01-1285	2002	Debre Zeit	104–118	White	1.6–2.2
Gola	DZ-01-2054	2003	Sirinka	82–90	Pale white	1.2–1.6

Table 9.9 (Continued)

Name						
Common name	Variety name	Year of release	Releasing centre	Days to mature	Seed colour	On-farm yield (t ha^{-1})
Ajora	PGRC/E 205396	2004	Areka	89–98	Pale white	1.6–1.8
Dega Tef	DZ-01-2675	2005	Debre Zeit	112–123	Pale white	1.4–2.2
Dima	DZ-01-2423	2005	Adet	92–106	Brown	1.6–2.1
Genete	DZ-01-146	2005	Debre Zeit	75–87	Pale white	1.2–1.6
Gimbichu	DZ-01-899	2005	Debre Zeit	118–137	Pale white	1.6–2
Yilmana	DZ-01-1868	2005	Adet	98–110	Pale white	1.7–2
Zobel	DZ-01-1821	2005	Sirinka	72–87	Pale white	1.2–1.6
Guduru	DZ-01-1880	2006	Bako	95–120	White	1.6–2
Mechare	Acc. 205953	2007	Sirinka	78–85	Pale white	1.4–1.8
Etsub	DZ-01-3186	2008	Adet	95–105	White	1.9–2.4
Kena	23-Tafi-Adi-72	2008	Bako	98–124	White	1.9–2.4
Werekiyu	Acc. 214746A	2014	Sirinka	94	White	
Using hybridisation technique						
Melko	DZ-Cr-82	1982	Debre Zeit	112–119	White	1.6–2
Menagesha	DZ-Cr-44	1982	Debre Zeit	95–140	White	1.8–2.2
Tsedey	DZ-Cr-37	1983	Debre Zeit	82–90	White	1.4–2.2
Gibe	DZ-Cr-255	1993	Debre Zeit	114–126	White	1.6–2.2
Ziquala	DZ-Cr-358	1995	Debre Zeit	76–138	White	2–2.7
Amarach	Ho-Cr-136	2006	Debre Zeit	63–87	Pale white	1.4–2.2
Quncho	DZ-Cr-387 RIL355	2006	Debre Zeit	86–151	Very white	1.8–2.6
Gemechis	DZ-Cr-387 RIL127	2007	Melkassa	67–90	Very white	1.6–1.8
Simada	DZ-Cr-285 RIL295	2009	Debre Zeit	75–87	White	1.6–2.4
Lakech	DZ-Cr-387 RIL273	2009	Sirinka	87–92	Very white	1.8–2
Boset	DZ-Cr-409 RIL 50d	2012	Debre Zeit	75–86	Very white	1.8–2.4
Kora	DZ-Cr-438 RIL 133B	2014	Debre Zeit	110–117	Very white	1.8–2.6

Source: Updated from MoA (2014).

released by Debre Zeit Agricultural Research Center, while 14 were released by other six centres. Of the total number of varieties released to date, only 12 varieties were developed through hybridisation, while the remaining 23 were developed using pure-line selection technique from the land races.

Four of the released varieties, namely *Magna* (DZ-01-196), *Enatite* (DZ-01-354), *Dukem* (DZ-01-974) and *Quncho* (DZ-Cr-387 RIL355), are widely adopted by farmers in areas with optimum rainfall in different parts of the country, while the relatively early-maturing varieties such as *Tsedey* (DZ-Cr-37), Gemechis (DZ-Cr-387 RIL127),

Simada (DZ-Cr-285 RIL295) and *Boset* (DZ-Cr-409 RIL50d) are recommended for terminal low moisture stress areas.

9.7.4.2 Genetic Gain

As shown in Figure 9.4, significant increase in both the area and production of tef has been achieved in the last 20 years. During the same period, the national tef yield has doubled from less than 0.8 t ha^{-1} in 1994 to 1.5 t ha^{-1} in 2013 (CSA, 2014).

Overall, the genetic gain study revealed that the grain yield potential of tef has not reached a plateau in Ethiopia. Thus, development of higher-yielding varieties should continue to increase tef grain yields if past trends are indicative of the future. In order to see the impact in the genetic progress research of tef, it is imperative to undertake large-scale popularisation of the released varieties, where the end-user farmers can see the impact of such improved varieties through demonstrations and scaling up activities, such as improved management practices.

9.7.4.3 Adoption of Improved Varieties

A number of improved tef varieties were developed and disseminated to farmers along with optimum management practices; but no systematic and comprehensive studies have been made to investigate the rate and intensity of adoption by smallholder farmers. In spite of this, the available evidences indicate that several improved tef varieties have been well adopted by farmers in the major growing regions. Until recently, the varieties such as *Enatite*, *Tsedey* and *Magna* were widely adopted in many areas (Tefera, Kelemework *et al.*, 2001; Beyene, 2008), and currently, the new tef variety called *Quncho* is rapidly expanding to most of the tef-growing areas of the country.

An adoption study conducted in East and West Shewa Zones showed that about 20% of the farmers grow improved tef varieties which accounted for 16% of the total tef acreage (Dadi, 1998). The adoption rate of fertiliser was higher than that of improved tef varieties. Fertilisers were applied on 93% of the total area allocated for tef. According to Beyene (Beyene, 2008), 66% of the total tef growers adopted improved varieties, while 20% of the total tef acreage was planted with improved varieties.

An evaluation of the national extension programme in 1999 showed that 15% of the farmers adopted the full package of improved tef technologies which consisted of varieties, fertiliser and herbicides, while 58% of them applied both fertiliser and herbicide on the local tef cultivar (Tefera, Kelemework *et al.*, 2001). A study in Lume and Minjar-Shenkora Districts unveiled that 84% of the tef farmers grow *Magna* while only 5% of the farmers grew *Quncho* in the 2008/09 cropping season (Ferede, 2012). These two varieties accounted for 71% and 4% of the total tef acreage in Lume and Minjar-Shenkora Districts, respectively.

At the national level, the use of inputs, particularly improved seed, is very low (Figure 9.4c). However, fertilisers and herbicides are widely applied in tef fields although the figures were not consistent. On the contrary, the adoption of fertiliser application is considerably high in tef than in the other cereal crops. About 45% of tef producers apply fertiliser on their farms, and this accounts for about 40% of the total tef area in the country.

It is important to note that data on tef technology adoption are lacking as compared to cereal crops such as wheat and maize. In addition, those little adoption studies on tef have some limitations. Some of these limitations are: (i) some of the studies were not

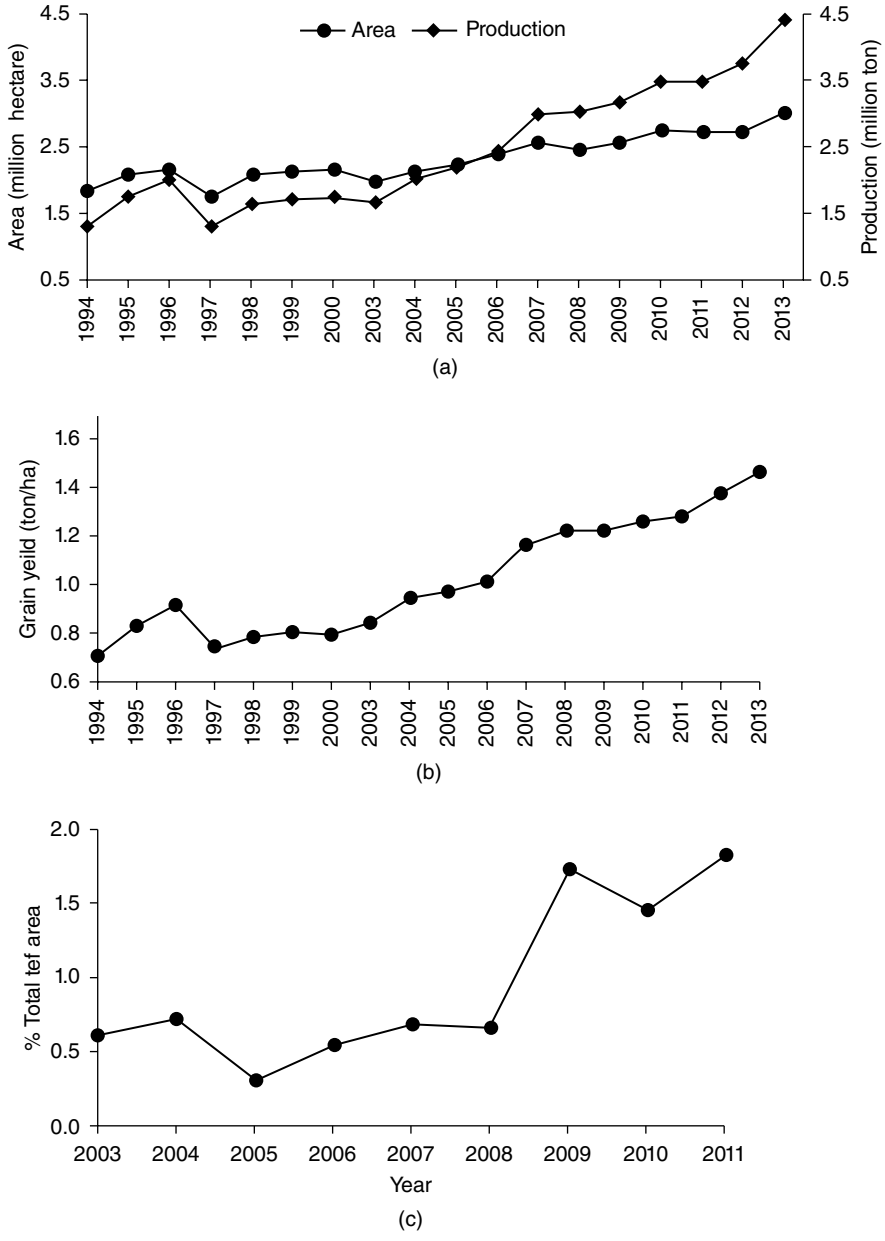

Figure 9.4 The trend in the cultivation, production and use of improved tef seed in Ethiopia. (a) Both the acreage and total production of tef were significantly increased; (b) the productivity of tef raised from only 0.7 t ha^{-1} in 1994 to 1.5 t ha^{-1} in 2013; (c) the proportion of tef farmers using improved seeds are extremely low. Adapted from (CSA, 2014).

properly designed, and hence, lack rigorous analysis; (ii) the outcomes of most of the studies do not show the adoption of a particular variety rather adoption of a group of varieties; (iii) sometimes data from different sources are contradictory and (iv) most of those limited studies were very fragmented to impart any policy implications. Additional

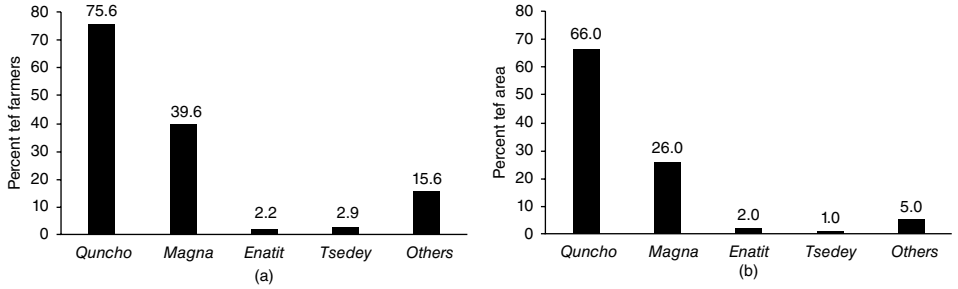

Figure 9.5 Adoption of improved tef varieties in three districts in the Central Highlands of Ethiopia in year 2011. (a) measured by the proportion of tef farmers growing improved varieties; (b) measured by the proportion of area allocated to improved tef varieties.

challenges related to tef adoption studies are that: (i) farmers often refer seeds saved from previous harvest or acquired through exchange from other farmers as local or unimproved seeds even though the seeds are actually improved ones; (ii) sometimes it is also difficult to identify the specific variety on farmers' fields due to seed contamination problem and (iii) most tef varieties have long and difficult to recall names. These complex names were retained during the release and dissemination of the improved tef varieties.

More recent adoption and impact-assessment studies of improved tef technologies in three Weredas (namely Minjar Shenkora, Ada and Lume) in the Central highlands of Ethiopia revealed that *Quncho* is the most widely adopted improved variety followed by *Magna*. Within the study area, *Quncho* variety was adopted by 76% while *Magna* by 40% of the respondent farmers (Figure 9.5a). By comparing this result with that of a similar survey conducted in the same area in 2008, the adoption of *Quncho* far exceeds expectation. For instance, its adoption rate has increased from 5% in 2008 to 76% in 2011. On the contrary, the adoption rate of *Magna* has dropped from 84% in 2008 40% in 2011.

In terms of intensity of adoption, which is measured by the proportion of total tef area allocated to a particular variety, *Quncho* comes first by covering 66%, while *Magna* accounted for 26% of the total tef acreage (Figure 9.5b). Similar to that of the adoption rate, the intensity of adoption for *Quncho* has increased from 4% in the 2008 to 66% in 2011. On the contrary, the adoption intensity of *Magna* has dropped from 71 to 26% in the respective years.

9.8 Crop and Pest Management

9.8.1 Land Preparation and Planting

The minute size of tef seeds requires a very fine, flat and smooth seedbed (Ebba, 1969). Conventionally, farmers plow their land before sowing the seeds, depending on the soil type and weed infestation conditions. The traditional plow known as '*maresha*' is largely used with oxen for the tillage operations, although horses or donkeys are used rarely. In spite of the conventional practice, recently it has been shown that tef can be grown

with reduced tillage involving pre-emergence application of roundup at 2 l ha^{-1} 2 weeks before sowing, and then practising tillage only once at the time of sowing.

Farmers in some areas also practise packing of the seedbeds before sowing using trampling with animals in the anticipation of facilitating good contact of seeds with the soil, avoiding and reducing weed infestation. However, experimental results at Debre Zeit showed that apart from facilitating germination and early stand establishment, packing did not significantly increase yields (DZARC, 1989).

Conventionally, farmers sow tef by hand-broadcasting of the seeds on the surface of the soil. Experimental results have indicated that sowing in rows, if not in increasing productivity, has agronomic advantages of easing up subsequent cultural operations such as weed control and harvesting, and facilitating efficient use of fertilisers by applying as row-side bands. However, for practical use by farmers, there has to be a user-friendly solution, such as the development of appropriate smallholder row-sowing implements.

Against the conventional farmers' practice of using 40–55 kg ha^{-1}, the recommended seed rate with the hand broadcasting method has been 25–30 kg ha^{-1}. According to the experiment conducted in Southern Ethiopia, a seed rate of 10–15 kg ha^{-1} was economically and technically feasible for tef (Laekemariam *et al.*, 2012).

9.8.2 Fertiliser Application

The recommended fertiliser rates for tef grown on different soil types ranges for nitrogen fertiliser from 40 kg ha^{-1} N for red soils and Nitosols to 75 kg ha^{-1} N for grey soils and black soils, while for phosphorus, it ranges from 50–60 kg ha^{-1} P_2O_5 for the different soil types (NFIU, 1993). However, the blanket fertiliser recommendation for tef for the major tef-growing areas has been 60 kg ha^{-1} N and 26 kg ha^{-1} P_2O_5 for heavy clay soils predominantly Vertisols and 40 kg ha^{-1} N and 26 kg ha^{-1} P_2O_5 for light soils. Commercial fertilisers in Ethiopia have so far been applied in the form of DAP (18% N and 46% P_2O_5) and Urea (46% N), and accordingly the blanket recommendation mentioned in the preceding text especially for the clay soils, has for practical purposes from the size of the packaging (the least package being 50 kg ha^{-1}) been approximated to 100 kg ha^{-1} DAP and 100 kg ha^{-1} urea.

The amount of fertilisers for tef grown on fields that have been previously used for legumes such as chickpeas, can be reduced by half. Moreover, it is recommended that the DAP fertiliser is applied at the time of sowing, while the urea for supplying the remaining of the recommended nitrogen rate should be applied at about the tillering stage (4–5 weeks after emergence) of the crops (Mamo *et al.*, 2001; Erkossa, 2003).

9.8.3 Important Weeds and Their Management

Weed management has remained one of the most back-breaking, labour-intensive and time-consuming operations in tef husbandry. The major weeds of tef recorded in Ethiopia have been listed in a weed research review in Ethiopia (Fessehaie and Tadele, 2001; Zewdie and Damte, 2013).

Generally, annual grass weeds pose the greatest challenge because of their morphological similarity to the tef crop and their extended period of germination that is difficult to control by manual hand weeding (Fessehaie and Tadele, 2001). These authors, however, also listed other problematic weeds in tef that include the parasitic witch weed, *Striga hermonthica* (Del.), the introduced alien invasive weed commonly known

as congress weed, *Parthenium hyterophorus* L., field bind weed, *Convolvulus arvensis*, and other noxious weeds. The latter include weeds with the following characteristics:

i) Those irritating to touch and interfere with weeding or harvesting operations thereby increasing weeding and/or harvesting time and costs (such as *Argemone mexicana*, *Xanthium spinosum*, *X. strumarium*, *Oxygonum sinuatum* and *Tribulus terristeris*);
ii) Those posing the biggest challenge because of their similarity to tef and extended period of germination (such as *Phalaris paradoxa* and *Setaria pumila*);
iii) Weeds that reduce the quality of tef grains harvested (such as *Phalaris paradoxa*, *Setaria pumila*, *Plantago lanceolata*, *Amaranthus* spp., *Guizotia scabra* and *Snowdenia polystachya*);
iv) Hard-to-pull-out perennial weeds (such as *cyperus esculentus*, *C. rotundus and Rumex bequarttii*).

Whilst the critical period of weed completion for tef is 3–4 weeks and 6–7 weeks post-emergence of the crops, a single application of post-emergence selective herbicides Starane M 64%b EC, Derby 175 SC, Mustang and 2,4-D Amine Salt 72% S about 25–30 days after crop emergence has proved effective in controlling the dominant broad-leaf weeds in tef, thereby giving significant yield increase, and this is then followed by twice hand weeding and the check with a single 2,4-D Amine Salt 72% SL application (Zewdie and Damte, 2013). These authors also maintained that one supplementary hand weeding in addition to the single post-emergence application of herbicides may be needed depending on the weed flora infestation and effectiveness of the herbicides in order to maximise yields.

9.8.4 Important Insect Pests and Their Management

The most important, generally sporadic ones in various tef-growing areas are, tef grasshopper (*Ailopus longicornis*), tef shoot fly (different species), red tef worm (*Mentaxya ignicollis*), Wello bush cricket (*Decticoides brevipennis* Ragge.), termites (*Macrotermus subhyalinus* and *Odontotermus* spp.) and black tef beetle (*Erlangerius niger*) (Damte, 2013).

The majority of the research on tef insect pest management to-date focussed on the identification of appropriate insecticides, to the exclusion of other management aspects such as cultural control (e.g. sowing date, seed rate, fertiliser rate, host plant resistance), biological control, and ecological methods (Damte, 2013).

9.8.5 Important Diseases and Their Management

Compared to the other cereals, tef suffers less from disease epidemics, but the significance of diseases should not be underestimated. More than 24 fungal pathogens and two nematodes have been reported to cause diseases on tef (Amogne *et al.*, 2001). Although most diseases are at least sporadically important, the major diseases are: tef rust (*Uromyces eragrostidis* Tracy), head smudge (*Heminthosporium miyakei* Nisikado) and damping-off caused by *Drechslera* spp. and *Epicoccum nigrum* Link (Bekele, 1986).

Tef rust is widely distributed in major tef-growing areas of Ethiopia. The disease, which usually appears at the post-flowering stage of the crop, was earlier reported to cause an average yield loss of 10–25% (Ebba, 1969) while in more recent studies at Debre Zeit, losses were estimated at 10–41% (DZARC, 1994).

9.9 Future Prospects

Tef, as a localised crop of importance only in Ethiopia, has remained an 'orphan crop' that has survived without the help of scientific improvement endeavours, which are currently outstanding. With respect to donors, tef remained largely marginalised particularly until the mid-1990s when the national tef research and development started obtaining the sustained generous support of the McKnight Foundation Collaborative Crop Research Program. However, low productivity, lodging, minute size of the seeds and labour-intensiveness of the cultural practices, still remain the major threats of tef husbandry.

It is worth highlighting that, over the past few years, there has been an assertion by development partners that poor African countries with a number of neglected crops of localised importance, should shift their farming systems to more productive crops of global significance. However to date, this notion has no longer been an issue of debate, for it has been proven that agricultural development in these countries cannot be realised without due consideration of the neglected crops of supreme local importance like tef and *Enset* in Ethiopia. Indeed, it has now been ascertained that even under the circumstances where the amount of effort and attention afforded to these crops is disproportionately low, the outcomes, as demonstrated by the remarkable achievement of developing and releasing the popular *Quncho* tef variety (Assefa, Aliye *et al.*, 2011) are worth the investments. Hence, countries like Ethiopia should 'nurture' their neglected crops, and indeed the issue now is not whether or not to invest in these crops, but rather *how* to bring about the required substantial improvements by using modern scientific techniques, including biotechnology that have been used extensively in other crops around the world.

In spite of the varied challenges that require commensurate attention, there have been ample opportunities and prospects for tef improvement and development. These are outlined in the following text.

i) *Availability of diverse wealth of genetic resources*: The tef genetic resources harbour a tremendous diversity in phenologic, agronomic and morphologic traits, coupled with unexploited aspects in terms of nutritional, and biotic and abiotic stress-tolerance traits. The wealth of diversity in the species offers ample opportunities for genetic improvement of the crop and to develop varieties suitable for different agro-ecologies, cropping systems and purposes.
ii) *New insights in breeding and overall research approaches*: The developments in agricultural sciences have opened new insights into how to tackle technical improvements by employing coordinated multi-faceted strategies involving conventional breeding, modern techniques including genomics and *in vitro* cultures, and crop and soil and water management, food science and mechanisation.

With respect to breeding in particular, the strategies to be employed involve: participatory research approaches, germplasm collection/acquisition, intensification of the hybridisation programme through increasing the number of crosses, use of intra-specific and inter-specific crossing, harnessing potentials of wide crosses (divergent crossing), targeted crossing (i.e. ideotype crossing for lodging resistance and semi-dwarf types with reduced length of peduncles and basal culm internodes, and thick basal culm internodes).

Likewise, modern biotechnological approaches such as *in vitro* culture techniques (especially DH production), molecular markers and linkage maps, QTL analysis, comparative genomics (association mapping), high-throughput techniques (TILLING and

Eco-TILLING), genome sequence and annotation (functional genomics), MAS, genetic transformation and harnessing important tef genes, offer new avenues for hastening the genetic improvement of the crop.
Furthermore, the productivity and production of tef can be enhanced by the integration of improved management, crop protection and farm implements and machinery. These value-added practices would also be useful to enhance the utilisation of the crop. Overall, the broadening of research and development endeavours in these various aspects would open and further latitudes and opportunities.

iii) *Brighter prospects to improve tef research and development*: The long-standing belief that tef is not amenable to improvement is now over. For the first time in history, the Ethiopian government has realised that transformation of the Ethiopian agriculture is impossible without considering its important local crops, most notably tef. The first thing to be aligned is the national recognition of tef in the priority agricultural commodities.

In line with the presently improved national attention, other areas are entailed including the development and release of the tef value-chain strategy, initiation of focus on the national tef-research capability, and improvements in the seed and extension system. In addition, there has been improved international attention especially by donors, namely the McKnight Foundation Collaborative Crop Research Program that has provided sustainable support to the national tef research project since the mid-1990s with commendable achievements. The partnership between the University of Bern in Switzerland and the Ethiopian Institute of Agricultural Research was key to develop semi-dwarf and lodging tolerant tef varieties which are at the present time at the advanced stage of field-testing before releasing to the farming community (Tadele, 2013).
Apart from the need for enhanced national support, the painstaking ventures of the tef improvement generally require enhanced external inputs and support in terms of collaboration, technical and knowledge support, financing and facilities. Furthermore, the increasing global interests in tef in recent years due to its gluten-free nature, health and performance food and noble stress-tolerance traits (such as drought resistance), promote attention, particularly in light of climate change.

References

Abate, E., Hussein, S., Laing, M. and Mengistu, F. (2013) Quantitative responses of tef [*Eragrostis tef* (Zucc.) Trotter] and weeping love grass [*Eragrostis curvula* (Schrad.) Nees] varieties to acid soil. *Australian Journal of Crop Science*, **7**, 1854–1860.

Admas, S. and Dagne, K. (2008) Meiotic behaviour of *Eragrostis tef* and *Eragrostis pilosa*. *African Crop Science Journal*, **16**, 237–241.

Alemu, D., Mwangi, W., Nigussie, M. and Spielman, D.J. (2007) An analysis of maize seed production and distribution systems in Ethiopia's Rift Valley, Research Report 72 Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia.

Amogne, S., Kassaye, Z. and Bekele, E. (2001) *Tef pathology research in Ethiopia*, EIAR, Addis Ababa, Ethiopia.

Asfaw, K.G. and Dano, F.I. (2011) Effects of salinity on yield and yield components of tef [*Eragrostis tef* (Zucc.) Trotter] accessions and varieties. *Current Research Journal of Biological Sciences*, **3**, 289–299.

Assefa, K., Aliye, S., Belay, G. *et al.* (2011) Quncho: the first popular tef variety in Ethiopia. *International Journal of Agricultural Sustainability*, **9**, 25–34.

Assefa, K., Chanyalew, S. and Metaferia, G. (2013) *Conventional and molecular tef breeding*, EIAR-University of Bern, Bern, Switzerland.

Assefa, K., Ketema, S., Tefera, H. *et al.* (1999) Diversity among germplasm lines of the Ethiopian cereal tef [*Eragrostis tef* (Zucc.) Trotter]. *Euphytica*, **106**, 87–97. doi: 10.1023/A:1003582431039

Assefa, K., Ketema, S., Tefera, H. *et al.* (2000) Trait diversity, heritability and genetic advance in selected germplasm lines of tef [*Eragrostis tef* (Zucc.) Trotter]. *Hereditas*, **133**, 29–37.

Assefa, K., Merker, A. and Tefera, H. (2003) Inter simple sequence repeat (ISSR) analysis of genetic diversity in tef [*Eragrostis tef* (Zucc.) Trotter]. *Hereditas*, **139**, 174–183.

Assefa, K., Tefera, H., Merker, A. *et al.* (2001) Quantitative trait diversity in tef [*Eragrostis tef* (Zucc.) Trotter] germplasm from Central and Northern Ethiopia. *Genetic Resources and Crop Evolution*, **48**, 53–61.

Assefa, K., Yu, J.K., Zeid, M. *et al.* (2011) Breeding tef [*Eragrostis tef* (Zucc.) trotter]: conventional and molecular approaches. *Plant Breeding*, **130**, 1–9.

Ayele, M., Dolezel, J., VanDuren, M. *et al.* (1996) Flow cytometric analysis of nuclear genome of the Ethiopian cereal Tef [*Eragrostis tef* (Zucc.) Trotter]. *Genetica*, **98**, 211–215.

Ayele, M. and Nguyen, H.T. (2000) Evaluation of amplified fragment length polymorphism markers in tef, *Eragrostis tef* (Zucc.) Trotter, and related species. *Plant Breeding*, **119**, 403–409.

Ayele, M., Tefera, H., Assefa, K. and Nguyen, H.T. (1999) Genetic characterization of *Eragrostis* species using AFLP and morphological traits. *Hereditas*, **130**, 33–40.

Bai, G., Tefera, H., Ayele, M. and Nguyen, H.T. (1999) A genetic linkage map of tef [*Eragrostis tef* (Zucc.) Trotter] based on amplified fragment length polymorphism. *Theoretical and Applied Genetics*, **99**, 599–604.

Bai, G.H., Ayele, M., Tefera, H. and Nguyen, H.T. (1999) Amplified fragment length polymorphism analysis of tef [*Eragrostis tef* (Zucc.) trotter]. *Crop Science*, **39**, 819–824.

Bai, G.H., Ayele, M., Tefera, H. and Nguyen, H.T. (2000) Genetic diversity in tef [*Eragrostis tef* (Zucc.) Trotter] and its relatives as revealed by Random Amplified Polymorphic DNAs. *Euphytica*, **112**, 15–22.

Baye, K. (2014) Teff: nutrient composition and health benefits, ESSP Working Paper 67, Washington, D.C. and Addis Ababa, Ethiopia.

Bekele, E. (1986) A review of research on diseases of barley, tef and wheat in Ethiopia. In Proceedings of the First Ethiopian Crop Protection Symposium, February 4–7, 1985, EIAR, Addis Ababa, Ethiopia.

Bekele, E. (1995) Electric field mediated fusion of *Eragrostis tef* and Sorghum bicolor protoplasts and their electroporation conditions. *Hereditas*, **123**, 199–203.

Bekele, E., Klock, G. and Zimmermann, U. (1995) Somatic embryogenesis and plant regeneration from leaf and root explants and from seeds of *Eragrostis tef* (Gramineae). *Hereditas*, **123**, 183–189.

Bekele, E. and Lester, R.N. (1981) Biochemical assessment of the relationships of *Eragrostis tef* (Zucc) Trotter with some wild *Eragrostis* species (Gramineae). *Annals of Botany-London*, **48**, 717–725.

Belay, G., Tefera, H., Getachew, A. *et al.* (2008) Highly client-oriented breeding with farmer participation in the Ethiopian cereal tef [*Eragrostis tef* (Zucc.) Trotter]. *African Journal of Agricultural Research*, **3**, 22–28.

Belay, G., Tefera, H., Tadesse, B. *et al.* (2006) Participatory variety selection in the Ethiopian cereal tef (*Eragrostis tef*). *Experimental Agriculture*, **42**, 91–101.

Berhe, T. (1975) *A break-through in tef breeding techniques*, FAO, Rome, pp. 11–13.
Berhe, T. and Miller, D.G. (1978) Studies of ethephon as a selective male gametocide in tef. *Crop Science*, **18**, 35–38.
Berhe, T., Nelson, L.A., Morris, M.R. and Schmidt, J.W. (1989a) Inheritance of phenotypic traits in tef. 1. Lemma color. *Journal of Heredity*, **80**, 62–65.
Berhe, T., Nelson, L.A., Morris, M.R. and Schmidt, J.W. (1989b) Inheritance of phenotypic traits in tef. 2. Seed color. *Journal of Heredity*, **80**, 65–67.
Berhe, T., Nelson, L.A., Morris, M.R. and Schmidt, J.W. (1989c) Inheritance of phenotypic traits in tef. 3. Panicle form. *Journal of Heredity*, **80**, 67–70.
Berhe, T., Nelson, L.A., Morris, M.R. and Schmidt, J.W. (2001) *The Genetics of Qualitative Traits in Tef*, EIAR, Addis Ababa.
Beyene, H. (2008) Adoption of improved tef and wheat production technologies in crop-livestock mixed systems in Northern and Western Shewa Zones of Ethiopia, in *PhD Thesis*, Pretoria University, South Africa.
Cannarozzi, G., Plaza-Wuthrich, S., Esfeld, K. *et al.* (2014) Genome and transcriptome sequencing identifies breeding targets in the orphan crop tef (*Eragrostis tef*). *BMC Genomics*, **15**, 581.
Chanyalew, S., Assefa, K. and Metaferia, G. (2013) *Phenotypic and Molecular Diversity in Tef*, EIAR-University of Bern, Bern, Switzerland.
Chanyalew, S., Singh, H., Tefera, H. and Sorrels, M. (2005) Molecular genetic map and QTL analysis of agronomic traits based on a *Eragrostis tef* x *Eragrostis pilosa* recombinant inbred population. *Journal of Genetics and Breeding*, **59**, 53–66.
Chanyalew, S., Tefera, H. and Singh, H. (2009) Genetic variability, heritability and trait relationships in recombinant inbred lines of tef [*Eragrostis tef* (Zucc.) Trotter]. *Journal of Agriculture and Biological Sciences*, **5**, 474–479.
Costanza, S.H., Dewet, J.M.J. and Harlan, J.R. (1979) Literature-review and numerical taxonomy of *Eragrostis tef* (Tef). *Economic Botany*, **33**, 413–424.
CSA (2010) Agricultural Sample Survey 2009/10. Report on farm management practices (private peasant holdings, Meher Season), in *Statistical Bulletin 468*, Central Statistical Agency, Addis Ababa, Ethiopia.
CSA (2014) Agricultural sample survey for 2013/14, in Statistical Bulletin 532, Central Statistical Agency, Addis Ababa, Ethiopia.
Cufodontis, G. (1974) Enumeration Planetarium Aethopiae Spermatophyta, Bulletin du Jardin Botanique, Brussels.
D'Andrea, A. (2008) Tef (*Eragrostis tef*) in ancient agricultural systems of highland Ethiopia. *Economic Botany*, **62**, 547–566.
Dadi, L. (1998) Adoption and diffusion of agricultural technologies: case of East and West Shewa Zone, Ethiopia, in PhD Thesis, Manchester University.
Damte, T. (2013) Insect pest management research in tef, EIAR-University of Bern, Bern, Switzerland.
DZARC (1989) Annual Research Progress Report for 1988/89, Debre Zeit Agricultural Research Center, Debre Zeit, Ethiopia.
DZARC (1994) Annual Research Report for the period 1991/92, Debre Zeit Agricultural Research Center, Debre Zeit, Ethiopia.
Ebba, T. (1969) Tef (*Eragrostis tef*): The cultivation, usage, and some of its known diseases and insect pests, in Part I. Experiment Station Bulletin No 60, Dire Dawa, Ethiopia.
Ebba, T. (1975) Tef cultivars: morphology and classification, Addis Ababa University, College of Agriculture, Dire Dawa, Ethiopia.

ENS (1959) A Report by Inter-Departmental Committee on Nutrition for National Defense, Ethiopian Nutrition Survey (ENS), Addis Ababa, Ethiopia.

Erkossa, T. (2003) *Some site-specific soil and water management technologies in the central highlands of Ethiopia*, EIAR, Addis Ababa.

Esfeld, K., Plaza-Wüthrich, S. and Tadele, Z. (2013) TILLING as a high-throughput technique of tef improvement, EIAR-University of Bern, Bern, Switzerland.

Esfeld, K., Uauy, C. and Tadele, Z. (2013) Application of TILLING for Orphan Crop Improvement, in Biotechnology of neglected and underutilized crops (eds S.M. Jain and S.D. Gupta), Springer, Dordrecht, pp. 83–113.

Espelund, M., Bekele, E., Holst-Jensen, A. *et al.* (2000) A molecular genetic analysis of *Eragrostis tef* (Zucc.) Trotter: non-coding regions of chloroplast DNA, 18S rDNA and the transcription factor VP1. *Hereditas*, **132**, 193–202.

Ferede, S. (2012) Tef seed system in Minjar-Shenkora and Lume-Ejere weredas of East Shewa. I, EIAR, Addis Ababa.

Ferede, S. (2013) Technological change and economic viability in tef production, EIAR-University of Bern, Bern, Switzerland.

Fessehaie, R. and Tadele, Z. (2001) Weed research in Tef, EIAR, Addis Ababa.

Frankel, Q.H. and Brown, A.H.D. (1984) Current plant genetic resources: a critical appraisal, Oxford and IBH Publishing Co., New Delhi, India.

Gebre, E., Gugsa, L., Schluter, U. and Kunert, K. (2013) Transformation of tef (*Eragrostis tef*) by Agrobacterium through immature embryo regeneration system for inducing semi-dwarfism. *South African Journal of Botany*, **87**, 9–17.

Ghebrehiwot, H., Burgdorf, R., Hussein, S. and Laing, M. (2015) The efficacy of four gametocides for induction of pollen sterility in *Eragrostis tef* (Zucc.) Trotter. *African Journal of Biotechnology*, **14**, 774–780.

Gugsa, L., Belay, G. and Ketema, S. (2001) *The cytogenetics of tef*, EIAR, Addis Ababa.

Gugsa, L., Kumlehn, J., Tadesse, A. *et al.* (2009) Haploidy in tef gynogenesis androgenesis, in *Advances in Haploid Production in Higher Plants* (eds A. Touraev, P. Brain, S. Forster and M. Jain), Springer, Netherlands, pp. 265–284.

Gugsa, L., Sarial, A.K., Lorz, H. and Kumlehn, J. (2006) Gynogenic plant regeneration from unpollinated flower explants of *Eragrostis tef* (Zuccagni) Trotter. *Plant Cell Reports*, **25**, 1287–1293.

Hamilton, D.G. (1951) Culm, crown, and root development in oats, wheat and barley as related to lodging. *Scientia Agricola*, **31**, 266–315.

Hundera, F., Arumuganathan, K. and Baenziger, P. (2000) Determination of relative nuclear DNA content of tef [*Eragrostis tef* (Zucc.) Trotter] using flow cytometry. *Journal of Genetics and Breeding*, **54**, 165–168.

Hundera, F., Tefera, H., Assefa, K. *et al.* (1999) Genetic variability and correlation of morpho-agronomic characters in tef landraces. *Tropical Science*, **39**, 140–146.

Ingram, A.L. and Doyle, J.J. (2003) The origin and evolution of *Eragrostis tef* (Poaceae) and related polyploids: evidence from nuclear waxy and plastid rps16. *American Journal of Botany*, **90**, 116–122.

Ishikawa, T., Kamei, Y., Otozai, S. *et al.* (2010) High-resolution melting curve analysis for rapid detection of mutations in a Medaka TILLING library. *BMC Molecular Biology*, **11**, 70.

Jones, B.M.G., Ponti, J., Tavassoli, A. and Dixon, P.A. (1978) Relationships of Ethiopian Cereal Tef (*Eragrostis tef* (Zucc.) Trotter) – Evidence from Morphology and Chromosome-Number. *Annals of Botany-London*, **42**, 1369–1373.

Kantety, R.V., Graznak, E.V., Tefera, H. and Sorrells, M. (2001) *Comparative mapping in tef*, EIAR, Addis Ababa.

Kearsey, M. and Pooni, H.S. (1996) The genetical analysis of quantitative traits, Stanley Thornes (Publishers) Ltd., Cheltenham, UK.

Kebebew, A., Gaj, M.D. and Maluszynski, M. (1998) Somatic embryogenesis and plant regeneration in callus culture of tef, *Eragrostis tef* (Zucc.) Trotter. *Plant Cell Reports*, **18**, 154–158.

Kedir, K., Jones, B.M.G. and Mekonen, D. (1992) Determination of outbreeding percentage in *Eragrostis tef* . *SEBIL*, **4**, 19.

Ketema, S. (1983) Studies of lodging, floral biology breeding techniques in tef [*Eragrostis tef* (Zucc.) Trotter], in *PhD Thesis*, London University, London.

Ketema, S. (1993) *Tef (Eragrostis tef): breeding, agronomy, genetic resources, utilization, and role in Ethiopian agriculture*, Institute of Agricultural Research, Addis Ababa, Ethiopia.

Ketema, S. (1997) *Tef, Eragrostis tef (Zucc.) Trotter*, Institute of Plant Genetics and Crop Plant Research Gatersleben/International Plant Genetic Resources Institute, Rome, Italy, p. 52.

Laekemariam, F., Gidago, G. and Taye, W. (2012) Participatory seeding rates evaluation on teff [*Eragrostis tef* (Zucc.) Trotter] using seed spreader in Wolaita, South Ethiopia: farmers evaluation and economic analysis. *Advances in Life Science and Technology*, **5**, 37–42.

Mamo, T., Erkossa, T. and Tulema, B. (2001) *Soil fertility and plant nutrition research in tef in Ethiopia*, EIAR, Addis Ababa.

Mekbib, M., Buchanan-Wollaston, V. and Mantell, S.H. (2001) Attachment study of *Agrobacterium tumefaciens* to tef [*Eragrostis tef* (Zucc.) Trotter], yam spp., and tobacco (*Nicotiana tabaccum* L.) explant SINET. *Ethiopian Journal of Science*, **24**, 185–195.

Mekbib, F., Mantell, S.H. and BuchananWollaston, V. (1997) Callus induction and in vitro regeneration of tef [*Eragrostis tef* (Zucc.) Trotter] from leaf. *Journal of Plant Physiology*, **151**, 368–372.

Mengiste, T. (1991) Genetic transformation of Eragrostis tef by Direct DNA transfer, University of London, MSc Thesis.

MoA (2014) Crop Variety Register Issue No. 15 Ministry of Agriculture, Animal and Plant Health Regulatory Directorate, Addis Ababa, Ethiopia.

NFIU (1993) Agronomic feasibility of the proposed recommendations and comparison with the previous recommendations, National Fertilizer and Inputs Unit (NFIU) General Paper 17, Addis Ababa, Ethiopia, pp. 191–200.

Peterson, P.M., Romaschenko, K. and Johnson, G. (2010) A classification of the Chloridoideae (Poaceae) based on multi-gene phylogenetic trees. *Molecular Phylogenetics & Evolution*, **55**, 580–598.

Pinthus, M.J. (1973) Lodging in wheat, barley and oats: the phenomenon, its causes and preventive measure. *Advances in Agronomy*, **25**, 209–263.

Plaza-Wüthrich, S., Cannarozzi, G. and Tadele, Z. (2013) Genetic and phenotypic diversity in selected genotypes of tef [*Eragrostis tef* (Zucc.)] Trotter. *African Journal of Agricultural Research*, **8**, 1041–1049.

Plaza-Wüthrich, S. and Tadele, Z. (2012) Millet improvement through regeneration and transformation. *Biotechnology and Molecular Biology Reviews*, **7**, 14.

Plaza-Wüthrich, S. and Tadele, Z. (2013) Regeneration and transformation studies on tef, EIAR-University of Bern, Bern, Switzerland.

Ponti, J. (1978) The systematics of *Eragrostis tef* (Gramineae) and related species, in *PhD Thesis*, University of London.

Spaenij-Dekking, L., Kooy-Winkelaar, Y. and Koning, F. (2005) The Ethiopian cereal tef in celiac disease. *New England Journal of Medicine*, **353**, 1748–1749.

Tadele, Z. (2013) Tef Improvement Project: harnessing genetic and genomic tools to boost productivity, EIAR, University of Bern, Bern, Switzerland, pp. 333–342. URL: http://www.ips.unibe.ch/unibe/philnat/biology/botany/content/e6537/e546913/tef_improvement.pdf

Tadele, Z., Mba, C. and Till, B.J. (2010) TILLING for mutations in model plants and crops, in *Molecular Techniques in Crop Improvement*, 2nd edn (eds S.M. Jain and D.S. Brar), Springer, Dordrecht, pp. 307–332.

Tavassoli, A. (1986) The cytology of *Eragrostis tef* with special reference to *E. tef* and its relatives, in *PhD Thesis*, University of London.

Tefera, H. (2001) *The genetics of quantitative traits in tef*, EIAR, Addis Ababa.

Tefera, H., Assefa, K. and Belay, G. (2003) Evaluation of interspecific recombinant inbred lines of *Eragrostis tef* x *E pilosa*. *Journal of Genetics and Breeding*, **57**, 21–30.

Tefera, H., Assefa, K., Hundera, F. *et al.* (2001) *Progress of Tef Breeding Research in Ethiopia*, Ethiopian Agricultural Research Organization, Addis Ababa.

Tefera, H. and Ketema, S. (2001) *Production and Importance of Tef*, EIAR, Addis Ababa, Ethiopia.

Tefera, H., Ketema, S. and Tesemma, T. (1990) Variability, heritability and genetic advance in tef [*Eragrostis tef* (Zucc) Trotter] cultivars. *Tropical Agriculture*, **67**, 317–320.

Tefera, H. and Peat, W.E. (1996) Gene action for some quantitative traits of tef (*Eragrostis tef*). *Ethiopian Journal of Agricultural Science*, **15**, 8–19.

Tefera, H. and Peat, W.E. (1997a) Genetics of grain yield and other agronomic characters in tef (*Eragrostis tef* Zucc Trotter). 2. The triple test cross. *Euphytica*, **96**, 193–202.

Tefera, H. and Peat, W.E. (1997b) Genetics of grain yield and other agronomic characters in tef (*Eragrostis tef* Zucc. Trotter). 1. Generation means and variances analysis. *Euphytica*, **96**, 185–191.

Tefera, H., Peat, W.E. and Chapman, G.P. (1992) Quantitative genetics in tef, in *Desertified Grasslands: Their Biology and Management* (ed. Chapman, G.D.), The Linnaean Society of London, pp. 283–296.

Tefera, T., Kelemework, F., Deresa, A. *et al.* (2001) *Tef Technology Transfer and Adoption*, EIAR, Addis Ababa.

Tesema, A. (2013) Genetic diversity of tef in Ethiopia, in *Achievements and Prospects of Tef Improvement* (eds K. Assefa, S. Chanyalew and Z. Tadele), EIAR-University of Bern, Bern, Switzerland, pp. 15–20.

USDA (2015) National Nutrient Database for Standard Reference Release 27, United States Department of Agriculture.

van Delden, S.H., Vos, J., Ennos, A.R. and Stomph, T.J. (2010) Analysing lodging of the panicle bearing cereal teff (*Eragrostis tef*). *New Phytologist*, **186**, 696–707.

Vavilov, I. (1951) *The Origin, Variation, Immunity and Breeding of Cultivated Plants*, Translated from the Russian by Chester KS, Ronald Press Co., New York.

Watson, L. and Dallwitz, M.J. (1992) *The Grass Genus of the World*, CAB International, Wallingford, UK.

Yu, J.K., Graznak, E., Breseghello, F. *et al.* (2007) QTL mapping of agronomic traits in tef [*Eragrostis tef* (Zucc) Trotter]. *BMC Plant Biology*, **7**, 30.

Yu, J.K., Kantety, R.V., Graznak, E. *et al.* (2006) A genetic linkage map for tef [*Eragrostis tef* (Zucc.) Trotter]. *Theoretical and Applied Genetics*, **113**, 1093–1102.

Yu, J.K., Sun, Q., La Rota, M. *et al.* (2006) Expressed sequence tag analysis in tef (*Eragrostis tef* (Zucc) Trotter). *Genome*, **49**, 365–372.

Zeid, M., Assefa, K., Haddis, A. *et al.* (2012) Genetic diversity in tef (*Eragrostis tef*) germplasm using SSR markers. *Field Crop Research*, **127**, 64–70.

Zeid, M., Belay, G., Mulkey, S. *et al.* (2011) QTL mapping for yield and lodging resistance in an enhanced SSR-based map for tef. *Theoretical and Applied Genetics*, **122**, 77–93.

Zeid, M., Yu, J.K., Goldowitz, I. *et al.* (2010) Cross-amplification of EST-derived markers among 16 grass species. *Field Crops Research*, **118**, 28–35.

Zewdie, K. and Damte, T. (2013) *Weed Research in Tef*, EIAR-University of Bern, Bern, Switzerland.

Zhang, D., Ayele, M., Tefera, H. and Nguyen, H.T. (2001) RFLP linkage map of the Ethiopian cereal tef [*Eragrostis tef* (Zucc) Trotter]. *Theoretical and Applied Genetics*, **102**, 957–964.

Zhu, Q.H., Smith, S.M., Ayele, M. *et al.* (2012) High-throughput discovery of mutations in tef semi-dwarfing genes by next-generation sequencing analysis. *Genetics*, **192**, 819–829.

10

Insect Pests of Millets and Their Host Plant Relations

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10.1 Insect Pests

10.1.1 Sorghum

Pest problems in sorghum start at the pre-sowing period and continue till harvest. There are around 150 insect pests recorded for sorghum globally. In India, the major insect pests of sorghum are shoot fly, stemborer, shoot bug, aphids and a complex of earhead pests such as head bug and grain midge (Jotwani and Young, 1971). Other notable pests are white grubs, cutworms, grasshoppers and leaf-eating beetles. In this chapter, all the major pests and the minor pests are discussed with relevant information. These insect pests are commonly associated with sorghum in the oriental region. Many of these pests attack other millet crops also.

10.1.1.1 Seedling Pest

10.1.1.1.1 Sorghum Shoot Fly, Atherigona soccata

The shoot fly, *Atherigona soccata* Rondani (Muscidae: Diptera), is strictly a seedling pest. It causes damage to 1-week to 30-days-old seedlings. The typical symptom of damage is the drying of central shoot called 'deadheart' (Figure 10.1). This is a major shoot fly species, a pest of economic importance and is found throughout Africa, the Mediterranean, the Middle East and Southeast Asia, where its principal host, sorghum is grown.

10.1.1.2 Stem and Leaf feeders

10.1.1.2.1 Spotted Stemborer, Chilo partellus

Many species of *Chilo* develop on cereal crops and wild grasses, mostly in the tropics. It is a serious pest of sorghum and maize. In 1-month crops, the damage is seen as deadheart, and in grown-up plants they cause stem tunnelling (Figure 10.2).

10.1.1.2.2 Sugarcane Stalk Borer, Chilo auricilius

This species is distributed in India, Nepal, Bangladesh, Myanmar, Sri Lanka, China, Malaysia, Indonesia, Papua New Guinea, Philippines, Taiwan, Thailand and Vietnam. The hosts of economic importance are sugarcane, sorghum, maize and rice.

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Figure 10.1 Sorghum shoot fly damage. (*See color plate section for the color representation of this figure.*)

Figure 10.2 Sorghum stemborer damage. (*See color plate section for the color representation of this figure.*)

10.1.1.2.3 Sugarcane Early Shoot Borer, **Chilo infuscatellus**

The species is distributed in South and Southeast Asia. It is primarily a pest of sugarcane. It also infests maize, sorghum and rice.

10.1.1.2.4 Sugarcane Internode Borer, **Chilo sacchariphagus**

It is distributed in Asia and Indian Ocean islands. This is also an important pest of sugarcane and also attacks sorghum and maize.

10.1.1.2.5 Asian Corn Borer, **Ostrinia furnacalis**

This species is distributed in South and Southeast Asia, Indian Ocean islands and Australia. It is a polyphagous species and causes yield losses in maize and sorghum. Eggs are laid in groups of 5–50. Larvae are light brown dorsally with three longitudinally running series of dark spots; matured larvae are about 2–3 cm; pupae are reddish-brown and 2–2.5 cm long.

10.1.1.2.6 Green-Striped Borer, **Maliarpha separatella**

This species is widely distributed in Africa. It is also reported from Asia especially India, Myanmar and China. It is a pest of rice, maize and sorghum.

Figure 10.3 Sorghum shoot bug damage. (*See color plate section for the color representation of this figure.*)

10.1.1.2.7 Cereal Pink Borer, Sesamia inferens

Pink stemborer is polyphagous and distributed in the Oriental and the Palearctic regions.

10.1.1.3 Sucking Pests

10.1.1.3.1 Shoot Bug, Peregrinus maidis

This species causes economic losses in maize and sorghum in the tropics and coastal areas of sub-tropical and temperate regions of all continents (Singh and Seetharama, 2008). Nymphs and adults suck the sap from leaves as well as stems. Severe damages result in complete drying of the plant (Figure 10.3). *Peregrinus maidis* vectored maize mosaic virus (MMV). The adult bugs show macropterous and brahypterous winged forms. In the macropterous wing, membranous region marked with radiating bands and a dark patch at the middle of anal margin. Brahypterous wing shows a distal thick dark patch and a small anal spot.

10.1.1.4 Aphids

10.1.1.4.1 Sugarcane Aphid, Melanaphis sacchari

It is a key pest on sorghum and sugarcane in many areas of Africa, Asia, Australia, the Far East and parts of Central and South America (Singh, Padmaja *et al.*, 2004a).

10.1.1.4.2 Corn Aphid, Rhopalosiphum maidis *(Fitch, 1856)*

It is distributed throughout the world and infests maize and sorghum. It transmits maize dwarf mosaic virus (MDMV). Massive populations are noticed during booting stage, and heavy earhead infestation just prior to harvest creates problems in harvesting because of honeydew secretion (Singh, Padmaja *et al.*, 2004b). Severe damages cause drying of plants (Figure 10.4).

Virgin Winged Female Head, thorax, antenna, legs and siphunculi are brownish black; yellow-green abdomen with brown marginal plates; antenna with secondary rinariums on segments 3–5; siphunculus shorter; bifuracated medial vein on fore wing, second branch very short, beginning near wing margin.

Figure 10.4 Sorghum aphid damage. (*See color plate section for the color representation of this figure.*)

Ovoid Apterous Female Grey–green or white–green body; head, legs and siphunculus are black; 7–8 abdominal tergites with dark transversal stripes; antenna without secondary rinariums; beak reaches to mid coxae; cylindrical siphunculus are short with a swelling at apex and with a constriction; marginal tubercles are small. Black oval eggs.

Sugarcane leafhopper, *Pyrilla perpusilla*, is a minor pest and sometimes assumes damaging proportions on sorghum. Several species of hemipterous bugs (*Cletus* sp., *Dolycoris indicus*, *Empoasca flavescens*, *Lygaeus* sp., *Menida histrio*, *Nephotettix virescens* and *Nezara viridula*) are reported on sorghum.

Some thrips, *Caliothrips indicus*, *Sorghothrips jonnachilus*, *Taeniothrips traegardhi* and *Xylaplothrips pellucidus*, are also reported on sorghum (Ananthakrishnan, 1973).

Mites (Figure 10.5) such as *Oligonychus indicus* cause serious damage in sorghum, especially in glasshouse conditions.

10.1.1.5 Leaf Feeders

The armyworm, *Mythimna separata*, causes damage (Figure 10.6) by defoliation (Kundu and Kishore, 1971; Sharma *et al*., 1982; Sharma and Davies, 1983) and severely damaged plants are left with only leaf midrib. The larvae are gregarious and feed mostly at night.

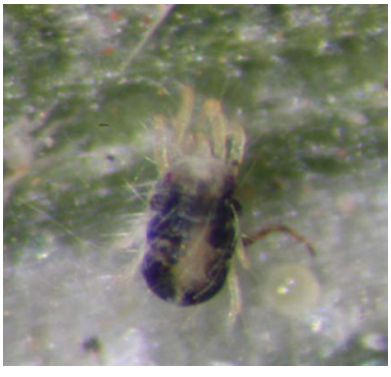

Figure 10.5 Spider mite on sorghum. (*See color plate section for the color representation of this figure.*)

Figure 10.6 Cutworm damage in sorghum. (*See color plate section for the color representation of this figure*.)

The red hairy caterpillar, *Amsacta moorei*, also causes defoliation (Srivastava and Goel, 1962). Occasional leaf-feeding caterpillars on sorghum foliage are *Euproctis virguncula*, *Amsacta albistriga*, *A. lactinea*, *Cnaphalocrosis trapezalis* and *Mocis frugalis.* Chrysomelid leaf beetles such as *Chaetocnema indica*, *Longitarsus* sp., *Aulacophora* sp. (Figure 10.7) and *Phyllotreta chaetonica* feed on leaves by making shot-holes. Ash weevil, *Myllocerus undecimpunctulatus maculosus*, causes damage to sorghum by feeding on the foliage and under severe infestations the entire leaf blade is eaten up leaving only the midribs (Kishore and Srivastava, 1976). Grasshoppers cause severe defoliation in Rajasthan and Gujarat states of India (Figure 10.8).

10.1.1.6 Earhead Pests

10.1.1.6.1 Sorghum Midge, Stenodiplosis sorghicola

This species is a native of Africa (Young and Teetes, 1977) and spread to other parts of the world. Coquillett first described the species as *Diplosis sorghicola* in 1898.

Figure 10.7 Sorghum leaf feeding by red pumpkin beetle. (*See color plate section for the color representation of this figure*.)

Figure 10.8 Grasshopper in sorghum. (*See color plate section for the color representation of this figure.*)

10.1.1.6.2 Head Bug, Calocoris angustatus *Lethierry, 1893*

Calocoris angustatus was first described by Lethierry in 1893 from the former state of Madras. The head bug, *Calocoris angustatus* Lethiery, is a key limiting factor in sorghum production (Young and Teetes, 1977). Apart from India, the bug was reported from Kenya and Rwanda (Seshu Reddy and Omolo, 1985).

Many species of lepidopteran caterpillars, viz., *Autoba silicula*, *Cryptoblabes gnidiella*, *Cydia* sp., *Dichocrocis punctiferalis*, *Ectomyclosis* sp., *Ephestia cautella*, *Eublemma* sp., *Euproctis limbata*, *Euproctis subnotata*, *Heliothis armigera*, *Porthesia xanthorrhoa* and *Sitotroga cerealella* (Figure 10.9), are also found feeding on developing grains.

Some beetle species (*Chiloloba acuta*, *Mylabris pustulata* and *Lytta tenuicollis*) are also found on earheads, especially during anthesis.

10.1.1.7 Root Feeders

White grubs, *Holotrichia serrata* and *Lachnosterna consanguinea*, sporadically gain the 'serious pest' status in India. The grubs feed on the roots of seedlings as well as older plants resulting in withering of plants. The infested plants wither and wilt in patches. Wire worms (Elateridae, Tenebrionidae: Coleoptera) also cause similar damages in sorghum seedlings.

The cutworms (Noctuidae: Lepidoptera), for example, *Agrotis ipsilon*, damage the plant by cutting the seedling at or little below the soil surface resulting in plant withering

Figure 10.9 Spodoptera on sorghum earhead. (*See color plate section for the color representation of this figure.*)

Figure 10.10 Termite damage in sorghum. (*See color plate section for the color representation of this figure.*)

and lodging. Termties (Figure 10.10), *Odontotermes* sp. and *Microtermes* sp., also cut the seedlings in some areas with sandy loam soils. Damages to germinating seeds by ants, especially *Monomorium salomonis* and *Pheidole sulcaticeps*, are also recorded.

10.1.2 Pearl Millet

Pearl millet is damaged by many insect pests, of which shoot fly, leaf-feeding beetles, caterpillars, stemborer and aphids are important.

10.1.2.1 Shoot Fly, *Atherigona approximata*

This species was first reported as cumbu (pearl millet) fly (Fletcher, 1917) on *Pennisetum typhoides* and also on *Sorghum bicolor*. Pont (1972) confirmed it as *Atherigona approximata.* The species is distributed in South and Western India. Shoot fly damage on pearl millet is similar to that in sorghum (Figure 10.11).

Other shoot flies occasionally found on pearl millet are *A. orientalis*, *A. soccata*, *A. oryzae* and *A. punctata.*

10.1.2.2 Stemborers

There are many lepidopteran borers, such as *Chilo partellus*, *Sesamia calamistis*, *S. cretica*, *S. inferens*, *Diatraea grandiosella*, *Coniesta igenfusalis*, *Busseola fusca*, *Ostrinia furnacalis*, *O.nubilalis* and *C. infuscatellus*, recorded to be damaging pearl millet across the world.

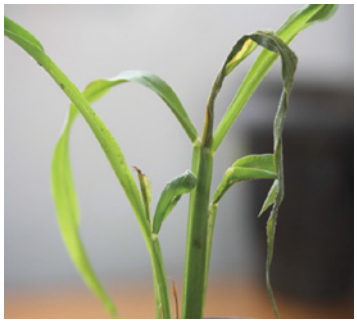

Figure 10.11 Shoot fly damage in pearl millet. (*See color plate section for the color representation of this figure.*)

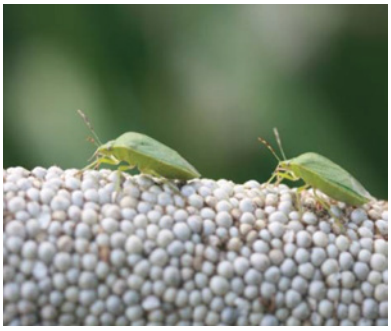

Figure 10.12 Green bug on pearl millet. (*See color plate section for the color representation of this figure.*)

10.1.2.3 Leaf Feeders

Lepidopteran caterpillars (*Amsacta moorei*, *Mythimna separata*, *M. loreyi*, *Cnaphalocrocis medinalis*, *Spodoptera exigua*, *S. frugiperda* and *S. mauritia*) and beetles and grasshoppers (such as *Diabolocatantops axillaris*, *Hieroglyphus banian*, *H. daganensis*, *Oedaleus senegalensis* and *Schistocerca gregaria*) feed on foliage and sometimes cause severe damage.

10.1.2.4 Sucking Pests

Bugs such as *Nizara viridula* (Figure 10.12), *Blissus leucopterus*, *Nysius niger* and hoppers, viz., *Cicadulina mbila*, *C. storey*, *Pyrilla perpusilla*, cause damage to the overall vigour of the plant stand. Aphids such as *Rhamphicarpa fistulosa*, *Rhopalosiphum maidis*, *Sitobion miscanthi* and *Hyalopterus pruni* appear on leaves and earhead, causing discolouration, curling and poor seed set.

10.1.2.5 Other Pests

Beetles, *Chiloloba acuta*, are found in large numbers on panicle, especially during anthesis. Earworm (*Heliocheilus albipunctella*) and millet midge (*Geiromiya penniseti*) are important in causing considerable damage to pearl millet. *Helicoverpa armigera*, *Spodoptera exempta*, *Spilarctia oblique*, *Pachnoda interrupta*, *Phyllophaga* sp., *Thrips hawaiiensis*, *Holotrichia consanguinea*, *H. serrata* are some of the sporadic pests on pearl millet.

10.1.3 Finger Millet

Finger millet is attacked by many insect pests, especially under irrigated condition. The cultivation is normally as transplanted crop under irrigated condition.

10.1.3.1 Root Feeders

Root aphid, *Tetraneura nigriabdominalis*, is a serious pest in finger millet. The affected plants show withering symptoms initially and finally dry up. A white grub, *Phyllophaga* sp. also causes considerable crop loss.

10.1.3.2 Shoot and Stem Feeders

Among borers, *Sesamia inferens* is the most serious pest in India. The affected plants produce deadheart symptom. The other borers such as *Chilo partellus*, *Busseola fusca* and *Saluria inficita* also occur in finger millet.

Shoot fly infestations are generally rare in this crop. There are some reports of occurrences of *Atherigona miliaceae* and *A. soccata*.

Stem weevil, *Listronotus bonariensis* is a minor pest in this crop.

10.1.3.3 Leaf Feeders

Hairy caterpillars (*Amsacta albistriga*, *A. transiens* and *A. moorei*); armyworm (*Mythimna separate*); leafhopper (*Cicadulina mobile*); leaf folder (*Cnaphalocrocis medinalis*); skipper (*Pelopidas mathia*); armyworms (*Spodoptera exempta* and *S. mauritia*); surface grasshopper (*Chrotogonus* sp.); migratory locust (*Locusta migratoria*); fire ant (*Solenopsis geminate*) and beetle (*Epilachna similis*) are the major leaf feeders in finger millet.

10.1.3.4 Sucking Pests

Aphids (*Metopolophium dirhodum*, *Rhopalosiphum maidis*, *Sitobion miscanthi* and *Brevennia rehi*) and leaf hoppers (*Cicadulina bipunctella bipunctella* and *C. chinai*) cause considerable damage to this crop.

10.1.4 Foxtail Millet

Foxtail millet is comparatively less attacked by insect pests. The most important pests are listed in the following sections.

10.1.4.1 Shoot Fly, *Atherigona atripalpis*

This species was recorded on *Setaria italica*, *S. glauca* and *S. plicata* in India, Sri Lanka, Myanmar, Nepal and China.

10.1.4.2 Other Important Pests

Stemborers (*Chilo partellus*, *Sesamia inferens* and *Ostrinia furnacalis*); armyworms, (*Mythimna separate* and *Spodoptera frugiperda*); leaf beetle (*Oulema melanopus*); leaf folder (*Cnaphalocrocis medinalis*); flea beetle (*Chaetocnema basalis*, *Madurasia* sp.); leaf roller (*Cnaphalocrosis trapezolis*); surface grasshopper (*Chrotogonus* sp.) and ant (*Sima* sp.) are the other important pests recorded on foxtail millet.

10.1.5 Kodo Millet

10.1.5.1 Shoot Fly, *Atherigona simplex*

This species becomes a serious pest in late-sown crop, and it is distributed widely in India. In some cases, *A. oryzae* and *A. soccata* were also recorded on kodo millet.

10.1.5.2 Other Pests

Stemborer (*S. inferens*), leaf roller (*Cnaphalocrosis patnalis*), leaf miner (*Hydrellia philippina*), army worm (*M. separata*), midge (*Orseolia* sp.), mealy bug (*Brevennia rehi*), leafhopper (*Nephotettix nigropictus*), skipper (*Pelopidas mathias*), thrips (*Stenchaetothrips biformis*), jassid (*Hecalus* sp.), grain bug (*Leptocorisa acuta*), green bug (Figure 10.13) and grasshopper (*Acrida exalta*) also attack kodo millet plants.

10.1.6 Proso Millet

10.1.6.1 Shoot fly, *Atherigona pulla*

It occurs on *Panicum* spp. And is distributed mainly in South India. Yellow vibrissal bristles in both sexes are the distinct features of this species. *Atherigona miliaceae* is also recorded on proso millet.

Figure 10.13 Green bug on kodo millet. (*See color plate section for the color representation of this figure*.)

10.1.6.2 Other Pests

Stemborers (*Chilo partellus, C. suppressalis, C. orichalcociliellus, S. inferens* and *Ostrinia furnacalis*); webworm (*M. trapezalis*); armyworms (*M. separate, M. unipuncta, Spodoptera exempta* and *S. frugiperda*); hairy caterpillar (*Spilarctia oblique*) (Figure 10.14,); leaf folder (*Cnaphalocrocis medinalis*); thrips (*Haplothrips aculeatus*); grasshoppers (*Hieroglyphus banian* and *Oxya chinensis*); aphids (*Sipha flava*) and seed bug (*Leptocorisa acuta*) attack proso millet.

Figure 10.14 Hairy caterpillar on proso millet. (*See color plate section for the color representation of this figure*.)

10.1.7 Little Millet

10.1.7.1 Shoot Fly, *Atherigona miliaceae*

It was first reported as China fly (Ramchandra Rao, 1924). This species was reported from India on *Panicum* spp.

10.1.7.2 Other Pests

Gall midge (*Orseolia* sp.), stink bug (*Nezara uiridula*), black pentatomid (*Dolycoris indicus*), jassid (*Kolla mimica*), grasshopper (*Acrida exalta*) and flea beetle (*Chaetocnema* sp.) are the other pests reported on little millet.

10.1.8 Barnyard Millet

10.1.8.1 Shoot Fly, *Atherigona falcata*

This species is distributed throughout the oriental region, and *Echinochloa frumentacea* was recorded as its main host. The species is comparatively large in size than other species.

10.1.8.2 Other Pests

Stemborer (*Sesamia inferens*), leafhopper (*Nephotettix cincticeps*), green bug (Figure 10.15) are found damaging the crop in India.

10.2 Host-Plant Selection by Insect Pests

A basket of stimuli associated with host and nonhost plants elicit a series of behavioural responses in phytophagous insects (Zhang and Schlyter, 2004; Liu *et al*., 2011). The host-finding process in insects is assisted by sensory receptors enabling them to perceive those stimuli. Plant stimuli involved include in varying proportions visual,

Figure 10.15 Green bug on barnyard millet. (*See color plate section for the color representation of this figure*.)

mechanical, gustatory and olfactory characteristics (Visser, 1986). Host plant selection is mainly a behavioural process which is governed primarily by chemoreception. Therefore, the emergence of specific insect/host plant relationships most likely results from evolutionary changes in the chemosensory systems of insects (Jermy, 1984).

Sorghum shoot fly, *Atherigona soccata* Rondani adults utilise specific blends of semiochemical cues for recognition of host plant and oviposition. Sorghum seedlings emit volatiles that are specific to both adult fly oviposition attraction and larval orientation. The susceptible genotypes and the younger seedlings emit different quantities of blends of volatiles than resistant or older ones. Females of *A. soccata* are attracted to the phototactic stimuli and the volatiles emitted by the susceptible seedlings that may facilitate orientation for oviposition (Nwanze *et al.*, 1998) and plant volatiles play an important role in determining susceptibility or resistance of a given sorghum cultivar (Padmaja *et al.*, 2010). The susceptible sorghum cultivar (e.g. Swarna) and the resistant one (e.g. IS 18551) produced different volatile profiles (Padmaja *et al.*, 2010). Plant volatiles are collected with air-entrainment chambers (Figure 10.16).

Electrophysiologically active components in volatiles released by sorghum were (Z)-3-hexen-1-yl acetate, (-)-α-pinene, (-)-(E)-caryophyllene, methyl salicylate, octanal, decanal, 6-methyl-5-hepten-2-one and nonanal (Padmaja *et al.*, 2010).

In case of spotted stem borer, *Chilo partellus* electrophysiologically active components such as linalool, acetophenone and 4-allylanisole in volatiles released by sorghum elicited large responses (Birkett *et al.*, 2006).

Figure 10.16 Air-entrainment chamber. (*See color plate section for the color representation of this figure.*)

Females of sorghum midge, *Stenodiplosis sorghicola* are attracted to sorghum plants in response to a combination of visual and chemical stimuli. Female midge flies are swiftly attracted to yellow and then in order of green, red and blue colors (Sharma and Franzmann, 2001; Sharma *et al.*, 2002). A combination of odour and optical spectral reflectance in sorghum genotypes influence host selection by midge flies and therefore, both visual and chemical stimuli play important role in host selection (Sharma *et al.*, 1990a; 2002). Oviposition in female midges was guided by the chemical stimuli from viable pollen and receptive stigmata (Sharma *et al.*, 1990a; 2002). Traps can be designed using those chemical and optical stimulants for monitoring and studying population levels of sorghum midge in the field (Sharma *et al.*, 1990a; 2002).

10.2.1 Host Preferences

Cultivated sorghum, *Sorghum bicolor* is the most preferred host of shoot fly *A. soccata* (Davies and Reddy, 1981a; 1981b) and is also recorded from maize, pearl millet, *Brachiaria*, *Cynodon*, *Echinochloa colonum*, *Eragrostis*, *Eriochloa procera*, *Cymbopogon* sp., *Panicum*, *Paspalum scrobiculatum*, *Pennisetum*, *Setaria*, *Sorghum halepense* and other *Sorghum* spp. (Seshu Reddy and Davies, 1977; Davies and Reddy, 1981a; Gahukar, 1991). *Sorghum halepense* is the most important alternative host plant for *A. soccata* (Davies and Reddy, 1981b). Importantly, the grasses, *Digitaria ascendens*, *Brachiaria reptans* and *Eleusine indica*, are the alternative food-plants of *A. soccata* in Thailand. Small populations of *A. soccata* persist on wild food-plants in the absence of sorghum (Davies and Reddy, 1981a; 1981b).

Atherigona soccata is the dominant species in sorghum growing areas of Africa and India (Davies *et al.*, 1980). In addition to *A. soccata*, *A. campestris*, *A. gilvifolia*, *A. tomentigera* and *A. secrecauda* were found in Uganda (Baliddawa and Lyon, 1974). *Atherigona approximata* infests pearl millet, *A. falcata* and *A. naqvii* infest wheat, maize and barley in India and Pakistan, *Pennisetum glacum* in Nigeria, wheat in Saudi Arabia. *A. oryzae* is a widespread pest of rice and other plants along with *A. simplex* in Pakistan (Pont, 1972).

The following are the most important cereal stem borers that cause severe economic loss in millets especially in Asia and Africa:

Family: Crambidae
Sub Family: Crambinae
Chilo partellus, *C. auricilius*, *C. infuscatellus*, *C. orichalcociliellus*, *C. sacchariphagus*
Sub Family: Pyraustinae
Coniesta ignefusalis, *Diatraea grandiosella*, *Ostrinia furnacalis*
Family: Pyralidae
Sub Family: Phycitinae
Eldana saccharina, *Maliarpha separatella*, *Saluria inficita*
Family: Noctuidae
Sesamia calamistis, *Sesamia inferens*, *Busseola fusca*

Spotted stem borer, *Chilo partellus* has a wide host range of cultivated cereals and wild grasses (Kfir, 2002). Among the hosts plant, the cultivated millets such as sorghum, pearl millet, finger millet and other small millets suffer the most due to *C. partellus* attack. Sorghum, maize and sugar cane were reported as the most preferred cultivated plant hosts for *C. partellus* (Swami and Bajpai, 2006).

Among the different host plants, sugarcane, sorghum, maize and barley, maize was found to be the most-preferred host and best for the development of stemborer. Among the other three hosts tested, sorghum was found almost at par with maize, closely following maize in all parameters (Swami and Bajpai, 2006). Nineteen cultivated and wild plants were identified as host plants of the stemborers of which sudan grass and elephant grass supported high numbers of larvae of *C. partellus*. During off-seasons *C. partellus* undergoes diapause depending upon the prevailing weather conditions. During the dry periods the larvae survive as diapausing larvae on crop residues, maize grown under irrigation and on wild host plants mainly grown in forest enclosure areas in Eritrea (Haile and Hofsvang, 2001).

The other *Chilo* species namely *C. auricilius*, *C. infuscatellus*, *C. orichalcociliellus* and *C. sacchariphagus* are known to survive in several grasses including cultivated cereals, millets and sugarcane.

Larvae of stem borer, *C. partellus* distributed in an aggregated fashion in the field (Jalali and Singh, 2001). Cultivated host plants showed higher incidences of whorl and stem damage than the grasses *Hyparrhenia tamba* (blue thatching grass) and *Panicum maximum* (guinea grass). *Chilo partellus* developed faster with bigger sized larvae in cultivated cereals (Rebe *et al.*, 2004). *Chilo partellus* larvae developed faster than *C. orichalcociliellus* in maize and sorghum. A comparative developmental biology between *C. orichalcociliellus* and *C. partellus* showed a competitive edge to the latter in terms of survival and rate of development. However, the ability of *C. orichalcociliellus* to complete development in two native grasses in which *C. partellus* did not survive may provide a refuge that has allowed *C. orichalcociliellus* to escape extirpation from the coastal area of Kenya (Ofomata *et al.*, 2000). In Uganda, with the exception of *Sorghum arundinaceum*, wild grasses play a minor role in the seasonal persistence of *C. partellus* (Kfir, 2002). *Chilo partellus* tend to oviposite on non hosts such as cowpea intercropped with sorghum and such oviposition behaviour reduced abundance in inter-cropping (Ampong-Nyarko *et al.*, 1994).

The other crambid borers are *Coniesta ignefusalis*, *Diatraea grandiosella* and *Ostrinia furnacalis.* There are several species of alternate hosts such as *Andropogon nardus*, *Coix lachryma-jobi*, *Cyperus rotundus*, *Echinochloa colonum*, *Eleusine coracana*, *Panicum frumentaceum*, *P. maximum* and *Pennisetum typhoides* recorded for those crambids in Asia and Africa.

The pyralid borers namely *Eldana saccharina*, *Maliarpha separatella* and *Saluria inficita* are known to survive in several grasses in Asia and Africa. The cultivated grasses such as sorghum, maize, sugarcane and millets are the most important host plants. The noctuids *Sesamia calamistis*, *S. inferens* and *Busseola fusca* are widely distributed in Africa. Wild species of *Eleucine* and cultivated *E. coracana*, *Sorghum bicolor* and *Zea mays* are the most preferred hosts.

Shoot bug, *Peregrinus maidis* is an oligophagy with maize and sorghum as the principal hosts. Shoot bug survives on *Pennisetum typhoides*, *Sorghum halepenise*, *Setaria italica*, *Echinochloa colona*, *E. frumentacca* and *Paspalum scrobiculatum* (Chelliah and Basheer, 1965). *Pennisetum purpureum*, *Paspalum urvillei*, *Saccharum officinarum*, *Trichachne insularis*, *Brachiaria mutica* and *Coix lacryma-jobi* are some of the other host plants of shoot bug (Namba and Higa, 1971). *P. maidis* is the vector of maize stripe virus (MStV) and maize mosaic virus (MMS). The bug is able to survive and transmit the two viral diseases in Itch grass, *Rottboellia exaltata* (Tsai, 1975). The host range of sugarcane aphid, *M. sacchari* spreads across the species of *Saccharum*,

Sorghum, *Setaria*, *Oryza* and *Panicum*, and *Zea mays*, *Cynodon dactylon*, *Paspalum sanguinale Pennisetum* (Wilbrink, 1922; van Rensburg, 1973; Agarwal and Abraham, 1985; Denmark, 1988).

Sorghum midge, *Stenodiplosis sorghicola* prefers to survive on species of the plant genus *Sorghum* that include *S. halapense*, *S. almum* and *S. sudanense*). Many wild non-sorghum grasses were also reported as hosts of *S. sorghicola.* Johnson grass, *S. halapense* is a key host plant in the population dynamics of the sorghum midge. *S. halapense* supports the early season populations of up to three generations of the midge before the start of the flowering in sorghum (Harris, 1961; 1979; Teetes, 1985; Franzmann *et al.*, 2006) and the peak adult emergence of overwintering midge coincides with the widespread flowering of Johnson grass in an area after spring rains (Sharma *et al.*, 1985; 1990a; 1990b; Franzmann *et al.*, 2006).

10.2.2 Mechanisms of Host Plant Resistance

Painter (1951) proposed the three classic mechanisms of insect resistance in plants – non-preference, antibiosis and tolerance and later the term 'non-preference' was replaced with 'antixenosis'(Kogan and Ortman, 1978). Antixenosis is a single or a set of plant traits that detrimentally affects insects as they attempt to use plants for food, oviposition or shelter. This leads to the rejection by the pest as an unsuitable host. Antixenosis is an important mechanism as it prevents the insect from selecting the plant for food or for survival. The antibiosis mechanism of resistance operates after the host plant infestation and affects the biology of the insect as it feeds on the plant. The tolerance mechanism is nothing but the inherent ability of a plant to regain or withstand the insect attack. Resistant plants may contain one or a combination of the three mechanisms that collectively contribute to the level of insect resistance. Each mechanism of resistance acts at some stage of the insect–plant relationship and is contributed to by physical or chemical plant characters that may be referred to as components of resistance.

10.2.3 Antixenosis

Non-preference or antixenosis is the property of the plant to render itself unattractive to insect pest for oviposition, feeding or shelter. This mechanism is governed by physicochemical characteristics of the host plant that affect insect behaviour adversely. Absence of physicochemical stimuli that are involved in the selection of host plant or presence of repellents, deterrants and antiffedants contribute to antixenosis. Sensory cues that mediate host selection for oviposition are visual, tactile and chemical stimuli. Oviposition non-preference is considered to be a primary mechanism of resistance to major insect pests of sorghum, viz., shoot fly, head bug and midge (Blum, 1967; 1968; 1969; 1972; Sharma and Lopez, 1990; Sharma and Vidyasagar, 1994; Dhillon, 2004; Dhillon *et al.*, 2005).

In sorghum shoot fly, *Atherigona soccata*, antixenosis is the most preferred mechanism of resistance because of the nature of damage by the insect. The first instar larva of shoot fly enters the shoot and cut the base of the growing shoot and at this point, operation of antibiosis would be of no use as the damage is done to the plant already. Non-preference for oviposition in sorghum is relative, since none of the known resistant cultivars were completely non-preferred for egg laying. There are certain plant traits correlated to lower oviposition preference by *A. soccata* in sorghum such as high

transpiration rate (Mate *et al*., 1988), leaf surface wetness (Nwanze *et al*., 1990), epicuticular wax (Nwanze *et al.*, 1992), leaf glossiness and trichomes on leaf surface (Blum, 1972; Sharma, 1997). Resistant genotypes have a smooth, amorphous wax layer with few wax crystals, while susceptible genotypes have significantly more wax in the epicuticle (Padmaja *et al.*, 2010). The frequency of lines with high vigour score was greater in the resistant group than in the susceptible group (Sharma, 1997). Although trichome density is significantly and negatively correlated with deadhearts, it does not have direct role in reducing deadhearts, but contributes to shoot fly resistance mainly through other traits (Karanjkar *et al*., 1992). Plants with eggs, deadhearts, leaf glossiness, trichomes on the abaxial surface of the leaf and leaf sheath pigmentation are the most reliable parameters, and these can be used as marker traits to screen and select for resistance to sorghum shoot fly. Sorghum midge, *Stenodiplosis sorghicola* is resisted by sorghum through structural morphology of spikelets in terms of small glume size and the extent of glume closure, length of glume, palea, lemma, anther and style length (Rossetto *et al*., 1975; Jadhav and Jadhav, 1978; Sharma, 1985; Sharma *et al*., 1990a; 1990b; 2002), The glumes of spikelets of resistant varieties were more tightly closed than those in susceptible varieties (Diarisso, 1997; Waquil *et al.*, 1986).

Odours emanating from the panicles of sorghum seem to attract the midge flies for oviposition.

The wild relatives of sorghum (except *S. halepense*) were not preferred for oviposition, and they were also less attractive to the sorghum midge females. Thus, wild relatives of sorghum can prove to be an alternative source of genes for resistance to sorghum midge (Sharma and Franzmann, 2001).

10.2.4 Antibiosis

Antibiosis is measured by means of biological traits of insects that feed on the plant. For example, retardation of growth and development, prolonged larval and pupal periods and poor emergence of adults on resistant genotypes provide evidence of antibiosis to sorghum shoot fly, *Atherigona soccata* (Sharma *et al*., 1977; Sharma, 1997). The larvae on the resistant genotypes are generally smaller, and the mortality of the first-instars was higher than on the susceptible genotypes (Ogwaro and Kokwaro, 1981).

Antibiosis and tolerance are operating against stem borer, *Chilo partellus* in sorghum (Jotwani and Srivastava, 1970; Jotwani, 1976). Due to antibiosis larval, pupal and the total development period are prolonged. Reduced pupal weight and low pupation and adult emergence were observed (Jotwani *et al.*, 1978; Lal and Pant, 1980; Lal and Sukhani, 1982; Singh and Verma, 1988; Verma *et al.*, 1992; Padmaja *et al.*, 2012). Secondary plant substances in the leaves or poor nutritional quality of the food, low sugar content, greater amounts of amino acids, tannins, total phenols, neutral detergent fibre, acid detergent fibre, lignins and silica content (Swarup and Chaugale, 1962; Narwal, 1973; Khurana and Verma, 1982; 1983) are associated with resistance to *C. partellus* in sorghum.

Decreased rates of post-embryonic growth, progeny development, survival, adult fecundity and increased mortality, and reduced size and weight of larvae of *Stenodiplosis sorghicola* are considered effects of antibiosis in sorghum (Sharma *et al.*, 1993; Wuensche, 1980). Similarly, in shoot bug, *Peregrinus maidis* antibiosis is expressed as increased mortality, prolonged nymphal development, and reduced fecundity while feeding on sorghum (Chandra Shekar, 1991; Singh and Rana, 1992).

10.2.5 Tolerance

Tolerance is also called recovery resistance in which the plant is able to withstand or recover from damage caused by an insect. Under shoot fly infestation synchronised tillering after the main shoot is killed is potentially a form of recovery resistance because the tillers in some genotypes express higher levels of resistance than the main shoots (Dogget, 1972). Tall seedlings and high-plant recovery were reported as the characteristics of resistant varieties (Sharma *et al.*, 1977). In a more generalized way, the varieties with high recovery resistance yield more under shoot fly infestation (Raina *et al.*, 1981; Raina, 1985; Rana *et al.*, 1985).

Seedling vigour and high rate of recovery are important characteristics of resistant cultivars (Sharma *et al.*, 1977). Recovery resistance does not appear to be useful mechanisms of resistance particularly when shoot fly population increases progressively as the rainy season continues (Singh and Rana, 1986). But the axial tillers often mature later than the main plants and often suffer greater damage by sorghum midge, *S. sorghicola* (Coq.), head bugs, *C. angustatus* (Leth.) and birds or may not be able to produce grain under drought stress (Dhillon, 2004).

10.2.6 Sources of Insect Resistance

Developing cultivars with insect resistance is an important aspect of the pest management. Much progress has been made in identifying sources and understanding the genetics and mechanisms of resistance to important pests of sorghum. Nevertheless, there were attempts to find genotypes with insect resistance in other millets especially in pearlmillet and finger millet. The existence of genetic differences in sorghum for resistance to shoot fly was first established by Ponnaiya (1951). A number of these varieties consistently showed little damage but none of them was found immune to shoot fly attack (Singh *et al.*, 1968). Several lines were identified in the All India Coordinated Sorghum Improvement Project (AICSIP). Identified resistance sources mostly come from maldandi (semi-compact head type) or dagadi (compact head type) races grown in post-rainy season in India (Rana *et al.*, 1985). Many of the resistant sources identified in the germplasm are poor in productivity due to a physiologically inefficient plant type, and are poor combiners for shoot fly resistance and the traits associated with resistance (Aruna and Padmaja, 2009). Wild species of sorghum (*S. purpureosericeum* and *S. versicolor*) possess very high levels of resistance to shoot fly (Mote, 1984). *Parasorghum* (*S. australience*, *S. purpureosericeum*, *S. brevicallosum*, *S. timorense*, *S. versicolor*, *S. matarankense* and *S. nitidum*) and *Stiposorghum* (*S. angustum*, *S. ecarinatum*, *S. extans*, *S.intrans*, *S. interjectum* and *S. stipoideum*) are reliable candidates for exploring resistant sources (Venkateswaran, 2003; Kamala *et al.*, 2009).

Several lines have been identified/developed with resistance to insects, of which IS 2123, ICSV 705, ICSV 708, SPSFR 94019, SPSFR 94006, SPSFR 94007, SPSFR 94011, SPSFR 94034, ICSV 93127, SPSFR 96069, SPSFR 86065, PS 23585 and ICSR 89058 are resistant to shoot fly; and IS 5448, IS 5470, IS 2205, IS 18573, ICSV 700 (sweet stalk) and ICSV 93046 (sweet stalk) are resistant to stemborer, *Chilo partellus* have been used in crop improvement in Asia, Africa, United States and Australia.

IS 3461, IS 9807, IS 10712, IS 18563, IS 19476, IS 21873, IS 21881, IS 22806, PM 15936-2 and ICSV 197 have high levels of resistance to sorghum midge (Sharma *et al.*, 2002).

Similarly, I 753, H 109, GIB, 3677B and IS 1055, IS 19349, IS 18657, IS 18677 and PJ 8 K(R) in sorghum are are promising resistant sources against *P. maidis* infestation

(Agarwal *et al.*, 1978; Chandra Shekar, 1991; Singh and Rana, 1992; Chandra Shekar *et al.*, 1992; Chandra Shekar, Reddy *et al.*, 1993; Chandra Shekar, Singh *et al.*, 1993). IS 3461, IS 9807, IS 10712, IS 18563, IS 19476, IS 21873, IS 21881, IS 22806, PM 15936-2 and ICSV 197 have high levels of resistance to sorghum midge (Sharma *et al.*, 2002).

Plants with eggs, deadhearts, leaf glossiness, trichomes on the abaxial surface of the leaf and leaf sheath pigmentation are the most reliable parameters, and these can be used as marker traits to screen and select for resistance to sorghum shoot fly. The genotypes showing resistance to stemborer leaf feeding, deadheart formation, stem tunnelling and/or compensation in grain yield can be used for sorghum improvement.

References

Agrawal, B.L. and Abraham, C.V. (1985) Breeding sorghum for resistance to shoot fly (*Atherigona soccata*) and midge (*Contarinia sorghicola*). *Proceedings of the International Sorghum Entomology Workshop*, July 15–21, 1984, International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh, India, pp. 371–383.

Agarwal, R.K., Verma, R.S. and Bharaj, G.S. (1978) Screening of sorghum lines for resistance against shoot bug, *Peregrinus maidis* Ashmead (Homoptera: Delphacidae). *JNKVV Research Journal*, **2**, 116.

Ampong-Nyarko, K., Seshu Reddy, K.V., Nyang'or, R.A. and Saxena, K.N. (1994) Reduction of insect pest attack on sorghum and cowpea by intercropping. *Entomologia Experimentalist et Applicata*, **70**, 179–184.

Ananthakrishnan, T.N. (ed.) (1973) *Thrips: Biology and Control*, Macmillan, New Delhi, India.

Aruna, C. and Padmaja, P.G. (2009) Evaluation of genetic potential of shoot fly resistant sources in sorghum (*Sorghum bicolor* (L.)). *Journal of Agricultural Sciences*, **147**, 71–80.

Baliddawa, C.W. and Lyon, W.F. (1974) Sorghum shoot fly species and their control in Uganda. *PANS*, **20** (1), 20–22.

Blum, A. (1967) Varietal resistance in sorghum to the sorghum shoot fly *(Atherigona varia soccata)*. *Crop Science*, **7**, 461–462.

Blum, A. (1968) Anatomical phenomena in seedlings of sorghum varieties resistant to the sorghum shoot fly, *(Atherigona varia soccata)*. *Crop Science*, **8**, 388–391.

Blum, A. (1969) Factors associated with tiller survival in sorghum varieties resistant to the sorghum shoot fly (*Atherigona varia soccata*). *Crop Science*, **9**, 508–510.

Blum, A. (1972) Sorghum breeding for shoot fly resistance in Israel, in *Control of sorghum shoot fly* (eds M.G. Jotwani and W.R. Young), Oxford and IBH Publishing Co., New Delhi, pp. 180–191.

Birkett, M.A., Chamberlain, K., Khan, Z.R. *et al.* (2006) Electrophysiological responses of the lepidopterous stemborers Chilo partellus and Busseola fusca to volatiles from wild and cultivated host plants. *Journal of Chemical Ecology*, **32** (11), 2475–2487.

Chandra Shekar, B.M. (1991) Mechanisms of resistance in sorghum to shoot bug, *Peregrinus maidis* (Ashmead) (Homoptera: Delphacidae), in *MSc thesis*, Andhra Pradesh Agricultural University, Hyderabad, AP, India, p. 106.

Chandra Shekar, B.M., Dharma Reddy, K., Singh, B.U. and Reddy, D.D.R. (1992) Components of resistance to corn planthopper, *Peregrinus maidis* (Ashmead), in sorghum. *Resistant Pest Management Newsletter*, **4**, 25.

Chandra Shekar, B.M., Reddy, K.D., Singh, B.U. and Reddy, D.D.R. (1993) Antixenosis component of resistance to corn planthopper, *Peregrinus maidis* (Ashmead) in sorghum. *Insect Science and Its Application*, **4**, 77–84.

Chandra Shekar, B.M., Singh, B.U., Reddy, K.D. and Reddy, D.D.R. (1993) Antibiosis component of resistance in sorghum to corn planthopper, *Peregrinus maidis* (Ashmead) (Homoptera: Delphacidae). *Insect Science and Its Application*, **14**, 559–569.

Chelliah, S. and Basheer, M. (1965) Biological studies of *Peregrinus maidis* (Ashmead) (Araeopidae: Homoptera) on sorghum. *Indian Journal of Entomology*, **27**, 466–471.

Davies, J.C. and Reddy, K.V.S. (1981a) Observations on oviposition of sorghum shoot fly, in *Atherigona soccata Rond. (Diptera: Muscidae)*, Sorghum Entomology Progress Report-4, International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh, India.

Davies, J.C. and Reddy, K.V.S. (1981b) Shoot fly species and their graminaceous hosts in Andhra Pradesh, India. *Insect Science and Its Application*, **2**, 33–37.

Davies, J.C., Reddy, K.V.S. and Skinner, J.D. (1980) *Attractants for Atherigona spp. Including Sorghum Shoot Fly (Atherigona soccata Rond., Muscidae: Diptera)*, International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh India, p. 16.

Denmark, H.A. (1988) *Sugarcane Aphids in Florida (Homoptera: Aphididae)*, Entomology Circular No. 302. Division of Plant Industry, Florida Department of Agriculture & Consumer Services.

Dhillon, M.K. (2004) Effects of cytoplasmic male-sterility on expression of resistance to sorghum shoot fly, *Atherigona soccata* (Rondani), in *PhD thesis*, Department of Entomology, Chaudhary Charan Singh Haryana Agricultural Univeristy, Hisar, Haryana, India, p. 382.

Dhillon, M.K., Sharma, H.C., Singh, R. and Naresh, J.S. (2005) Mechanisms of resistance to shoot fly, *Atherigona soccata* in sorghum. *Euphytica*, **144** (3), 301–312.

Diarisso, N.Y. (1997) Spikelet flowering time and morphology as causes of sorghum resistance to sorghum midge (Diptera: Cecidomyiidae), in *PhD thesis*, Texas A&M University, College Station.

Dogget, H. (1972) Breeding for resistance to sorghum shoot fly in Uganda, in *Control of Sorghum Shoot Fly* (eds M.G. Jotwani and W.R. Young), Oxford and IBH Publishing Co., New Delhi, pp. 192–201.

Fletcher, T.B. (1917) Report of the Proceedings of the Second Entomological Meeting, Pusa, India, p. 47, 53–55, 68, 83, 87, 91, 99, 179, 187, 189, 199, 203.

Franzmann, B.A., Lloyd, R.J. and Zalucki, M.P. (2006) Effect of soil burial depth and wetting on mortality of diapausing larvae and patterns of post-diapause adult emergence of sorghum midge, Stenodiplosis sorghicola (Coquillett) (Diptera: Cecidomyiidae). *Australian Journal of Entomology*, **45**, 192–197.

Gahukar, R.T. (1991) Recent developments in sorghum entomology research. *Agricultural Zoology Reviews*, **4**, 23–65.

Haile, A. and Hofsvang, T. (2001) Effect of sowing dates and fertilizer on the severity of stemborer (Busseola fusca Fuller, Lepidoptera: Noctuidae) on sorghum in Eritrea. *International Journal of Pest Management*, **47**(4), 259–264; 37 ref.

Harris, K.M. (1961) The sorghum midge, *Contarinia sorghicola* (Coq.) in Nigeria. *Bulletin of Entomological Research*, **52**, 129–146.

Harris, K.M. (1979) Descriptions and host ranges of the sorghum midge, *Contarinia sorghicola* (Coquillett) (Diptera. Cecidomyiidae), and of eleven new species of *Contarinia* reared from Gramineae and Cyperaceae in Australia. *Bulletin of Entomological Research*, **69**, 161–182.

Jadhav, R. and Jadhav, L.D. (1978) Studies on preliminary screening of some sorghum hybrids and varieties against earhead midge (*Contarinia sorghicola* Coq.). *Journal of the Maharashtra Agricultural Universities*, **3**, 187–188.

Jalali, S.K. and Singh, S.P. (2001) Studies on the thermal requirements of estimating the number of generations of *Chilo partellus* (Swinhoe) and its natural enemies in the field. *Annals of Plant Protection Sciences*, **9** (2), 213–219.

Jermy, T. (1984) Evolution of insect/host plant relationships. *American Naturalist*, **124**, 609–630.

Jotwani, M.G. (1976) Insect pests of jowar and their control. *Pesticide Information*, **2**, 37–39.

Jotwani, M.G. and Srivastava, K.P. (1970) Studies on sorghum lines resistant against shoot fly *Atherigona soccata* Rond. *Indian Journal of Entomology*, **32**, 1–3.

Jotwani, M.G. and Young, W.R. (1971) Sorghum insect control – here's what's working in India. *World Farming*, 6–11.

Jotwani, M.G., Chaudhari, S. and Singh, S.P. (1978) Mechanism of resistance to *Chilo partellus* (Swinhoe) in sorghum. *Indian Journal of Entomology*, **40**, 273–276.

Kamala, V., Sharma, H.C., Manahor Rao, D. *et al.* (2009) Wild relatives of sorghum as sources of resistance to sorghum shoot fly, *Atherigona soccata*. *Plant Breeding*, **128** (2), 137–142.

Karanjkar, R.R., Chundurwar, R.D. and Borikar, T. (1992) Correlations and path analysis of shoot fly resistance in sorghum. *Journal of Maharashtra Agricultural Universities*, **17**, 389–391.

Kfir, R. (2002) Increase in cereal stemborer populations through partial elimination of natural enemies. *Entomologia Experimentalis et Applicata*, **104** (2/3), 299–306.

Khurana, A.D. and Verma, A.N. (1982) Amino acid contents in sorghum plants, resistance/susceptible to stemborer and shoot fly. *Indian Journal of Entomology*, **44**, 184–188.

Khurana, A.D. and Verma, A.N. (1983) Some biochemical plant characters in relation to susceptibility of sorghum to stemborer and shoot fly. *Indian Journal of Entomology*, **45**, 29–37.

Kishore, P. and Srivastava, K.P. (1976) Occurrence of cotton grey weevil as a serious pest of sorghum. *Entomologists' Newsletter*, **6** (3), 30–31.

Kogan, M. and Ortman, E.E. (1978) Antixenosis – a new term proposed to replace Painter's 'non-preference' modality of resistance. *Bulletin of Entomological Society of America*, **24**, 175–176.

Kundu, G.G. and Kishore, P. (1971). A note on the varietal differences in leaf damage due to *Pseudaletia separate* (Walker) in sorghum. Pages 153-155 in *Investigations on insect pests of sorghum and millets (1965-1970):final technical report* (Pradhan, S. *et al.* investigators). New Delhi, India: Indian Agricultural Research Institute.

Lal, G. and Pant, J.C. (1980) Laboratory and field testing for resistance in maize and sorghum varieties to *Chilo partellus* (Swinhoe). *Indian Journal of Entomology*, **42**, 606–610.

Lal, G. and Sukhani, T.R. (1982) Antibiotic effects of some resistant lines of sorghum on post-larval development of *Chilo partellus* Swinhoe. *Indian Journal of Agricultural Sciences*, **52**, 127–129.

Liu, Z., Wang, B., Xu, B. and Sun, J. (2011) Monoterpene variation mediated attack preference evolution of the bark beetle *Dendroctonus valens*. *PLoS ONE*, **6(7)**: e22005. doi:10.1371/journal.pone.0022005.

Mate, S.N., Phadanwis, B.A. and Mehetre, S.S. (1988) Studies on growth and physiological factors in relation to shoot fly attack on sorghum. *Indian Journal of Agricultural Research*, **22**, 81–84.

Mote, U.N. (1984) Sorghum species resistant to shoot fly. *Indian Journal of Entomology*, **46** (2), 241–243.

Namba, R. and Higa, S.Y. (1971) Host plant studies of the corn planthopper, *Peregrinus maidis* (Ashmead), in Hawaii. *Proceedings of the Hawaiian Entomological Society*, **21**, 105–108.

Narwal, R.P. (1973) Silica bodies and resistance to infection in jowar (*Sorghum vulgare* Pers.). *Agra University. Journal of Research (Science)*, **22**, 17–20.

Nwanze, K.F., Nwilene, F.E. and Reddy, Y.V.R. (1998) Fecundity and diurnal oviposition behaviour of sorghum shoot fly, *Atherigona soccata* Rondani (Diptera: Muscidae). *Entomon*, **23** (2), 77–82.

Nwanze, K.F., Pring, R.J., Sree, P.S. *et al.* (1992) Resistance in sorghum to the shoot fly, *Atherigona soccata*: epicuticular wax and wetness of the central whorl leaf of young seedlings. *Annals of Applied Biology*, **120**, 373–382.

Nwanze, K.F., Reddy, Y.V.R. and Soman, P. (1990) The role of leaf surface wetness in larval behaviour of the sorghum shoot fly, *Atherigona soccata*. *Entomologia Experimentalis et Applicata*, **56**, 187–195.

Ofomata, V.C., Overholt, W.A., Lux, S.A. *et al.* (2000) Comparative studies on the fecundity, egg survival, larval feeding, and development of *Chilo partellus* and *Chilo orichalcociliellus* (Lepidoptera: Crambidae) on five grasses. *Annals of the Entomological Society of America*, **93** (3), 492–499.

Ogwaro, K. and Kokwaro, E.D. (1981) Development and morphology of the immature stages of the sorghum shoot fly, *Atherigona soccata* Rondani. *Insect Science and Its Application*, **1**, 365–372.

Padmaja, P.G., Aruna, C. and Patil, J.V. (2012) Evidence of genetic transmission of antibiosis and antixenosis resistance of sorghum to the spotted stemborer, *Chilo partellus* (Lepidoptera: Pyralidae). *Crop Protection*, **31**, 21–26.

Padmaja, P.G., Madhusudhana, R. and Seetharama, N. (2010) Epicuticular wax and morphological traits associated with resistance to shoot fly, *Atherigona soccata* Rondani in sorghum. *Sorghum bicolor. Entomon*, **34** (3), 137–146.

Painter, R.H. (1951) *Insect Resistance in Crop Plants*, University Press of Kansas, Lawrence.

Ponnaiya, B.W.X. (1951) Studies in the genus *Sorghum*. I. Field observations on sorghum resistance to the insect pest, *Atherigona indica* M. *Madras Agricultural Journal*, **21**, 96–117.

Pont, A.C. (1972) The oriental species of *Atherigona* Rondani, in *Control of Sorghum Shoot Fly* (eds M.G. Jotwani and W.R. Young), Oxford & IBH Publishing, New Delhi, India, pp. 27–104.

Raina, A.K. (1985) Mechanisms of resistance to shoot fly in sorghum. A review, in *Proceedings of International Sorghum Entomology Workshop, July 15–21, 1984*, Texas A & M University, College Station, TX USA. ICRISAT, Patancheru, Andhra Pradesh, India, pp. 131–136.

Raina, A.K., Thindwa, H.K., Othieno, S.M. and Cork-Hill, R.T. (1981) Resistance in sorghum to the sorghum shoot fly: larval development and adult longevity and fecundity on selected cultivars. *Insect Science and Its Application*, **2**, 99–103.

Ramchandra Rao, Y. (1924) The genitalia of certain Anthomyiid flies (*Atherigona* spp.). *Report of the Proceedings of 5th Entomology Meeting, 1923*, Pusa, Bihar, India, Superintendent Government Printing, India, pp. 330–335.

Rana, B.S., Singh, B.U. and Rao, N.G.P. (1985) Breeding for shoot fly and stemborer resistance in sorghum. *Proceedings of the International Sorghum Entomology Workshop*, July 15–21, 1984, Texas A&M University, College Station, TX, USA, pp. 347–360.

Rebe, M., van den Berg, J. and McGeoch, M.A. (2004) Colonization of cultivated and indigenous graminaceous host plants by *Busseola fusca* (Fuller) (Lepidoptera: Noctuidae) and *Chilo partellus* (Swinhoe) (Lepidoptera: Crambidae) under field conditions. *African Entomology*, **12** (2), 187–199.

Rossetto, C.J., Goncalves, W. and Diniz, J.L.M. (1975) Resistencia de variedade AF-28 a mosca do sorgo, *Contarinia sorghicola*, no ausencia de outras variedades. *Anais Da Sociedade Entomologica Do Brazil*, **4**, 16–20.

Seshu Reddy, K.V. and Davies, J.C. (1977) Species of shoot fly *Atherigona* sp. present in Andhra Pradesh. *International Journal of Pest Management*, **23**, 379–383.

Seshu Reddy, K.V. and Omolo, E.O. (1985) Sorghum insect pest situation in eastern Africa, in *Proceedings of the International Sorghum Entomology Workshop*, July 15–21, 1984, Texas A&M University and ICRISAT, pp. 31–36.

Sharma, G.C., Jotwani, M.G., Rana, B.S. and Rao, N.G.P. (1977) Resistance to the sorghum shoot fly, *Atherigona soccata* (Rondani) and its genetic analysis. *Journal of Entomological Research*, **1**, 1–12.

Sharma, H.C. (1985) Screening for sorghum midge resistance and resistance mechanisms, in *Proceeding of the International Sorghum Entomology Workshop*, Texas A&M University and ICRISAT, pp. 89–95.

Sharma, H.C. (1997) Plant resistance to insects: basic principles, in *Plant Resistance to Insects in Sorghum* (eds H.C. Sharma, F. Singh and K.F. Nwanze), International Crop Research Institute for Semi Arid Tropics, Patancheru, pp. 24–31.

Sharma, H.C., Bhatnagar, V.S. and Davies, J.C. (1982) Studies on *Mythimna separata* at ICRISAT, in *Sorghum Entomology Progress Report, 1980/81*. International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh, India, (Limited distribution), pp. 1–44.

Sharma, H.C. and Davies, J.C. (1983) The oriental armyworm, *Mythimna separata* (Wlk.), in *Distribution, biology and control: a literature review. Miscellaneous Report*, Centre for Overseas Pest Research, No. 59, p. 24.

Sharma, H.C. and Franzmann, B.A. (2001) Orientation of sorghum midge, *Stenodiplosis sorghicola*, females (Diptera: Cecidomyiidae) to color and host-odor stimuli. *Journal of Agricultural and Urban Entomology*, **18** (4), 237–248.

Sharma, H.C., Franzmann, B.A. and Henzell, R.G. (2002) Mechanisms and diversity of resistance to sorghum midge. *Stenodiplosis sorghicola. Euphytica*, **124**, 1–12.

Sharma, H.C., Leuschner, K. and Vidyasagar, P. (1990a) Factors influencing oviposition behaviour of the sorghum midge, *Contarinia sorghicola* Coq. *Annals of Applied Biology*, **116**, 431–439.

Sharma, H.C., Leuschner, K. and Vidyasagar, P. (1990b) Componental analysis of the factors influencing resistance to sorghum midge. *Contarinia sorghicola Coq. Insect Science and Its Application*, **11** (6), 889–898.

Sharma, H.C. and Lopez, V.F. (1990) Mechanisms of resistance in sorghum to head bug. *Calocoris angustatus. Entomologia Experimentalis et Applicata*, **57** (3), 285–294.

Sharma, H.C. and Vidyasagar, P. (1994) Antixenosis component of resistance to sorghum midge. *Contarinia sorghicola Coq. in Sorghum bicolor (L.) Moench. Annals of Applied Biology*, **124**, 495–507.

Sharma, H.C., Vidyasagar, P. and Subramanian, V. (1993) Antibiosis component of resistance in sorghum to sorghum midge, *Contarinia sorghicola*. *Annals of Applied Biology*, **123**, 469–483.

Singh, B., Sung, L.K., Matusop, A. *et al.* (2004) A large focus of naturally acquired *Plasmodium knowlesi* infections in human beings. *Lancet*, **363**, 1017–1024.

Singh, B.K., Millard, P., Whiteley, A.S. and Murrell, J.C. (2004) Unravelling rhizosphere-microbial interactions: Opportunities and limitations. *Trends in Microbiology*, **12**, 386–393.

Singh, B.U., Padmaja, P.G. and Seetharama, N. (2004a) Biology and management of the sugarcane aphid, Melanaphis sacchari (Zehntner) (Homoptera: Aphididae), in sorghum: a review. *Crop Protection*, **23**, 739–755.

Singh, B.U., Padmaja, P.G. and Seetharama, N. (2004b) Stability of biochemical constituents and their relationship with resistance to shoot fly, *Antherigona soccata* (Rondani) in seedling sorghum. *Euphytica*, **136**, 279–289.

Singh, B.U. and Rana, B.S. (1986) Resistance in sorghum to the shoot fly, *Atherigona soccata* Rondani. *Insect Science and Its Application*, **7**, 577–587.

Singh, B.U. and Rana, B.S. (1992) Stability of resistance to corn planthopper, *Peregrinus maidis* (Ashmead) in sorghum germplasm. *Insect Science and Its Application*, **13**, 251–263.

Singh, B.U. and Seetharama, N. (2008) Host plant interactions of the corn planthopper, *Peregrinus maidis* Ashm. (Homoptera: Delphacidae) in maize and sorghum agroecosystems. *Arthropod–Plant Interactions*, **2**, 163–196.

Singh, S.P. and Verma, A.N. (1988) Antibiosis mechanism of resistance to stemborer, *Chilo partellus* (Swinhoe) in sorghum. *Insect Science and Its Application*, **9**, 579–582.

Singh, S.R., Vedamoorthy, G., Thoi, V.V. *et al.* (1968) *Resistance to stemborer, Chilo zonellus (Swinhoe) and stem fly, Atherigona socaata Rond*, In the world sorghum collection in India. Memoirs of the Entomological Society of India, Entomological Society of India, p. 79.

Srivastava, A.S. and Goel, G.P. (1962) Bionomics and control of red hairy caterpillar (*Amsacta moorei*). *Proceedings of the National Academy of Sciences of India, Section B*, **32** (2), 97–100.

Swami, H. and Bajpai, N.K. (2006) Preference of graminaceous host plants to stemborer, *Chilo partellus* (Swinhoe) at Udaipur, India. *Journal of Plant Protection and Environment*, **3** (2), 67–71.

Swarup, V. and Chaugale, D.S. (1962) A preliminary study on resistance to stemborer, *Chilo zonellus* (Swinhoe) infestation on sorghum, *Sorghum vulgare* Pers. *Current Science*, **31**, 163–164.

Teetes, G.L. (1985) Sorghum midge biology, population dynamics and integrated pest management. In: *Proc Int workshop Sorghum Insect pests*. Texas A&M University and ICRISAT, pp. 233–245.

Tsai, J.H. (1975) Occurrence of a corn disease in Florida transmitted by *Peregrinus maidis*. *Plant Disease Reporter*, **59**, 830–833.

van Rensburg, N.J. (1973) Notes on the occurrence and biology of the sorghum aphid in South Africa. *Journal of the Entomological Society of South Africa*, **36**, 293–298.

Venkateswaran, K. (2003) Diversity analysis and identification of sources of resistance to downy mildew, shoot fly and stemborer in wild sorghums, in *PhD thesis*, Department of Genetics, Osmania University, Hyderabad, Andhra Pradesh, India.

Verma, O.P., Bhanot, J.P. and Verma, A.N. (1992) Development of *Chilo partellus* (Swinhoe) on pest resistant and susceptible sorghum cultivars. *Journal of Insect Science*, **5**, 181–182.

Visser, J.H. (1986) Host odor perception in phytophagous insects. *Annual Review of Entomology*, **31**, 121–144.

Waquil, J.M., Teetes, G.L. and Peterson, G.C. (1986) Adult sorghum midge (Diptera: Cecidomyiidae) nonpreference for resistant hybrid sorghum. *Journal of Economic Entomology*, **79**, 455–458.

Wilbrink, G. (1922) An investigation on spread of the mosaic disease of sugarcane by aphids. *Medid Procfst. Java Suikerind*, **10**, 413–456.

Wuensche, A.L. (1980) An assessment of plant resistance to the sorghum midge, in *Contarinia sorghicola, in selected lines of Sorghum bicolour. PhD thesis*, Texas A&M University, College Station, TX, USA, p. 193.

Young, W.R. and Teetes, G.L. (1977) Sorghum entomology. *Annual Review of Entomology*, **22**, 193–218.

Zhang, Q.H. and Schlyter, F. (2004) Olfactory recognition and behavioural avoidance of angiosperm nonhost volatiles by conifer-inhabiting bark beetles. *Agriculture and Forest Entomology*, **6**, 1–19.

11

Millet Diseases: Current Status and Their Management

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11.1 Introduction

Millets are important crops in the semi-arid tropics of Africa and Asia, with 97% of millet production happening in developing countries. They can be grown under agricultural conditions where other cereals fail to produce an acceptable yield. Millet-growing dryland areas are mostly inhabited by the world's poorest people. Millets are high-energy, nutritious and healthy food, especially recommended for children, and the elderly. Under changing climatic conditions, these are the crops for future consideration. Disease-problems are one of the major constraints in millet production. In future, these problems are likely to increase because of climate change. Major diseases of millets are grain mould, downy mildew, blast, smut, rust, ergot, leaf spot, brown spot, and occasionally viral and bacterial diseases. In this chapter, major diseases of millets are discussed under three sub-headings, viz., sorghum diseases, pearl millet diseases and small millet diseases.

11.2 Sorghum Diseases

Sorghum is mostly grown in rainy (*kharif*) or post-rainy (*rabi*) season. Disease incidence is more during rainy season compared to post-rainy season. Major adverse effects of diseases include loss in productivity, production of quality grain in grain sorghum, fodder yield and quality in forage sorghum and sugar yield in sweet sorghum. Fungal diseases have major impact in sorghum followed by viral and bacterial diseases. Economic significance of a particular disease varies with location, environment, cropping season and type of sorghum. Diseases such as grain mould, anthracnose, downy mildew, ergot, smut, leaf blight and leaf spots are common worldwide. A list of common diseases of sorghum is given in the Table 11.1. In grain sorghum, grain mould, downy mildew, anthracnose and ergot are major diseases during rainy season, whereas root and stalk rot and viral diseases are common during post-rainy season. Other diseases like rusts, leaf spots, pokkah boeng and smuts occur sporadically. Diseases that are of importance on forage are foliar diseases, such as leaf spots, sooty stripes, leaf blight, downy mildew, anthracnose and rust. Other diseases such as viral diseases, sugary disease and head mould are important under specific agro-climatic environments.

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Table 11.1 Common diseases of sorghum.

Disease	Pathogen
Grain mould	*Fusarium, Curvularia, Alternaria, Phoma spp.*
Anthracnose	*Colletotrichum sublineolum*
Downy mildew	*Peronosclerospora sorghi*
Ergot/sugary disease	*Claviceps sorghi; C. sorghicola; C. africana*
Rust	*Pucciniap urpurea*
Leaf blight	*Bipolaris turcica*
Sooty stripe	*Ramulispora sorghi*
Zonate leaf spot	*Gleocercospora sorghi*
Grey leaf spot	*Cercospora sorghi*
Target leaf spot	*Phyllachora sacchari*
Loose smut	*Sporisorium cruenta*
Covered smut	*Sporisorium sorghi*
Head smut	*Sporisorium reilianum*
Long smut	*Tolyposporium ehrenbergii*
Charcoal rot	*Macrophomina phaseolina*
Pokkahboeng	*Fusarium moniliforme var. subglutinans*
Fusarium stalk rot	*Fusarium moniliforme*
Pythium root rot	*Pythium arrhenomanes*
Bacterial leaf stripe	*Pseudomonas andropogonis*
Bacterial leaf streak	*Xanthomonas axonopodis pv. holcicola*
Bacterial leaf spots	*Pseudomonas syringae pv. syringae*
Viral diseases	Maize stripe virus, maize mosaic virus

Leaf diseases destroy active leaf area, adversely affect accumulation of sugar and thus interfere with the quantity and quality of fodder. Sweet sorghum or high-energy sorghum has immense potential as a bio-energy maker and has great relevance in the renewable energy security. In addition to the grain, the juice from stalk, stover and bagasse can be used to produce alcohol (ethanol). Most of the diseases of grain sorghum crop up in sweet sorghum, depending on the growing conditions and environment. Leaf anthracnose, red-rot, leaf blight, downy mildew, rust, sugary disease, head mould and virus diseases are common in sweet sorghum. Many fungal, viral and bacterial diseases are reported on sorghum but all are not economically important.

11.2.1 Grain mould

Grain mould is a major biotic constraint on the production, marketing and utilisation of quality sorghum grain. It is one of the most important diseases of sorghum in many countries in Asia, Africa, North America and South America. The disease is particularly important on improved short- and medium-duration sorghum cultivars that mature during the rainy season under humid climates. Late-maturing, sorghums generally escape grain mould. The disease becomes severe in India because of widespread

cultivation of white grain, bold-seeded hybrids and varieties. It is common in the states of Maharashtra, Karnataka, Andhra Pradesh and Tamil Nadu. Grain mould has severe implication on grain quality and productivity. Major loss is due to quality deterioration and yield loss. Mouldy grain looses lustre and fetches far less market price than the normal one (Audilakshmi *et al.*, 2007). Yield loss occurs mostly due to reduction in seed size and weight, and rotting of grain. Seed value of grain gets affected because of loss of germination in mouldy seed. Production losses range from 30 to 100% depending on cultivar and weather (Singh and Bandyopadhyay, 2000). Economic losses are around US$130 million in Asia and Africa (ICRISAT, 1992) and US$50 – 80 million in India (Das and Patil, 2013). The disease has significant impact on human and livestock population and crop pattern. Nutritive value of food and feed, and the cooking quality of the grain get deteriorated. Mycotoxins present in mouldy grains are harmful to human, animal and poultry. In India, fumonisin B levels between 0.1 and 2.7 mg/kg grains have been reported in sorghum (Chatterjee and Mukherjee, 1994). Consumption of fumonisin-contaminated grains may be a possible reason of an acute disease outbreak among tribal in several parts of India. An outbreak of food poisoning characterised by abdominal pain and diarrhoea, attributed to the ingestion of fumonisin-contaminated mouldy sorghum and maize had been reported from a number of villages in South India (Bhat *et al.*, 1997). Major share of the rainy-season sorghum grains are utilised as feed for animal and poultry. There is report of health risk if mouldy grains are continuously fed to the livestocks including porcine pulmonary edema, liver toxicity and liver cancer in rats, atherosclerosis in monkeys and immunosuppression in poultry (Norred, 1993).

The first visible symptom of mould infection is pigmentation of the spikelet tissues. Anthers and filaments are also infected, depending on the severity of infection. Under humid conditions, infected grain may be covered by fungal growth even before physiological maturity, and such grains disintegrate under small pressure. Premature disintegration of mouldy grain is termed as 'pre-mature seed rotting' (Das *et al.*, 2012). The colour of infected grains varies from whitish, pinkish, greyish, to shiny black, depending on the fungus species. Fungal colonisation of grain may lead to sprouting of grains, which become soft due to the digestion of parts of the endosperm by amylase enzyme. Signs of mould infection on mature grain become prominent when pink, orange, grey, white or black colour fungal bloom appear on the grain surface. Discolouration is more prominent on white grain than on brown/red grain sorghum. Sometimes grain may not show external symptoms but develops fungal growth under inappropriate storage conditions.

Grain mould can be caused by one or many fungi, which may be weakly parasitic, pathogenic or saprophytic in nature. Among the parasites/pathogens, *F. moniliforme*, *C. lunata*, *A. alternate* and *P. sorghina* are predominant. Many saprophytic fungi may colonise mature grain under the condition of high humidity. Common fungi are *Bipolaris* spp., *Colletotrichum* spp., *Aspergillus* spp., *Cladosporium* spp., *Exerohilum* spp. etc. Among the *Fusarium* spp., *F. andiyazi*, *F. nygamai*, *F. proliferatum*, *F. Thapsinum* and *F. verticillioides* and among *Curvularia* spp., *C. lunata* are the most frequently occurred species. Infection occurs on spikelet tissues at the time of flowering by airborne conidia under moderate temperature (25 to 35 °C) and high humidity (>90%) (Thakur *et al.*, 2006). Frequent rains during grain development and maturity stage provide favourable conditions for saprophytic mould development. Plant residues and soil debris containing fungal hyphae and conidia are the primary sources of inoculums in the field. Crop residue buried deep in soil survives longer than the surface residue

(Nelson *et al.*, 1983). Under moist conditions, senescent leaves of sorghum plants produce abundant spores which are readily disseminated by wind and rain. Cool and dry weather is not favourable for grain mould development. Best option for management of grain mould is to use cultivars that mature during a period of no rains. However, this option is hardly practicable when rainfall pattern is erratic. Use of mould-tolerant cultivars and harvesting the crop at physiological maturity followed by drying of grain is the second best option to avoid grain deterioration due to saprophytic mould. Development of grain mould resistant cultivar is a big challenge as many different mechanisms of resistance are in operation (Mansuetus *et al.*, 1988; Esele *et al.*, 1993; Audilakshmi *et al.*, 1999; Aruna and Audilakshmi, 2004; Rodriguez-Herrera *et al.*, 2006; Katile *et al.*, 2010). These mechanisms could hardly be incorporated into a high-yielding bold-seeded cultivar. Therefore, disease-escape mechanism is more important for grain mould management. Long-duration cultivar that matures during rain-free periods generally escapes the disease. Chemical sprays may be useful if not washed out by frequent rains. However, it is hardly economical because of low price of sorghum grain and high price of the chemicals and labourers. For high-value seed production plot, spraying panicles with fluorescent pseudomonad may be undertaken that reduces grain mould severity and improves seed quality (Kannababu *et al.*, 2009).

11.2.2 Anthracnose

Anthracnose was first reported from Togo, West Africa in 1902 (Sutton, 1980). Since then, the disease has been observed in most of the regions of the world. The disease is common in many countries in Africa (Nigeria, Kenya, Togo, Mali, Zimbabwe, Ethiopia, South Africa), North America (South, Central and North America), South America (Brazil, Argentina, Guatemala) and Asia (India, China, Thailand). Anthracnose appears on several plant parts causing seedling blight, leaf blight, stalk rot and head blight. In India, it occurs on forage sorghum in moderate to severe form and sporadically on grain sorghum. The disease is common in Northern and Western India on forage and in Central and Southern India on grain sorghum. Losses due to anthracnose vary based on severity of infection and on plant parts infected. Seedling blight phase of anthracnose causes seedling mortality, which affects final plant stand in the field. Leaf anthracnose destroys photosynthetic leaf area and thus reduces grain filling, sugar accumulation and yields. Red rot phase of the disease damages stalk tissue and may affect movement of sap/nutrients to the earhead. Loss varies with level of incidence, environment and cultivar. Major economic loss occurs due to leaf anthracnose, which has negative impact on grain and fodder yield. Grain-yield losses of 50% can occur under severe epidemics, and it may go up to 70% on highly susceptible cultivars (Harris *et al.*, 1964; Thomas *et al.*, 1995; Mathur *et al.*, 2002). Estimation of monetary loss is complex and the quantitative data are not available. The disease has impacts on human and cattle population.

Anthracnose may infect seedlings as well as adult plants and symptoms can occur on any plant part. Leaf symptoms appear as small, elliptic to circular spots, usually 5 mm or less in diameter. Centre of the spot is straw-coloured with wide margin. Colour of the margin may be red, orange, purple or tan, depending on the pigment present in the cultivar (purple or tan). Under favourable conditions, the spots increase in number and combine to give a blighted appearance on the leaf. The fungi produce black dot-like fruiting structure at the centre of the spot, called acervulus (plural: acervuli). Under

favourable conditions, creamy to pinkish masses of spores are produced in the acervulus. The disease may defoliate plants, reducing growth and further development. In severe disease conditions, plants die before reaching maturity. Infected plants may also develop red rot symptom which is characterised by the presence of continuous to discontinuous type of reddish discolouration inside stalk tissue. If infection occurs at seedling stage plants become stunted and yellow and often do not produce tiller. In severe cases, the seedling wilts and dies. Anthracnose is caused by *Colletotrichum graminicola* (Synonym: *C. sublineolum*). The fungus has perfect state in *Glomerella graminicola*. Mycelium of *C. graminicola* is grey to olivaceous, septate, and sparingly branched when grown on culture medium. Acervuli produce numerous erect, hyaline, non-septate conidiophores on which conidia are borne terminally. The conidia are hyaline, non-septate, and obclavate but become sickle-shaped with age (Frederiksen, 1986). More than 40 races/pathotypes have been reported from different geographical areas of the world (Nakamura, 1982; Casela and Ferreira, 1988; Prom *et al.*, 2012) including nine from India (Pande *et al.*, 1991) using different sets of putative host differentials.

The fungus may infect plant part below or just above the ground. If infection is early and severe, pre-emergence damping-off may occur. There are contradictory reports about host specificity and host range of *C. graminicola* isolates from different graminiceous hosts (Mathur *et al.*, 2002). Conidia from crop residues or probably from wild sorghum species serve as the primary inoculums, which are spread by wind or rain. Conidia germinate by producing germ tubes, which develop into an appressoria that penetrates through the epidermis or stomata. Subsequently the pathogen establishes itself inside leaf tissue and develops visible symptoms on leaf. Warm, humid and wet weather predisposes plant to severe disease. Conidia are produced on lesions under conditions of high humidity or high moisture and require about 14 h to mature at 22 °C (Frederiksen, 1986). The fungus can survive as mycelium in host residue, wild sorghum species and some weeds and as conidia or mycelium in seed. Survival may be up to 10 months in plant debris buried in the soil (Mishra and Siradhana, 1979). Few isolates of *C. graminicola* can produce sclerotia (Rao *et al.*, 1998). Sclerotia survive up to 18 months in stalk residue placed on the soil surface, and their viability reduces when residues are buried deep in soil (Casela and Frederiksen, 1993). The infection can be controlled or minimised by cultural practices, crop rotation, clean cultivation and use of resistant cultivars. Collection and destruction of crop residues help eliminate sources of inoculum and chances of infection. Available resistant sources can be utilised for cultivar development against different pathotypes. There may be different genes conferring resistance to leaf, stalk and grain anthracnose. Resistance is controlled by single dominant or recessive genes, depending on the crosses (Mehta *et al.*, 2005; da Costa *et al.*, 2011). Various molecular markers such as Random Amplified Polymorphic DNA (RAPD) (Boora *et al.*, 1998), Restriction Fragment Length Polymorphism (RFLP) (Perumal *et al.*, 2009), Single Sequence Repeat (SSR) (Murali Mohan *et al.*, 2010) and Single Nucleotide Polymorphism (SNP) (Upadhyaya *et al.*, 2013) have been used for the identification of resistant genes for genetic improvement of anthracnose resistance.

11.2.3 Downy Mildew

Downy mildew of sorghum was first reported by Butler from India (Butler, 1907). Since then the disease has been reported from many countries in the tropical and sub-tropical zones. It was initially originated in Africa and Asia and subsequently spread to the

Americas in the late 1950s (Frederiksen, 1980). It is a potentially destructive disease in peninsular India (Karnataka, Tamil Nadu, Andhra Pradesh and Maharashtra). The disease causes significant loss in grain and fodder yield. The disease was in check for quite long time but has recently been showing increasing trends in India (Das and Madhusudhana, 2005). Systemic infection of downy mildew results in a barren inflorescence whereas local infection affects productive leaf area. Under favourable conditions the disease may outbreak as an epidemic. Crop losses estimated due systemic infection were found to vary from 2 to 20%. Annual yield loss was reported to be around 0.1 million tonnes in parts of India (Payak, 1975). In a single season in the United States, a downy mildew epidemic in Texas caused an estimated loss of US$2.5 million (Frederiksen *et al.*, 1969). The disease has impact on livestock population as the loss of stover yield can cause significant losses in income to poor farmers from crop–livestock production system. The disease has quarantine significance because of its seed-borne nature.

Sorghum downy mildew produces two sets of symptoms resulting from two types of infections – systemic and local. Infection in apical meristematic tissue is developed into systemic infection, under which seedlings develop pale yellow or light-coloured streaking or mottling on the leaf. The infected plants are chlorotic and stunted and may die prematurely. Symptoms are first expressed on the lower surface of the leaf that becomes covered by a white, downy growth consisting of conidia and conidiophores in cool humid weather. During later stages of the disease, leaves emerging from the whorl exhibit parallel stripes of green and white tissue. The infected areas die, turn brown, and disintegrate, resulting in a shredded appearance of the leaf. Systemically infected plants normally do not produce earhead but sometimes plant may recover and produce earhead (Singh and Milliano, 1989). Conidia produce in the infected plants become airborne and cause local infection on leaves. Local lesions are rectangular in shape, initially pale yellow in colour that later turn brown. The disease is caused by *Peronosclerospora sorghi* (Synonym: *Sclerospora sorghi*). The obligate parasites require living tissue for growth and generally do not grow in artificial media. However, there is report of *P. sorghi* successfully growing in dual culture with host tissue on a modified White's medium (Kaveriappa, 1980). Oospores are produced in the mesophyll tissue between the vascular bundles. They are spherical, hyaline to yellow, and enclosed in an irregularly thickened wall.

Systemic infection of young seedlings occurs either from oospores in soil or from conidia produced on early-infected plants. Infection normally occurs a week after emergence. The fungus grows internally, infects meristematic tissues and produces systemic symptoms. Both conidia and oospores germinate by a germ tube. Conidia production, dispersal and infection process require specific temperature and relative humidity (Pande *et al.*, 1997). The optimum temperature for conidia production is 18 °C. Oospores require low soil temperature (10 °C) and low soil moisture for infection. Production of conidia and infection process are favoured by a cool environment and high humidity. *Peronosclerospora sorghi* survives as oospore in soil and plant debris and spreads through oospores in the glumes of sorghum seeds and in plant debris. Conidia are fragile and play no role in the long distance dissemination. The pathogen may be present as mycelium in infected seeds, but mycelium is inactivated when seeds are dried. Therefore, seed-borne infection seemed to have negligible importance in spreading the disease. *Peronosclerospora sorghi* can also infect grasses such as *Euchlaena*, *Panicum*, *Pennisetum* and *Zea* spp. and can produce conidia and oospores on them. The collateral hosts serve as source of inoculums for the sorghum crop. Pathotypes

have been reported in isolates of *P. sorghi* from different geographic regions including the United States (Craig and Frederiksen, 1983), Brazil (Fernandes and Schaffert, 1983), Honduras (Craig and Odovody, 1992), Zimbabwe (de Milliano and Veld, 1990) and India (Pawar *et al.*, 1985). SSR markers have been developed from *Peronosclerospora* genomic DNA to distinguish isolates within several species of the oomycetes that cause downy mildew diseases (Perumal *et al.*, 2008).

Cultural practices including deep ploughing, rouging of infected plants, adjusting the sowing dates and crop rotation are recommended for the management of the disease. Use of disease-resistant cultivars is the best practice and the present-day cultivars have moderate level of field resistance. However, resistance is often broken down due to the development of pathogen race and repeated use of resistant cultivars. Continuous effort to develop resistant cultivars with new sources of resistance is required. Kamala *et al.* (2002) identified potential new sources of resistance genes from wild and weedy sorghums. Many accessions from Australia exhibited immunity to downy mildew. Chemical spray becomes necessary to control downy mildew if conditions are favourable for disease development. Seed treatment with Ridomyl-MZ @ 6 g/kg seed followed by a spray of Ridomyl-MZ @ 3 g/l reduces downy mildew incidence. Judicious use of metalaxyl is recommended as there is chance of resistance development against this fungicide. *Peronosclerospora sorghi* isolates from the downy mildew outbreak region in Texas were found to be resistant to metalaxyl fungicide, which had been used as an effective seed treatment for many years (Perumal *et al.*, 2008).

11.2.4 Ergot or Sugary Disease

Ergot of sorghum was first reported from India in 1917 (McRae, 1917) and in Australia in 1996 (Ryley, 1996). Now it is prevalent in many countries in Asia, Africa, South America, North America and Australia. The disease causes direct loss in seed yield, seed quality, germination, and indirect loss through rejection of seed lots due to contamination with ergot. Production of hybrid seed generally suffers from risk of ergot. Estimated production loss is about 10 to 80% in India and South Africa (Bandyopadhyay *et al.*, 1996). In addition to hybrid, ergot can cause wide-spread damage to popular varieties when environmental conditions are favourable. The disease has quarantine implications and seeds harvested from infected fields are often rejected in trading.

Exudation of honeydew-like droplet from infected floret is the indication of ergot infection. The exudates contain micro- and macro-conidia of the causal fungus. The symptom can be seen on a single, few or all florets in a panicle depending on the severity of infection. Honeydews fall on leaf and turn it black due to growth of saprophytic fungi. Infected florets do not produce grain and a wart-like fungal structure, called sclerotium, gradually evolves in place of grain. Sclerotia vary in shape, size, colour, and compactness depending upon the host genotype and environmental conditions. In sorghum, the sclerotium develops later from within the sphacelium and generally remains attached to a remnant of the sphacelium. Under warm and dry conditions sphacelia harden and form solid dense sclerotia known as ergot. Sclerotia of *Claviceps africana* are always found in association with sphacelia. Both are physically associated with one another and it is difficult to distinguish between them. Sclerotia are black in colour, elongated in shape, hard in texture, and bigger than sorghum seed. Three different species of *Claviceps*, cause ergot in different parts of the world. Distribution of *C. africana* is widespread across continents and found in Southern and Eastern Africa, South America, Australia,

Southeast Asia and India. Distribution of *C. sorghi* is limited to India (Kulkarni *et al.*, 1976) and Southeast Asia and *C. sorghicola* to Japan (Tsukiboshi *et al.*, 1999). Macroconidia of *C. africana* produces large numbers of secondary conidia, which become airborne and cause infection. They are oval to oblong, slightly constricted at the centre, and have two polar vacuoles. Macroconidia germinate to produce pear-shaped secondary conidia outside the surface of sticky honeydew. Sclerotia act as resting spore and widely vary in colour, shape, size and mass (Ramakrishnan, 1948; Kulkarni *et al.*, 1976) depending on genotypes, climate and stage of development. On germination, sclerotium produce one or more (1 – 7) elongated and pigmented stipes (Sangitrao and Bade, 1979). Each stipe develops a sub-globose, capitulum, inside which perithecia are developed. Perithecia contain asci, which on maturity produce filliform and hyaline ascospores.

Primary infection of ergot takes place either by ascospores or by conidia. Conidia are produced on collateral grass weeds, wild sorghums and infected panicles or on plant debris in the soil. Honeydew produced on the infected florets contains numerous macroconidia and secondary conidia that help in secondary spread of the disease. Several conidial cycles are completed in a season and conidia are spread by wind, rain and insects. Low night temperatures (<12 °C) during the period between 3 and 4 weeks before flowering to 5 days after flowering, high RH (>90%) or cloudy weather favour ergot disease development (Tonapi *et al.*, 2002). The pathogen survives via infected panicles left in the field or via sclerotia. Collateral hosts (*Pennisetum typhoides*, *Ischaemum pilosum* and *Panicum maximum*) also play a role in survival. Early sowing avoids the occurrence of the sugary disease (Anahosur and Patil, 1982). Removal of collateral host plants from the field helps to reduce pathogen inoculum and disease. Mechanical removal of sclerotia from seeds, by washing in 30% salt water followed by three times rinsing in plain water before sowing reduces seed contaminated infection. Ensuring synchrony of flowering between A and R lines avoids the occurrence of disease in seed production plots. Spraying panicles with fungicides (Bavistin/Tilt/Mancozeb) minimises disease and its subsequent spread (Nagarajan and Saraswathi, 1971; McLaren, 1994). First spray should be done at initiation of flowering and rest two sprays at 10 days interval.

11.2.5 Rust

Rust is common in almost all sorghum-growing countries in Africa, Asia, North and South America. The disease occurs regularly in many places, but rarley becomes severe. Rust infection weakens the plant and makes it vulnerable to other diseases. Early-sown crops often escape rust injury and the disease mainly observed on late sown crops. Present-day cultivars, especially tan type varieties and hybrids possess tolerance to sorghum rust. Purple-pigmented sorghums are generally susceptible to rust (Singh *et al.*, 1994). The disease may become severe under cool humid weather.

Sorghum rust is caused by *Puccinia purpurea* Cook. The fungus produces urediniospores and teleutospores on sorghum. Reddish brown rust pustules appear first on both the surfaces of the lower leaves, the upper half being more severely affected than the lower half. Later the infection may spread to the younger leaves. Several pustules (rust sori) may combine to form large patch on leaves and the infected leaves die prematurely giving the plants an unhealthy appearance. Severely affected plant may fail to produce earhead. Yield loss due to rust may vary from 29 to 65% under certain condition (Bandyopadhyay, 1986; Hepperly, 1990).

Urediniospores survive on sorghum in the field or on perennial and collateral hosts. The airborne spores cause primary infection. Urediniospores on freshly infected plants serve as source of secondary inoculum. *Oxalis corniculata* serves as alternate hosts. Use of resistant cultivars is the best known control measure for sorghum rust as is true in other cereal rusts. Foliar spray of Mancozeb @ 0.2% effectively controls the disease.

11.2.6 Leaf Blight

Leaf blight causes considerable economic losses to sorghum. First report of the disease was from India (Butler, 1918; Mitra, 1923). The disease is prevalent in areas with tropical humid weather and common in India, United States, Mexico, Brazil, Argentina, Kenya, Zimbabwe, Sudan and other sorghum-growing countries (Frederiksen, 1978; Ngugi *et al.*, 2002). In India the disease occurs almost every year in moderate to severe form in almost every state (Anahosur, 1992) and particularly on forage sorghum in Rajasthan, Haryana, Uttarakhand, Uttar Pradesh and Maharashtra. Financial loss due to leaf blight varies with incidence, severity, prevailing environment, growth stage of the crop and resistance in cultivar. Infection before flowering causes more damage than late infection. If the disease is established on susceptible varieties before panicle emergence, 50% losses in grain yield may occur (Frederiksen, 1986). Leaf blight reduces current photosynthesis because of loss of leaf areas. The pathogen produces toxins that may be partially responsible for the death and collapse of host cells (Tuleen and Frederiksen, 1977). Seedling blight phase sometimes become severe and affect final plant stand in the field. Damages on leaf areas result in reduced yield of grain as well as fodder. The epidemiological outbreaks of the disease have been reported in post-rainy sorghum in Karnataka, (Desai, 1998) and in rainy sorghum in Rajasthan (Mathur and Bunker, 2001).

Typical symptoms of leaf blight include appearance of long elliptical, spindle-shaped necrotic lesions which are straw coloured in the centre with dark brown margins, especially in older plants. Colour of lesion varies with pigment present in the plant and lesion shape and size varies with the level of resistance in a genotype. Lesion size varies from 5 to 155 mm in length and 2–20 mm in width (Bunkar and Mathur, 2010). Many long spots may coalesce to form large necrotic areas that may lead to the wilting of leaf and premature death of the plant. Under humid conditions, the pathogen produces numerous spores on the surface of lesions, and gives a dark grey appearance to the leaf. Severely infected crop gives a blighted look when viewed from a distance. The disease is caused by *Exserohilum turcicum* (Pass.) Leonard and Suggs (Synonym: *Helminthosporium turcicum* (Pass.); *Bipolaris turcica* (Pass.) Shoemaker; and *Dreschslera turcica* (Pass.) Subramanian & Jain). The perfect state is *Trichometasphaeria turcica* Luttrell. *Exserohilum turcicum* produces light grey, straight or curved, 3–8 septate conidium singly on the conidiophore. The conidia have a truncate and protuberant hilum in their basal cell. Conidia germinate by polar germ tubes. Pseudothecia have been observed under controlled conditions (Leonard and Suggs, 1974). Pathogen *E. turcicum* infects hosts such as maize, Johnson grass, teosinte, paspalum and other cereals. Variation in pathogenic properties of this fungus has been reported in sorghum (Mathur *et al.*, 2011). However, there are no reports on the existence of races of *E. turcicum* from sorghum.

Foliar pathogens favour moderate temperature, extended periods of cloudy weather, high humidity, dew and warm and humid weather. Intermittent rains and cool winds favour secondary spread within fields and also for long-distance dissemination of

pathogen by wind. Leaf blight pathogen persists as mycelia and conidia in infected crop residues on or in the soil and on the glumes of sudangrass seed. Airborne conidia are responsible for secondary spread within and between fields. Infection and disease development is favoured by moderate temperatures (18–25 °C) and high humidity. Minimum temperatures between 14 and 16 °C and mean temperatures between 20 and 22 °C with high humidity are most favourable for disease development (Thakur *et al.*, 2007). At least two types of resistance are known: polygenic resistance, characterised by few and small lesions, and monogenic resistance, characterised by a hypersensitive fleck and little or no lesion development. Use of good quality and healthy seeds, crop rotation with non-hosts once in 2 years, clean cultivation before taking up planting and after planting, cultural practices such as adjusting sowing window, proper tillage and intercropping with non-hosts reduce disease incidence. Destruction of weeds, volunteer, wild sorghum and alternate hosts help to reduce primary inoculum. Need-based use of fungicides (metalaxyl, captan) with right dosage and at right time is beneficial. However, use of disease-resistant cultivars is the best option considering the cost of chemical treatments.

11.2.7 Leaf Spots

Many leaf spots caused by fungi and bacteria are reported on sorghum. Sooty stripes (*Ramulispora sorghi*), zonate leaf spot (*Gleocercospora sorghi*), grey leaf spot (*Cercospora sorghi*), rough leaf spot (*Ascochyta sorghina*), target leaf spot (*Bipolaris sorghicola*), oval leaf spot (*Ramulispora sorghicola*) and tar spot (*Phyllachora sacchari*) are caused by fungi while bacterial leaf stripe (*Pseudomonas andropogonis*), leaf streak (*Xanthomonas axonopodis* pv. *holcicola*) and bacterial leaf spots (*Pseudomonas syringae* pv. *syringae*) are caused by bacteria. Fungal leaf spots are not much damaging in general. They are more visible on purple or red pigment lines and relatively less on tan cultivars. Few have little economic importance while others assume significance under specific conditions. Bacterial leaf streak and bacterial leaf spot are less common in tropical or subtropical climate and more common in temperate areas and at higher elevations in the tropics.

Sooty stripe is characterised by small, circular to elongated reddish brown spots on leaf with distinct yellow haloes. Lesions coalesce to form necrotic areas with blackish or sooty centre. Numerous sclerotia are formed on the surface of the lesion giving it a rough appearance. Zonate leaf spots appear as circular, reddish purple bands alternating with straw-coloured areas. Alternating bands with irregular borders form a zonate pattern on leaves. The spots often occur along the margins of leaves forming semi-circular patterns. Symptoms may also occur on leaf sheaths and these can also become infected. Pink to salmon coloured gelatinous spore masses are formed above stomata in favourable weather. High incidence during seedling stage may result in severe defoliation or death of infected plants. Grey leaf spot is characterised by narrow rectangular lesions delimited by veins. A small spot is formed in between veins that later may enlarge longitudinally to develop irregular blotches. Target leaf spot is characterised by the appearance of oval to cylindrical spots with irregular margin. The spots are purple to red in colour and occasionally with straw-coloured centre. Many spots may combine to form large lesions. Bacterial leaf stripe is characterised by the presence of interveinal stripe on leaves. Bacterial exudates can be seen on careful observation of the lesions. Bacterial leaf streak is characterised by the presence of short interveinal red stripes with water-soaked appearance on leaves. Later, lesions become irregular with necrotic centre and

red margin. In bacterial leaf spot, small water-soaked lesions are developed on the leaf or leaf sheath. Lesions become irregular with red margin.

Moderate temperature, long cloudy weather, high humidity, heavy dew and warm and humid weather are favourable for leaf spot development. Intermittent rains and cool winds favour the secondary spread within fields and also for long-distance dissemination of pathogen by wind. Sooty stripe pathogen survives as sclerotia in leaf residue on or below the soil surface. When conditions become favourable, sclerotia produce conidia, which are disseminated by wind and rain. The fungus survives on some perennial hosts, such as *Sorghum bicolor* subsp. *bicolor*, *S. halepense*, and *S. purpureosericeum* (Frederiksen, 1986). Zonate leaf spot pathogen over seasons as sclerotia formed within the dead tissue of old leaf lesion. They are also produced abundantly on millet and other grasses, and sclerotia from these hosts may also function in the survival of the pathogen. The sclerotia germinate and form conidia, which infect the next crop. During wet weather, conidia are produced on the new lesions and cause further spread of the disease. The fungus may also be carried on seed. Bacteria causing leaf diseases on sorghum mostly survive in soil-borne crop residues. Seed-borne nature of these bacteria is not yet known except for *Pseudomonas syringae* causing leaf spot of sorghum. Their dissemination to plant mostly takes place by rain splash.

Use of good-quality and healthy seeds, crop rotation with non-hosts once in 2 years, clean cultivation before taking up planting and after planting, cultural practices like adjusting dates of sowing, proper tillage and inter-cropping with non-hosts reduces foliar disease incidence. Primary inoculums may be reduced by destruction of weeds, volunteer and wild sorghum and alternate hosts. Need-based use of fungicide or bactericide in supplement with host resistance are beneficial for management of the disease.

11.2.8 Smuts

Four different types of smuts are observed in sorghum in almost all sorghum-growing regions in the world. Presently, sorghum smuts do not cause much economic damage. In India, they are found here and there, and are of minor importance. Their importance has been reduced, especially after the advent of seed-treatment fungicides. Different types of smuts are covered smut (*Sporisorium sorghi*), loose smut (*Sporisorium cruenta*), head smut (*Sporisorium reilianum*) and long smut (*Tolyposporium ehrenbergii*). In covered smut, sori are formed in the place of healthy grains, where most of the grains of an infected ear are replaced by smut sori. The membrane-like structure covering the spore masses generally persist up to threshing. In loose smut, the affected plants are stunted, produce thinner stalks, more tillers and earlier to flower than the healthy plants. All the spikelets of an infected earhead get malformed and hypertrophied. The membrane-like structure covering the spore masses generally ruptures soon after head emergence. In head smut, a sorus fully covered with a greyish-white membrane emerges from the boot leaf in place of inflorescence. When fully emerged the fungal membrane ruptures releasing spore masses in the air leaving filamentous vascular tissues of the host. In long smut, the sorus is covered by a whitish to dull yellow, fairly thick membrane and is much longer than those of the other two smuts.

Loose and covered smuts are externally seed-borne and easily controlled by seed dressing with sulphur (@ 4 g kg/1 seed). Collecting smutted heads in cloth bags and dipping in boiling water to kill the pathogen will reduce the inoculum potential for the next

year's crop. Long smut is airborne and difficult to control. Adjusting sowing dates seems to help in avoiding the disease.

11.2.9 Charcoal Rot

Macrophomina stalk rot, popularly known as charcoal rot, is a common disease and is reported from all the diverse areas in the tropics, sub-tropics and temperate regions. It is a stress-related disease that becomes severe under post-flowering moisture stress conditions. In India, the disease is prevalent in post-rainy sorghum-growing tracts of Maharashtra, Karnataka and Andhra Pradesh. Charcoal rot mainly affects high-yielding cultivars and land races are less affected. The pathogen infects root and stalk and may block water movement through vascular bundles. Rotting and weakening of the basal internodes cause lodging of the crop. Grain-filling process in such plants is greatly affected. Yield losses vary, depending on weather and the growth stage of cultivars. In general, the disease becomes conspicuous near crop maturity. In some hybrid sorghums, more than 50% of the plants may break over at the base. There may be four different types of crop losses that include poor crop stands due to seedling blight; loss in yield and quality of grain due to premature lodging of plant and improper grain filling; post-production loss of grain yield in lodged plants due to destruction of such plants by termites and rodents in the field and loss in quality and quantity of fodder due to infection and destruction of the stalk. Grain-yield loss depends on the stage of the crop when lodging takes place and the extent of lodging. Crop lodging of 100% could cause 23–64% loss in grain yield under experimental conditions (Mughogho and Pande, 1984). Loss in grain weight may vary from 15 to 55%. In the diseased stalk, the pathogen produces many toxins. The toxin phaseolinone, produced by *M. phaseolina*, can cause anaemia in mice (LD_{50} 0.98 g/kg/body wt) (Bhattacharya *et al.*, 1994). Thus, the disease has indirect implications on animal health. Diseased stalks cannot be stored for long time as it loses moisture and becomes unfit for consumption by cattle.

Lodging of the crop and poor grain filling indicate that the crop is infected by charcoal rot pathogen. Infected roots and lower stem of the infected plant show water-soaked lesions that slowly turn brown or black. Affected stalks become soft at the base and often lodge even due to moderate wind. Thus pre-mature lodging is the most apparent symptom of charcoal rot. When infected stalk is split open, the pith is found disintegrated across several nodes. The cortical tissues are disintegrated and vascular bundles get separated from one another. The vascular tubes contain numerous charcoal-coloured sclerotia of the pathogen. The disease may appear both during post-flowering and seedling stages. The disease is caused by *Macrophomina phaseolina* (Tassi.) Goid (Perfect state: *Sclerotium bataticola* Taub). The fungus is highly variable in size of sclerotia and presence or absence of pycnidia. Sclerotia are called microsclerotia, which are loose type, brown to black, irregular in shape and size, and are highly variable within an isolate. Pycnidia stage is uncommon in sorghum. Physiological specialisation has been reported in this pathogen (Cloud and Rupe, 1991). Chlorate-sensitive biotypes score significantly high disease than chlorate-resistant ones (Das *et al.*, 2008a). *Macrophomina phaseolina* is present in most cultivated soils and can infect about 500 plant species worldwide, including a wide range of agriculturally important crops (Dhingra and Sinclair, 1978).

The fungus is soil-borne that survives as sclerotia on the infected plant debris. The sclerotia, which can survive for 2–4 years in the soil, serve as primary source of inoculum.

Shallow burial of infected stalk pieces increased survival of the pathogen compared to material buried deeply (Singh and Kaiser, 1991). Dry weather, high temperature and low soil moisture are the important factors predisposing sorghum plants to infection by *M. phaseolina*. Germination of sclerotia is triggered by root exudates from sorghum seedlings. If infection occurs before the emergence of secondary roots, the plants die. Fungal mycelium colonises the xylem vessel and blocks the translocation of water and carbohydrate to the upper plant parts. The prevalence of high soil temperature (35–38 °C) and low soil moisture during the post-flowering stage are the most important factors predisposing sorghum plants to charcoal rot. Under the condition of stress (moisture, temperature and photosynthesis) that often coincide with the onset of flowering, the activity of *M. phaseolina* increases many folds, leading to rapid and extensive rotting of roots and stalks that result in lodging of the crop.

Chemicals are not generally used for management of sorghum diseases. Deep sowing, conservation of soil moisture, optimum plant density, wheat straw mulching and mixed cropping with pigeonpea are some of the practices recommended for management of charcoal rot. Early-maturing varieties generally escape disease. High level of genetic resistance is not available. Strong relation of the disease with yield and environmental stresses, particularly moisture and temperature, makes the task of evaluating host resistance more challenging. Drought-tolerant, lodging-resistant and non-senescing sorghum genotypes are supposed to have good tolerance to charcoal rot. However, finding such genotypes with high grain yield under desirable agronomic background are often not easy. Seed treatment with talc formulation of *Pseudomonas chlororaphis* SRB127 is reported to reduce disease and increase seed weight (Das *et al.*, 2008b).

11.2.10 Viral Diseases

Three groups of plant viruses, viz., potyvirus, tenuivirus and rhabdovirus, infect sorghum. Among potyviruses, sugarcane mosaic virus (SCMV), maize dwarf mosaic virus (MDMV), Johnson grass mosaic virus (JGMV) and sorghum mosaic virus (SrMV); among tenuiviruses, maize stripe virus or MStV (formerly MStpV); and among rhabdoviruses, maize mosaic virus (MMV) have been reported to naturally infect sorghum crop in different countries. MStV, MMV and SRSV are economically important for sorghum in India. The sorghum chlorotic stripe virus was the variants of MStV and designated as MStV-Sorg (or MStV-S) to distinguish it from MStV. Sorghum mosaic was first observed on sorghum in peninsular India during 1988 (Naidu *et al.*, 1989). There is report of the occurrence of sorghum red stripe in India from Maharashtra (Mali and Garud, 1977). A potyvirus naturally infecting sorghum grown in Maharashtra was termed as sugarcane mosaic virus-Jg (SCMV-Jg) (Garud and Mali, 1985). Later, the virus was named as sorghum red stripe virus-Indian isolate (SRSV-Ind). Sorghum red stripe virus (SRSV) was reported to be related to potyvirus SCMV, but was distinct from MDMV-A, MDMV-B and SrMV (Mali and Thakur, 1999).

Viral disease incidence may vary from 4 to 14%. On average, yield loss of 2–4% for grain and 2–8% for fodder is common. Yield losses vary with the stage of infection. Infection at early stages results in higher grain and fodder losses in comparison to that at later stages. Reduction of plant height, earhead weight and grain mass to the extent of 73, 93 and 25%, respectively has been reported in the variety CSV15 (Revuru and Garud, 1998). Apart from effects on grain, viral diseases have adverse effect on forage quality. Leaf protein content was reduced by 16.98 and 37.58% in forage cultivar MKV

Chari-1 and SSG 59-3, while the total soluble solid content reduction was 3.25 and 3.19%, respectively (Rathod *et al.*, 2004). Infection with SRSV significantly reduced plant height, leaf area, juice yield and chlorophyll content.

Symptoms of viral diseases vary depending on the virus. There may be single or multiple viral infection leading to complex symptom development. Occurrence of maize stripe virus on sorghum (MStV-S) was first reported in India during the 1990s (Peterschmitt *et al.*, 1991). The symptoms on sorghum include appearance of continuous chlorotic stripes between the veins of the infected leaf progressing from the base towards the tip of the leaves. The infection is systemic and subsequent leaves appear with yellow stripes. Early-infected plants die sooner or later without the emergence of earhead. Plants infected at later stages appear dwarfish with short internodes, show partial exertion of earhead. The disease is also known as chlorotic stripe stunt or sorghum stripe disease, the name derived from its characteristic stripe symptoms on leaf. In an infected plant, expression of first chlorotic symptom can take place on any leaf starting from the 4th to the 11th leaf (Das and Prabhakar, 2002). Sorghum mosaic virus (MMV-S) is characterised by fine discontinuous chlorotic streaks between the veins on leaf. Infected plants become stunted in growth with short internodes. Early-infected plants die sooner or later without the emergence of earhead. Sorghum red stripe virus (SRSV) infection is characterised by systemic symptoms of mosaic followed by necrotic red stripe and temperature-dependent red leaf. Severely infected crops may develop necrosis and produce burning appearance when viewed from a distant. Recently there was an outbreak of red stripe disease in Maharashtra India (Narayana *et al.*, 2011).

MStV-S and MMV-S are transmitted by insect vector *Peregrinus maidis*, which is known as shoot bug and is also a major pest on sorghum in India (Chellaiah and Basheer, 1965). Shoot bug sucks sap from the leaves, leaf sheaths and stem and transmits virus from the diseased to the healthy plants. The vector requires feeding on the infected plant for at least 4 hours to acquire the virus and another 8–22 days for infection of a new plant. The vector requires a minimum of 1 hour feeding to transmit the virus in a plant. A viruliferous vector retains the virus until its death and transmits it from one generation to another through eggs in a persistent manner (Nault and Gordon, 1988). The nymphs and macropterous females are more efficient transmitters of MStV-S and MMV-S than the males. Neither of these two viruses is transmitted by seed or mechanically by sap. Mode of transmission of sorghum red stripe virus (SRSV) is not yet known. The potyvirus SCMV, which is related to SRSV, may be transmitted mechanically by plant sap and by various aphids in non-persistent manner. Plant growth stages between 36 and 65 days after emergence have been identified as highly susceptible for the development of chlorotic stripe virus in rabi sorghum. Both the MStV-S and MMV-S can infect wild Johnson grass which can serve as important sources for primary inoculums at the beginning of the season. The trans-ovarial nature of transmission across insect generations contributes greatly to the perpetuation of the disease. Viral diseases can be managed by clean cultivation, vector control and adjustment of sowing time. The practice of uprooting and burning of the infected plants help to reduce source of inoculum for the vector and thus reduce spread of the disease in the field. There is strong relation between vector population and field incidence of MStV and MMV (Reynaud *et al.*, 2009). Spraying of Imidachlorpid @ 1.5 ml/L water effectively reduces vector population and the disease. Disease incidence in India is reported to be reduced as sowing of post-rainy sorghum is shifted from September to October (Das and Raut, 2002).

11.3 Pearl Millet Diseases

Pearl millet is the most widely cultivated cereal in India after rice and wheat (Table 11.2). India produces more than half the world's pearl millet. Presently, it is cultivated in an area of 7.2 million ha. Rajasthan is the major pearl millet growing state, covering 50% of the total area. Around 40% areas are in the states of Maharashtra, Gujarat, Uttar Pradesh and Haryana. Pearl millet is a crop that is grown under dry climate, yet it suffers from infection of many diseases. Compared to fungal diseases incidence of bacterial and viral diseases are negligible. King (1992) ranked relative importance of pearl millet diseases as downy mildew 45%, striga 32%, smut 9%, ergot 7%, rust 3%, viruses, >1% and other diseases 3%. Downy mildew is important in India and to some extent in Western Africa, and striga is important in Western Africa. Downy mildew, leaf blast, ergot, smut and rust occur almost regularly in low to severe form in pearl millet growing areas across India.

11.3.1 Downy Mildew

Downy mildew is considered the important disease of pearl millet due to its widespread occurrence sometimes in epidemic form, and extensive damaging effect on vegetative as well as reproductive parts. The disease is present in all pearl millet growing regions

Table 11.2 Common diseases of pearl millet.

Disease	Pathogen
Downy mildew	*Sclerospora graminicola*
Blast	*Pyricularia grisea*
Ergot	*Claviceps fusiformis*
Smut	*Moesziomyces penicillariae*
Rust	*Puccinia penisetti (P. substriata var. indica)*
Top rot	*Fusarium moniliforme*
Head mould	Various fungi
Bipolaris leaf spot	*Bipolaris setariae*
Cercospora leaf spot	*Cercospora penniseti*
Curvularia leaf spot	*Curvularia penniseti*
Dactuliophora leaf spot	*Dactuliophora elongata*
Drechslera leaf spot	*Drechslera dematioidea*
Myrothecium leaf spot	*Myrothecium roridum*
Phyllachora leaf spot	*Phyllachora penniseti*
Zonate leaf spot	*Gloeocercospora sorghi*
Exserohilum leaf blight	*Exserohilum rostratum*
Phyllosticta leaf blight	*Phyllosticta penicillariae*
Rhizoctonia blight	*Rhizoctonia solani; Rhizoctonia zeae*
Southern blight	*Sclerotium rolfsii*

in India and Africa. However, it has not yet been reported on pearl millet in the United States. In India, Gujarat, Rajasthan, Haryana in the northwest and Tamil Nadu and Karnataka in the south are the major downy mildew-prone areas for pearl millet. In fields, the range of downy mildew incidence was up to 90%, depending on the location and specific cultivar (AICPMIM, 2011–2014). Pearl millet hybrids developed during 1970s and 1980s in India were the worst affected due to severe outbreak of this disease. Downy mildew epidemics caused substantial yield losses in F1 hybrids during 1970–1976, during 1983 and 1984 and again in 1987 and 1988 (Singh *et al.*, 1993) and many popular hybrids were then withdrawn from cultivation. The epidemic was mainly due to the narrow genetic base of parental lines of the hybrids. Presently, the downy mildew disease is under control as the hybrids are based on diverse genetic backgrounds. The disease affects grain yield, and there is highly significant ($p = 0.05$) negative linear correlation between disease incidence and severity on yield (Gwary *et al.*, 2009). Apart from yield, the disease can also adversely affect fodder quality. Total soluble sugars were reported to be reduced in diseased plants compared to healthy plants of pearl millet hybrids (Upasana *et al.*, 2010).

In pearl millet, downy mildew is mostly developed as a systemic disease. Symptoms of systemic infection are expressed in the leaf and earhead. Chlorosis or yellowing symptoms on the lower leaves progressively spread to upper leaves and gradually all the leaves become infected. Frequently, only the lower part of a leaf shows symptoms, which is known as 'half leaf' symptoms. Numerous spores are produced on the lower side of the infected leaves. Severely infected plant become stunted and may fall short to produce earhead. Sometimes the infected plant produces symptom only on earhead in the form of leafy structure. Downy mildew at this stage is known as 'green ear' disease or virescence. Green ear can also produce asexual spores if conditions are favourable. Local lesion symptoms are rare in pearl millet. The disease is caused by *Sclerospora graminicola*, an obligate oomycetes that reproduces both asexually by producing sporangia and sexually by means of oospores. Two mating types have been identified in *S. graminicola.* The fungus is heterothallic but homothalism has also been reported (Michelmore *et al.*, 1982; Pushpavathi *et al.*, 2006). The existence of mating types and their frequency greatly contribute towards the variability of the pathogen. *Sclerospora graminicola* may be even highly cultivar-specific (Singh and Singh, 1987). Molecular characterisation of the pathogen has been carried out using SSR, ISSR, RFLP and RAPD for studying variability (Sastry *et al.*, 1995; Sudisha *et al.*, 2009; Sharma *et al.*, 2010). A SCAR primer pair (UOM3-Sg-Path1-F/R) has been developed for rapid identification and specific detection of *S. graminicola* pathotype-1 (Sudisha *et al.*, 2009).

Primary infection of pearl millet downy mildew takes place at the underground part of the seedling from germinating oospores in the soil. Systemically infected leaves produce abundant sporangia, which become airborne and cause secondary infection. Optimum temperature and humidity for the production of sporangia is 20–25 °C and RH 95–100%. Sporangia are short-lived, can survive for about 24 h at low temperature (5–15 °C). Sporangial infectivity is limited by seedling age, from the time of seed germination to the 1–2 leaf stage. Thereafter, the susceptibility decreases sharply (Singh and Gopinath, 1985). Zoospore produces germ tube that penetrates the leaves directly through the epidermal cells. The pathogen colonises the leaf tissue inter- and intra-cellularly (Celia Chalam, 1996). Oospores are produced in infected leaves when compatible mating types of *S. graminicola* are present in the same tissue, or when homothallism is functioning. The role of alternate/collateral hosts in the survival of pathogen is not clear. Although

many graminaceous species have been reported as hosts of *S. graminicola* (Bhat, 1973) their role in disease epidemiology is doubtful. The disease is assumed to be seed-borne in the form of seed-carried oospores, however, internal seed transmission has been a subject of controversy (Safeeulla, 1976; Thakur and Kanwar, 1978; Shetty *et al.*, 1980).

The disease can be well managed by use of resistant varieties and hybrids. Present-day hybrids having wider genetic base hold a good degree of tolerance to downy mildew. Varieties show better tolerance to downy mildew than hybrids. Efforts have been made to utilise recovery resistance in which systemically infected plants outgrow the disease and produce healthy panicles. Both the protective and systemic fungicides have been used but protective fungicides are not as effective as the systemic ones. Seed treatment with metalaxyl, a systemic fungicide, at 2 g a.i./kg seed control the disease for about the first 5 weeks after sowing (Dang *et al.*, 1983). However, seed treatment coupled with a single foliar application was found much superior to the seed treatment alone (Shankara Rao *et al.*, 1987). Anaso and Anaso (2010) reported that Apron Star 42WS, a new formulation of metalaxyl, for seed dressing is cost-effective and sustainable in the downy mildew endemic areas of northern Nigeria. Seed priming with chitosan protected pearl millet plants systemically against downy mildew disease (Manjunatha *et al.*, 2009).

11.3.2 Blast

Leaf spot or blast is a common disease of pearl millet and is noticed wherever the crop is grown. The disease was first recorded in Uganda in 1933. In India, the disease was first reported from Kanpur, Uttar Pradesh (Mehta *et al.*, 1953). It is an important disease for grain and forage pearl millet in India, United States and in many African countries. Blast is generally more severe in finger millet than in pearl millet but recently the disease is increasing in pearl millet (Lukose *et al.*, 2007; AICPMIP, 2013). It is a serious disease of forage pearl millet in southern coastal plains of the United States (Wilson and Gates, 1993). In India, the disease is becoming common in the states of Rajasthan, Gujarat, Maharashtra and Madhya Pradesh. Both the seedlings and adult plants of forage and grain pearl millets are affected by this disease resulting in premature drying of leaves and reduction in yield. Blast incidence is negatively correlated with forage yield, dry matter yield and digestive dry matter (Wilson and Gates, 1993). Mean disease severity ranges from 10 to 30% and sometimes may go up to 50% on hybrids and varieties depending on season. A survey in Uganda revealed around 60% incidence and severity of leaf blast in pearl millet causing severe loss in grain yield (Lubadde *et al.*, 2014).

Blast of pearl millet is caused by *Pyricularia grisea* (teleomorph: *Magnaporthe grisea* (Herbert) Barr). The disease appears as greyish, water-soaked lesions on foliage that turn brown upon drying. The lesions are elliptical or diamond-shaped with grey centre. Often, each lesion is surrounded by a chlorotic halo, which turns necrotic, giving the appearance of concentric rings. Widespread chlorosis causes premature drying of young leaves. The symptom may appear on leaves, leaf sheath and stem. Lesions produce abundant sporulation under high humid conditions. Sexual stage of this pathogen *Magnaporthe grisea* is a haploid, filamentous, heterothallic ascomycetous fungus that parasitises over 50 grasses. The pathogen infects many cereals including rice, wheat, pearl millet, finger millet and foxtail millet, and several grasses. *Pyricularia grisea* are highly specialised in its host range and the population that infects rice or any other

hosts does not infect pearl millet and vice versa. A high degree of pathogenic variation in this fungus is reported from rice, finger millet, foxtail millet, wheat and several weed hosts (Prabhu *et al.*, 1992; Nakayama *et al.*, 2005; Takan *et al.*, 2012). Because of this variation, there is frequent race change in this pathogen. Race development is a big challenge for the development of durable resistance against this pathogen in other crops. In rice, resistance in most of the cultivars breaks down in a few years because of the rapid change in pathogenicity of the blast fungus (Suh *et al.*, 2009). In pearl millet too, this may be true, but till now only little information is available on this pathogen infecting this crop.

The pathogen survives in the crop residues and on other cereals, which acts as collateral hosts. The initial inoculum probably comes from weeds or some collateral hosts. The fungus spreads mainly by the airborne conidia. Temperature of 25–30 °C, relative humidity of 90% or more, cloudy weather with intermittent rainfall, are favourable for disease development and rapid spread of the disease (Thakur *et al.*, 2011). Nitrogen fertilisation increases the incidence of the disease. Use of resistant cultivar is the best method for blast management. Management practices such as wide plant spacing and regulating the amount of nitrogenous fertiliser applied to the crop are important measures to minimise the occurrence of blast disease. A number of chemicals are widely used for controlling blast. Two sprays of carbendazim (0.05%) at 15-day intervals are reported to reduce the blast intensity and increase the grain and fodder yields (Lukose *et al.*, 2007). There are reports of use of biological control agents for management of pearl millet blast (Ramteke *et al.*, 2011) but their efficacies under field conditions have been hardly testified.

11.3.3 Ergot

Ergot is a major disease of pearl millet in India and has quarantine implication. The disease is also reported from many African countries including Sudan, Ethiopia, Eritrea, Benin, Togo, Central African Republic, Ghana, Senegal, Tanzania, Cameroon and Nigeria (Marley *et al.*, 2002). Pearl millet ergot was first reported from India during 1940s (Thomas *et al.*, 1945). The first epiphytotic form of the disease was reported from Maharashtra, India, in 1956 (Bhide and Hegde, 1957). With the introduction of new hybrids HB1 and HB3 during the late 1960s, ergot became severe and occurred almost every year in India (Sundaram *et al.*, 1975). Presently the disease is familiar in many states of India including Rajasthan, Maharashtra, Karnataka, Haryana and Uttar Pradesh. Ergot infection causes loss in seed yield, seed quality, germination and seedling emergence. Grain yield loss has been estimated to be as high as 58–70% in hybrids (Khairwal, 2007). Sclerotia contain alkaloids that affect the health of human beings and animals. The alkaloid is reported to cause milklessness in female pigs (Loveless, 1967) and weakening of legs in chicks (Bhat *et al.*, 1976).

Ergot in pearl millet is caused by *Claviceps fusiformis*, an ascomycetous fungus. The first visible symptom is the appearance of exudates of a viscous liquid from diseased florets. The honeydew-like exudate contains numerous micro- and macro-conidia of the pathogen. Infection is spread to adjoining florets through mechanical contact. Infected florets produce fungal sclerotium, which are light pink to dark brown to black in colour, round or elongated in shape, larger than seed, and with a pointed apex that protrudes from the florets in place of grain. Sclerotia germinate by producing 1–16 fleshy, stipes which bears a globular, dark brown capitulum at its head (Thakur

et al., 1984). Asci are produced inside pyriform perithecia. Each perithecium bears hyaline, nonseptate and filliform ascospores.

Sclerotia present in the seed or left in the soil serve as source of primary inoculum. A germinated sclerotia produces thread-like ascospores, which become airborne and cause infection in the floret. Chance of infection is more when pollination does not happen after emergence of stigma. Infected florets produce honeydew symptoms under high relative humidity and moderate temperature (Thakur *et al.*, 2011). Disease management practices like cultural, chemical and biological control can be followed for management of ergot. The disease can also be managed by pollen management that includes continuous supply of pollen by maintaining heterogeneous plant populations of open-pollinated varieties. Deep ploughing and removal of weeds from around pearl millet help to reduce the inoculum. Healthy seed can be separated from ergot mixed or infected seed either manually or by soaking in salt solution. However, the use of resistant cultivars is the most cost-effective method for the control of ergot.

11.3.4 Smut

Pearl millet smut is a common disease in India, Western Africa and the United States. In India, the disease incidence varies from 2 to 20%, depending on the season and result in direct loss of grain yield (up to 30%) CCMS-based single-cross hybrids get more smuts than the open-pollinated varieties (Thakur *et al*., 1989). The disease is also important on commercial F1 hybrids in India and on exotic early-maturing cultivars in Africa.

Smut of pearl millet is caused by *Tolyposporium penicillariae* (synonym: *Moesziomyces penicillariae*), a basidiomycetes fungus, that survives as teleutospore in infected seed or in soil. Teleutospore germinates to produce sporidia, which becomes airborne and causes infection. The infected ovary is converted into a spore-bearing structure called sorus, which is bright or shiny green in colour and turns brown on maturity. The sorus is large and appears as an enlarged body in place of grain. Mature sorus ruptures to release teleutospores. The secondary infection in same-aged crops is rare as the spores have long latent period.

The use of resistant cultivars is an economic way of rust management, while cultural and chemical methods are not cost-effective. The disease can also be managed by efficient pollen management. It is suggested that ergot resistance ensures smut resistance, but the opposite is not true.

11.3.5 Rust

Rust of pearl millet is observed in Asia, Africa, North America and South America. Recently, the disease appeared in damaging proportion in central Brazil (de Carvalho *et al.*, 2006). In India, the disease is common in the states of Tamil Nadu, Karnataka, Rajasthan, Gujarat and Maharashtra. Disease severity across India varies from 10 to 45% depending on season. It has little effect on grain yield but may affect forage crop. Rust has greater importance in multicut forage hybrids in which the disease may cause losses of digestible dry matter yield (Wilson *et al.*, 1991).

Pearl millet rust is caused by *Puccinia substriata* var. *indica* Ramachar & Cumm (synonym: *Puccinia substriata* Ell. & Barth. var. *penicillariae* de Carvalho *et al.*; *Puccinia penniseti* Zimm). It is a heteroecious rust and it needs two different host plants to complete its life cycle. The fungus survives on alternate host brinjal (*Solanum melongena*),

on which it produces spermagonia, acea and aeciospores (de Carvalho *et al.*, 2006). Airborne aeciospores infect the leaves, and produce ureadia and then telia. Teleutospores produced in telia infect alternate host and thus complete the life cycle. The distal half of the leaf is commonly infected first, then pustules (sori) spread over both the surfaces. Highly susceptible cultivars develop large pustules on leaf blade and leaf sheath. Symptoms also may appear on stem and other plant parts. Occurrence of physiological races has been reported from the United States (Tapsoba and Wilson, 1996).

Removal of alternate hosts and grassy weeds and use of resistant cultivars are the cost-effective methods for the control of rust.

11.4 Small Millet Diseases

The minor millets account for about 1% of the food grain production in the world. These minor cereals are not important in terms of world food production, but essential as food crops in their respective agro-ecosystems. They are mostly grown in marginal lands or under agricultural conditions where other cereals fail to consistently produce an acceptable harvest. The major members of the small millets group are finger millet or ragi (*Eleusine coracana*), Italian or foxtail millet (*Setaria italica*), common or proso millet (*Panicum miliaceum*), little millet (*Panicum miliare*) (renamed *P. sumatrense*), kodo millet (*Paspalum scrobiculatum*), barnyard millet (*Echinochloa frurnentacea*) (renamed *E. colona*), fonio (*Digitaria exilis*) and teff (*Erogrotis teffi*). All these are cultivated mostly in the semi-arid regions of western and eastern Africa and Asia, particularly India and Nepal. In India, small millets occupy about 4.5% of the total cultivated area. Globally, India is the leading producer of small millets, with about 20% of the area under these crops. Annual planting area of small millets is around 2.5 million ha. Due to poor management practices, crops succumb to various biotic stresses including diseases such as blast, leaf spot, brown spot, downy mildew, smut, rust and viral diseases. A list of fungal diseases reported on small millets is given in Table 11.3.

It should be noted that all diseases of small millets are not economically important. Many of them are minor and not much information available on them. A particular disease may be important for one millet crop but not for others. In the following discussion, only those diseases will be considered for which substantial research works have been done and information is available.

11.4.1 Blast

Blast disease is a major constraint to finger millet production in most crop-growing environments. The disease is common on finger millet in India and Africa. In India, the disease was first reported from Tanjore delta of Tamil Nadu by McRae (1920). It is common in Tamil Nadu, Karnataka, Andhra Pradesh, Maharashtra, Orissa, Bihar, Uttaranchal, Madhya Pradesh, Gujarat and Himachal Pradesh. The extent of crop loss depends on the severity and the time of onset of disease. The pathogen can infect the crop at all stages and seedlings may be killed under epidemic condition. Depending on the time and severity of infection the infected ears become completely chaffy or produce shrivelled grains. Neck infection is the most serious phase of the disease that causes major loss in grain number and grain weight. Yield loss varies depending on weather and plant variety. The average loss has been reported to be around 28–36%,

Table 11.3 Common diseases of small millets.

Crop	Disease	Pathogen
Finger millet	Blast	*Pyricularia grisea*
	Seedling and leaf blight	*Helminthosporium nodulosum*
	Banded blight	*Rhizoctonia solani*
	Smut	*Melanopsichium eleusinis*
	Downy mildew	*Sclerophthora macrospora*
	Wilt or foot rot	*Sclerotium rolfsii*
	Rust	*Puccinia substriata*
	Bacterial leaf blight	*Pseudomonas avenae*
Foxtail millet	Blast	*Pyricularia setariae*
	Rust	*Uromyces setariae italic*
	Smut	*Ustilago crameri*
	Downy mildew	*Sclerospora graminicola*
	Udbatta	*Ephelis sp*
	Bacterial leaf blight	*Pseudomonas avenae*
Kodo millet	Head smut	*Sorosporium paspali*
	Rust	*Puccinia substriata*
	Udbatta	*Ephelis sp*
Barnyard millet	Head smut	*Ustilago crus-galli*
	Kernel smut	*Ustilago paradoxa*
	Bacterial leaf blight	*Pseudomonas avenae*
Proso millet	Head smut	*Phacelotheca destruens*
	Bacterial leaf blight	*Pseudomonas avenae*
Little millet	Rust	*Uromyces linearis*

which may go up to 90% in endemic areas (Bisht, 1987; Rao, 1990; Nagaraja *et al.*, 2007). There is report of high quantity of avoidable loss of grain yield (35.8%) and fodder yield (43.7%) in Gujarat (Prajapathi *et al.*, 2013). Blast pathogen produces a phytotoxic metabolite, pyrichalasin H, which has a toxic effect on seed germination and seedling growth of blast-resistant and susceptible varieties (Sanmathi Kumar *et al.*, 2006).

Finger millet blast is caused by the fungus *Pyricularia grisea*, whose sexual stage is called *Magnaporthe grisea.* Typical symptoms are the appearance of elliptical or diamond-shaped lesions with grey centre and dark brown margin. Often, lesions are surrounded by chlorotic halo. Adjacent lesions may coalesce to form large necrotic areas. Symptoms may appear on leaf, stem, peduncle and finger. Infection in peduncle is known as neck blast and causes premature breaking of panicle. Finger blast occurs on panicle branches (finger), causing huge loss to the crop. One, two or all the fingers may be infected in a panicle. Infected finger become straw in colour and dry and can be easily identified from healthy green fingers. Crop loss is greater when the disease appears on the neck and ears during flowering and grain-development phase. Blast pathogen can infect around 50 grasses, including economically important crops such

as wheat, rice, barley and millets. Despite wide host range, *M. grisea* populations mainly exist as host-specific forms, capable of infecting a single host (Todman *et al.*, 1994; Viji *et al.*, 2000). Within a particular host organ specificity most probably does not occur in this pathogen, and cross-infectivity might happen at the three plant-growth stages (Puri and Kumar, 2012). Extensive work on biology and variability has been done in the rice-blast pathosystem, whereas such studies are very limited for the finger millet-blast pathosystem (Singh and Kumar, 2010; Takan *et al.*, 2012). Genetic diversity and population structure of 72 *M. grisea* isolates collected from finger millet, foxtail millet, pearl millet and rice from major crop-growing areas in India were studied using 24 SSR markers. Results suggested presence of high degree of genetic variability among isolates (Babu *et al.*, 2013).

Blast pathogen is very sensitive to minute change of temperature and other environmental factors. The life cycle of the fungi in nature is very complicated. It can parasitise many grasses. The primary inoculum comes from weeds or some collateral hosts. The fungus spreads mainly by airborne conidia. A temperature of 25–30 °C, and an RH >90% with intermittent rainfall are favourable for the rapid spread of the disease. The disease incidence increases with increasing N levels (Kumar and Rashmi, 2012).

Management practices such as plant spacing and regulating the amount of nitrogenous fertiliser are important measures to minimise the occurrence of blast disease. Sprays of carbendazim @ 0.1% or tricyclazole @ 0.05% or collimation of mancozeb 63% + carbendazim 12% were recommended by the AICSMIP (2006). Spraying of fungicide combined with seed treatments gave better management of the disease. Nagaraja *et al.* (2012) observed that seed treatment to resistant varieties with either carbendazim @ 2 g/kg or *Pseudomonas fluorescens* 6 g/kg was found to reduce blast disease incidence by two and a half times over control besides recording high mean yield of 25.67 and 24.98 q/ha as against 21.06 q in susceptible variety. They further suggested that, instead of trying sprays of different chemicals on a susceptible variety, it is worthwhile to select resistant variety and give simple seed treatment with carbendazim @ 2 g/kg or *Pf* @6 g/kg. Recently, Prajapathi *et al.* (2013) claimed that, with the proper protection measures, 70.5, 67.7 and 62.9% disease of leaf blast, neck blast and finger blast can be controlled, respectively. Silica fertilisers, such as calcium and sodium silicate were reported to reduce neck blast in finger millet (Krishnappa *et al.*, 2013).

Development of varieties with inbuilt genetic resistance is the best means of disease control. Search for blast resistance began in the early 1990s, and as a result resistant varieties like GPU 28, VL 149, GPU 48 and L 5 were released in India. These varieties, however, had juvenile susceptibility to leaf blast (Nagaraja *et al.*, 2012). Durable resistance is desirable for increasing shelf life of a resistant cultivar. Recently, Ignacimuthu and Ceasar (2012) developed leaf blast resistance in finger millet transgenic using rice chitinase (*chi*11) gene.

11.4.2 Leaf Spots

Among all the leaf spots, the brown spot of finger millet caused by *Helminthosporium nodulosum* is the most important. The pathogen also causes seedling blight when infection occurs in the emerging seedling. The disease is prevalent in Asia (India, Japan) and Africa. In India, it is common in the states of Madhya Pradesh, Andhra Pradesh, Maharashtra, Uttar Pradesh, Bihar, Tamil Nadu and Karnataka. It affects all the parts of the plants including leaf blade, leaf sheath, culms, neck and fingers and cause considerable

yield loss. Symptoms appear as small light brown lesion on leaf. Lesions may coalesce forming large dark brown patches. Infection on sheath, neck and finger cause poor grain filling and discolouration of seed.

Moderate temperature and high humidity favour disease development. Grewal and Pal (1965) reported contamination of seed by the pathogen. The pathogen can also survive on crop residues. The primary infection is caused by seed-born inoculum, and secondary spread is through airborne conidia. Several other cereals are infected by this organism, including *Cynodon dactylon*, *Echinochloa colonum*, *Echinochloa frumentacea*, *Eleusine indica*, *Panicum miliaceum*, *P. miliare*, *P. ramosum*, *P. repens*, *Setaria glauca*, *S. italica*, *Oryza sativa*, *Sorghum vulgare* and *Zea mays* (Mitra, 1931). Seed treatment with fungicides controls the pre-emergence damping off and seedling blight. The secondary infection in the field can be reduced by protective sprayings with suitable fungicides.

11.4.3 Smut

Among the smuts the grain smut is common on finger, foxtail and barnyard millet, while head smuts is common in kodo, barnyard and proso millet. Generally, smuts are minor diseases and not much literature is available on this topic, barring a few reports. Practice of clean cultivation and seed treatment with fungicides effectively controls the disease under check.

Finger millet smut (*Melanopsichium eleusinis*) is gaining importance recently. On infection by airborne spores smut sori are developed in the grains, main rachis or in peduncle. The pathogen may also convert floral organs into smut sori. Smut disease in foxtail millet is caused by *Ustilago crameri* mainly in the southern states of India. The fungus is externally seed-borne and soil-borne. Head smuts are common in kodo, barnyard and proso millet. In kodo millet, head smut (*Sorosporium paspali*) is important and causes considerable yield loss in Madhya Pradesh, Andhra Pradesh, Bihar, Tamil Nadu and Karnataka. The entire panicle is transformed into a long sorus which may be enclosed in the flag leaf and may not emerge properly. The membrane bursts and exposes the black spores. The disease is mainly seed-borne. The spores adhere to the surface of the grains and infect the seedlings. Two types of smuts are reported on barnyard millet: head smut (*Ustilago crus-galli*) and grain smut (*Ustilago paradoxa*). Head smut is recently reported from Uttarakhand in India (Kumar *et al*., 2008).

Systematic breeding for development of smut resistance variety has not been common. Cultural practices are mainly followed for management of the disease and fungicidal seed treatment also used occasionally.

11.4.4 Rust

Among small millets, rust is observed on foxtail, finger, kodo and barnyard millets. Two different pathogens cause rust on them. Finger and kodo millets are infected by *Puccinia substriata*. Foxtail and little millets, on the other hand, are attacked by *Uromyces* spp. Rust on millet is not a regular disease, which occur sporadically causing small damage to the crop. There are reports of the rust becoming serious recently.

Uromyces rust produces small brown uredia that are arranged linearly on both surfaces of the leaves. Symptoms can be seen in all plant parts and infection can occur at any plant growth stage. Uredia produce brown colour uredniospores that germinate readily to cause infection. The teleutospores are produced later after urediniospores.

Uromyces setariae italic produces light-yellow-coloured single-celled teleutospore, whereas *U. linearis* produces black-coloured teleutospores. *Puccinia substriata* develops small, brown, oval and raised spots (uredia) on upper surfaces of leaf and leaf sheath. Uredia produce urediniospores that germinated in water drops and cause infection. Telia are usually produced on the lower surface of leaf and leaf sheath. Red-brown pustules may be surrounded by a yellow halo. The pathogen can survive on grasses. Brinjal is known to act as alternate host in which aecia are produced (de Carvalho *et al.*, 2006). Little information is available on systemic research on this disease on small millets.

11.4.5 Downy Mildew

Pathogen *Sclerospora graminicola* infects both pearl millet and foxtail millet, whereas *Sclerophthora macrospora* infects finger millet. Downy mildew incidence on small millets is not as severe as in pearl millet. Affected finger millet plants are generally stunted with shortened internodes and profuse tillers. The plant looks a bunchy and bushy appearance. The green ear ear disease expresses itself at the time of grain formation and converts the earhead into green narrow leafy structures causing complete sterility. The disease is mainly observed in peninsular India, particularly in Tamil Nadu and Karnataka. The fungus is internally as well as externally seed-borne. It has a wide host-range including maize, wheat, oat, *Eragrostis pectinacea* and *Digitaria marginata*. Physiologic specialisation and races of the pathogen are reported. Seed treatment with fungicides is desirable for management of the disease.

11.4.6 Udbatta

Udbatta caused by *Ephelis* sp., is reported in kodo and foxtail millets. The disease is noticed on several host plants such as grasses *Cynodon dactylon*, *Pennisetum* sp. and *Ergostis tenufolia*. It is a sporadic disease and incidence go up to 19.6% (Nagaraja *et al.*, 2010). Symptom appears during panicle initiation stage, and the entire panicle converts into hard-silver-coloured cylindrical spikes resembling the udbatta disease in paddy. No grains are formed on the affected panicle. Use of clean cultivation, disease-free seeds and hot-water treatment of seed can be practised for the management of this disease.

References

AICPMIP (2011–2014) *Progress reports. All India Coordinated Pearl Millets Improvement Project Mandore*, Indian Council of Agricultural Research, India, Rajasthan.

AICPMIP (2013) *Proceedings of the 48th Annual Pearl Millet Workshop*, All India Coordinated Pearl Millet Improvement Project, Junagadh Agricultural University, Junagadh, AICPMIP Mandor, Jodhpur, p. 51.

AICSMIP (2006) *Technology for Increasing Finger Millet and Other Small Millets Production in India*, Project Coordination Cell, All India Coordinated Small Millets Improvement Project, Gandhi Krishi Vignan Kendra, Bangalore, pp. 1–41.

Anahosur, K.H. and Patil, H.S. (1982) Effect of date of sowing on the incidence of ergot of sorghum. *Indian Phytopath.*, **35**, 507–509.

Anahosur, K.H. (1992) Sorghum diseases in India: knowledge and research needs, in *Sorghum and Millets Diseases: A Second World Review* (eds W.A.J. de Millano, R.A. Frederiksen and G.D. Bengston), ICRISAT, Patancheru, Andhra Pradesh, India, pp. 45–46.

Anaso, C.E. and Anaso, A.B. (2010) Cost-effectiveness of seed dressing with a new formulation of metalaxyl (Apron Star 42 WS) for sustainable pearl millet production in northern Nigeria. *Arch. Phytopath. Pl. Prot.*, **43**, 154–159.

Aruna, C. and Audilakshmi, S. (2004) Genetic architecture of grain hardness – a durable resistance mechanism for grain molds in sorghum [*Sorghum bicolor* (L.) Moench]. *Indian J. Genet. Pl. Breed.*, **64**, 35–38.

Audilakshmi, S., Aruna, C., Solunke, R.B. *et al.* (2007) Approaches to grain quality improvement in rainy season sorghum in India. *Crop. Prot.*, **26**, 630–641.

Audilakshmi, S., Stenhouse, J.W., Reddy, T.P. and Prasad, M.V.R. (1999) Grain mould resistance and associated characters of sorghum genotypes. *Euphytica*, **107**, 91–103.

Babu, T.K., Sharma, R., Upadhyaya, H.D. *et al.* (2013) Evaluation of genetic diversity in *Magnaporthe grisea* populations adapted to finger millet using simple sequence repeats (SSRs) markers. *Physiol. Mol. Pl. Patholo.*, **84**, 10–18.

Bandyopadhyay, R. (1986) Rust, in *Compendium of Sorghum Diseases* (ed. R.A. Frederiksen), American Phytopathological Society, St Paul, MN, USA,. pp. 23–24.

Bandyopadbyay, R., Frederickson, D.E., McLaren, N.W. and Odvody, G.N. (1996) Ergot– a global threat to sorghum. *Int. Sorghum. Millet Newslett.*, **37**, 1–32.

Bhat, R.V., Roy, D.N. and Tulpule, P.G. (1976) The nature of alkaloids of ergot of pearl millet or bajra and its comparison with alkaloids of ergot of rye and ergot of wheat. *Toxic. Appl. Pharmacol.*, **36**, 11–17.

Bhat, R.V., Shetty, P.H., Amruth, R.P. and Sudershan, R.V.A. (1997) Food-borne disease outbreak due to the consumption of moldy sorghum and maize containing fumonisins mycotoxins. *J. Toxicol. Clin.Toxicol.*, **35**, 249–255.

Bhat, S.S. (1973) Investigations on the biology and control of *Sclerospora graminicola* on bajra, in *PhD thesis*, University of Mysore, Mysore, Karnataka, India, p. 165.

Bhattacharya, G., Siddiqui, K.A.I. and Chakraborty, S. (1994) The toxicity of phaseolinone to mice. *Indian J. Pharmacol.*, **26**, 121–125.

Bhide, V.P. and Hegde, R.K. (1957) Ergot on bajra [*Pennisetum typhoides* (Burm) Stapf. & Hubbard] in Bombay State. *Curr. Sci.*, **26**, 116.

Bisht, I.S. (1987) Blast tolerance and yield loss in finger millet. *Indian J. Agri. Sci.*, **50**, 954–955.

Boora, K.S., Frederiksen, R. and Magill, C. (1998) DNA-based markers for a recessive gene conferring anthracnose resistance in sorghum. *Crop Sci.*, **38**, 1708–1709.

Bunker, R.N. and Mathur, K. (2010) Pathogenic and morphological variability in *Exserohilum turcicum* isolates causing leaf blight of sorghum (*Sorghum bicolor*). *Indian J. Agric. Sci.*, **80**, 888–892.

Butler, E.J. (1907) Some diseases of cereals caused by *Sderospora graminicola*. *Memoirs Dept. Agric. India Bot. Ser.*, **2**, 1–24.

Butler, E.J. (1918) *Fungi and Diseases in Plants*, Thacker Spink and Co., Calcutta, p. 206.

Casela, C.R. and Ferreira, A.S. (1988) Identification of sources of resistance to *Colletotrichurn graminicola*, causal agent of sorghum anthracnose. *Fitopatol. Brasil.*, **13**, 351–353.

Casela, C.R. and Frederiksen, R.A. (1993) Survival of *Colletotrichum graminicola* sclerotia in sorghum stalk residue. *Pl. Dis.*, **11**, 825–827.

Celia Chalam, V. (1996) Studies on the mechanisms of resistance in pearl millet genotypes to downy mildew disease, in *PhD thesis*, Acharya NG Ranga Agricultural University, Rajendranagar, Hyderabad, p. 132.

Chatterjee, D. and Mukherjee, S.K. (1994) Contamination of Indian maize with fumonisin B1 and its effects on chicken macrophage. *Lett. Appl. Microbiol.*, **18**, 251–253.

Chellaiah, S. and Basheer, M. (1965) Biological studies of *Peregrinus maidis* (Ashmead) (Araccopidae: Homoptera) on sorghum. *Indian J. Entomol.*, **27**, 466–471.

Cloud, G.L. and Rupe, J.C. (1991) Morphological instability in a chlorate medium of isolates of *Macmphomina phaseolina* from soybean and sorghum. *Phytopathology*, **81**, 892–895.

Craig, J. and Frederiksen, R.A. (1983) Differential sporulation of pathotypes of *Peronosclerospora sorghi* on inoculated sorghum. *Pl. Dis.*, **67**, 278–279.

Craig, J. and Odvody, G.N. (1992) Current status of sorghum downy mildew control, in *Sorghum and Millet Diseases: A Second World Review* (eds W.A.J. de Milliano, R.A. Frederiksen and G.D. Bengston), International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh, India, pp. 213–217.

da Costa, R.V., Zambolim, L., Cota, L.V. *et al.* (2011) Genetic control of sorghum resistance to leaf anthracnose. *Pl. Pathol.*, **60**, 1162–1168.

de Carvalho, A., Soares, D., Carmo, M. *et al.* (2006) Description of the lifecycle of the pearl millet rust fungus – *Puccinia substriata* var. *penicillariae* with a proposal of reducing var. *indica* to a synonym. *Mycopathologia*, **161**, 331–336.

Dang, J.K., Thakur, D.P. and Grover, R.K. (1983) Control of pearl millet downy mildew caused by *Sclerospora graminicoia* with systemic fungicides in an artificially contaminated plot. *Annal. Appl. Bio.*, **102**, 99–106.

Das, I.K., Audilakshmi, S., Annapurna, A. *et al.* (2012) Relationship among seed germination and other characters associated with Fusarium grain mold disease in sorghum (*Sorghum bicolor* L. Moench) using path coefficient analysis. *Can. J. Pl. Path.*, **34**, 203–212.

Das, I.K., Fakrudin, B. and Arora, D.K. (2008a) RAPD cluster analysis and chlorate sensitivity of some Indian isolates of *Macrophomina phaseolina* from sorghum and their relationships with pathogenicity. *Microbiol. Res.*, **163** (2), 215–224.

Das, I.K., Indira, S., Annapurna, A. *et al.* (2008b) Biocontrol of charcoal rot in sorghum by fluorescent pseudomonads associated with rhizosphere. *Crop Prot.*, **27** (11), 1407–1414.

Das, I.K. and Madhusudhana, R. (2005) Incidence of sorghum downy mildew during Rabi season. *Jowar Samachar*, **1** (2), 2–3.

Das, I.K. and Patil, J.V. (2013) Assessment of economic loss due to grain mold of sorghum in India, in *Compendium of Papers and Abstracts: Global Consultation on Millets Promotion for Health and Nutritional Security* (eds S. Rakshit, I.K. Das, G. Shyamprasad *et al.*), December 18–20, 2013, Society for Millet Research, Directorate of Sorghum Research, Hyderabad, AP, India, pp. 59–63 (356 pp.).

Das, I.K. and Prabhakar (2002) Effect of growth stages of winter sorghum on susceptibility of stripe disease. *Indian Phytopath.*, **55**, 313–314.

Das, I.K. and Raut, M.S. (2002) Effect of sowing dates and weather parameters on the occurrence of stripe disease in winter sorghum. *Indian J. Mycol. Pl. Path.*, **32**, 21–24.

de Milliano, W.A.J. and Veld, M.I. (1990) Incomplete resistance of the sorghum variety QL-3 (India) against sorghum downy mildew in Zimbabwe. *Sorghum Newslett.*, **31**, 03.

Desai, A. (1998) A note on the epiphytotic outbreak of leaf blight of sorghum in India. *Kar. J. Agric. Sci.*, **11**, 5–11.

Dhingra, O.D. and Sinclair, J.B. (1978) *Biology and pathology of Maaophomina philseolina Vicosa, Brazil*, Imprensia Universitaria, Vniversidade Federal de Vicosa, p. 166.

Esele, J.P., Frederiksen, R.A. and Miller, F.R. (1993) The association of genes controlling caryopsis traits with grain mold resistance in sorghum. *Phytopathology*, **83**, 490–495.

Fernandes, F.T. and Schaffert, R.E. (1983) The reaction of several sorghum cultivars to a new race of sorghum downy mildew (*Peronosclerospora sorghi*) in southern Brazil in 1982–1983. *Agron. Abstr.*, **27**, 63.

Frederiksen, R.A., Amador, J., Jones, B.L. and Reyes, L. (1969) Distribution, symptoms and economic loss from downy mildew caused by *Sclerospora sorghi* in grain sorghum in Texas. *Pl. Dis. Report.*, **53**, 995–998.

Frederiksen, R.A. (1986) *Compendium of Sorghum Diseases, The American Phytopathological Society and Department of Plant Pathology and Microbiology*, Texas A&M University, Texas, USA, p. 82.

Frederiksen, R.A. (1980) Sorghum downy mildew in the United States: overview and outlook. *Pl. Dis.*, **64**, 903–908.

Frederiksen, R.A. (1978) Sorghum leaf blight, in *Sorghum Disease – A World Review, Proceedings of the International Workshop on Sorghum Diseases*, sponsored jointly by Texas A & M University (USA) and ICRISAT, Hyderabad, India, pp. 243–248.

Garud, T.B. and Mali, V.R. (1985) A red stripe virus disease of sorghum in India. *Indian Phytopath.*, **36**, 545–546.

Grewal, J.S. and Pal, M. (1965) Seed Microflora-1. Seed-borne fungi of ragi, their distribution and control. *Ind. Phytopath.*, **18** (1), 33–37.

Gwary, D.M., Bdliya, B.S. and Bdliya, J.A. (2009) Appraisal of yield losses in pearl millet due to downy mildew pathogen (*Sclerospora graminicola*) in Nigerian Sudan savannah. *Arch. Phytopath. Pl. Prot.*, **42**, 1010–1019.

Harris, H.B., Johnson, B.J., Dobson, J.W. and Luttrell, E.S. (1964) Evaluation of anthracnose on grain sorghum. *Crop Sci.*, **4**, 460–462.

Hepperly, P.P. (1990) Sorghum rust II. Control and losses. *J. Agrrc. Unrv. Puerto Rico*, **74**, 37–44.

ICRISAT (1992) *The Medium Term Plan, Vol 2*, International Crops Research Institute for Semi-Arid Tropics, Patancheru, Andhra Pradesh, India.

Ignacimuthu, S. and Ceasar, S.A. (2012) Development of transgenic finger millet (*Eleusine coracana* (L.) Gaertn.) resistant to leaf blast disease. *J. Biosci.*, **37** (1), 135–147.

Kamala, V., Singh, S.D., Bramel, P.J. and Manohar Rao, D. (2002) Sources of resistance to downy mildew in wild and weedy sorghums. *Crop Sci.*, **42**, 1357–1360.

Kannababu, N., Das, I.K. and Seetharama, N. (2009) Effect of chemicals and bioagents on control of molds and improvement of seed quality of rainy season sorghum (*Sorghum bicolor*). *Indian J. Agric. Sci.*, **79**, 461–465.

Katile, S.O., Perumal, R., Rooney, W.L. *et al.* (2010) Expression of pathogenesis-related protein PR-10 in sorghum floral tissues in response to inoculation with *Fusarium thapsinum* and *Curvularia lunata*. *Mol. Pl. Path.*, **11**, 93–103.

Kaveriappa, K.M., Safeeulla, K.M. and Shaw, C.G. (1980) Culturing *Sclerospora sorghi* in callus tissue of sorghum. *Proc. Indian Acad. Sci. Pl. Sci.*, **89**, 31–38.

Khairwal, I.S., Rai, K.N., Diwakar, B. *et al.* (2007) *Pearl Millet: Crop Management and Seed Production Manual*, International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh, India, p. 104.

King, S.B. (1992) World review of pearl millet diseases: Knowledge and future research needs, in *Sorghum and Millet Diseases: A Second World Review* (eds W.A.J. de Milliano, R.A. Frederiksen and G.D. Bengston), International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh, India, pp. 95–108 (370 pp).

Krishnappa, P., Ramaswamy, G.R. and Jyothi, V. (2013) Role of silica fertilizers on blast (*Pyricularia grisea* Sacc.) disease development in finger millet [*Eleusine coracana* (L.) Gaertn.]. *Pl. Dis. Res.*, **28** (2), 207–208.

Kulkarni, B.G.P., Seshadri, V.S. and Hegde, R.K. (1976) The perfect stage of *Sphacelia sorghi* McRae. *Mysore J. Agric. Sci.*, **10** (2), 286–289.

Kumar, B., Kumar, J. and Srinivas, P. (2008) First record of head smut of barnyard millet from mid hills of Uttarakhand. *J. Mycol. Pl. Pathol.*, **38** (1), 142.

Kumar, B. and Rashmi, Y. (2012) Influence of nitrogen fertilizer dose on blast disease of finger millet caused by *Pyricularia grisea*. *Indian Phytopath.*, **65** (1), 52–55.

Leonard, K.J. and Suggs, E.G. (1974) Setosphaeria prolatum. *The ascigerous state of Exserohilum prolatum. Mycologia*, **66**, 281–297.

Loveless, A.R. (1967) *Claviceps fusiformis* sp. nov., the causal agent of an agalactia of sows. *Trans. Br. Mycol. Soc.*, **50**, 5015–5018.

Lubadde, G., Tongoona, P., Derera, J. and Sibiya, J. (2014) Major pearl millet diseases and their effects on farm grain yield in Uganda. *African J. Agric. Res.*, **9**, 2911–2918.

Lukose, C.M., Kadvani, D.L. and Dangaria, C.J. (2007) Efficacy of fungicides in controlling blast disease of pearl millet. *Indian Phytopath.*, **60**, 68–71.

Mali, V.R. and Garud, T.B. (1977) Studies on sorghum red stripe virus disease in Maharashtra. *Indian J. Mycol. Pl. Path.*, **7**, 201–203.

Mali, V.R. and Thakur, R.P. (1999) Reactions and virus titres of differential sorghum inbred lines mechanically inoculated with an Indian isolate of sorghum red stripe potyvirus (SRSV-Ind). *Sugar Tech.*, **1**, 13–18.

Manjunatha, G., Niranjan, R.S., Geetha, N.P. *et al.* (2009) Nitric oxide is involved in chitosan induced systemic resistance in pearl millet against downy mildew disease. *Pest. Manag. Sci.*, **65**, 737–743.

Mansuetus, A.S.B., Frederiksen, R.A., Waniska, R.D. *et al.* (1988) The effects of glume and caryopses characteristics of sorghum on infection by *Fusarium moniliforme* Sheldon. *Sorghum Newslett.*, **31**, 100.

Marley, P.S., Diourtk, M., Neya, A. *et al.* (2002) Sorghum and pearl millet diseases in West and Central Africa, in *Sorghum and Millets Diseases* (ed. J.F. Leslie), Iowa State Press, pp.419–425.

Mathur, K. and Bunker, R.N. (2001) *Annual Report of All India Coordinated Sorghum Improvement Project (AICSIP) Sorghum Pathology*, AICSIP Main Centre Udaipur, Rajasthan College of Agriculture, Udaipur, pp. 1–40.

Mathur, K., Thakur, R.P., Neya, A. *et al.* (2002) *Sorghum anthracnose – problem and management strategies, in Sorghum and Millets Diseases* (ed. J.F. Leslie), Iowa State Press, Iowa, pp. 211–220 (504 pp.).

Mathur, K., Thakur, R.P., Rao, V.P. *et al.* (2011) Pathogenic variability in *Exserohilum turcicum* and resistance to leaf blight in sorghum. *Indian Phytopath.*, **64**, 32–36.

McLaren, N.W. (1994) Efficacy of systemic fungicides and timing of preventative sprays in the control of sugary disease of grain sorghum (*Sorghum bicolor*). *South African J. Pl. Soil.*, **11**, 30–33.

McRae, W. (1917) Notes on South Indian Fungi, in *Madras Agricultural Year Book*, Madras Agric. Dept., pp. 108–111.

McRae, W. (1920) *Detailed Administration Report of the Government Mycologist for the Year 1919–20*, Madras Agric, Dept.

Mehta, P.J., Wiltse, C.C., Rooney, W.L. *et al.* (2005) Classification and inheritance of genetic resistance to anthracnose in sorghum. *Field Crops Res.*, **93**, 1–9.

Mehta, P.R., Singh, B. and Mathur, S.C. (1953) A new leaf spot disease of bajra (*Pennisetum typhoides*) Staph and Hubbard) caused by a species of *Piricularia*. *Indian Phytopath.*, **5**, 140–143.

Michelmore, R.W., Pawar, M.N. and Williams, R.J. (1982) Heterothallism in *Sclerospora graminicola*. *Phytopathology*, **72**, 1368–1372.

Mishra, A. and Siradhana, B.S. (1979) Studies on the survival of sorghum anthracnose (*Colletotrichum graminicola*) pathogen. *Phil. Agric.*, **62**, 141–152.

Mitra, M. (1923) *Helminthosporium* in cereals and sugarcane in India. *I. Diseases of Zea mays and Sorghum vulgure caused by species of Helminthosporium. India Dept. Agric. Mem. Bot. Ser.*, **11**, 219–242.

Mitra, M. (1931) *Report of the Imperial Mycologist 1929-1930, Sci. Rept. Imperial Agric. Res. Inst. (Pusa, India)*, 59–71.

Mughogho, L.K. and Pande, S. (1984) Charcoal rot of sorghum, in *Sorghum Root and Stalk Rots – A Critical Review: Proceedings of the Consultative Group Discussion on Research Needs and Strategies for Control of Sorghum Root and Stalk Rot Diseases, November 27–December 2, 1983*, Bellagio, Italy, ICRISAT, Patancheru, Andhra Pradesh, India.

Murali Mohan, S., Madhusudhana, R., Mathur, K. *et al.* (2010) Identification of quantitative trait loci associated with resistance to foliar diseases in sorghum [*Sorghum bicolor* (L.) Moench]. *Euphytica*, **176**, 199–211.

Nagaraja, A., Anjaneya Reddy, B. and Govindappa, M.R. (2010) Occurrence of Udabatta disease on kodo millet (*Paspalum scrobiculatum* L.): A new report from South India. *J. Mycopathol. Res.*, **48** (1), 163–164.

Nagaraja, A., Kumar, J., Jain, A.K. *et al.* (2007) *Compendium of Small Millets Diseases*, Project Coordination Cell, All India Coordinated Small Millets Improvement Project, UAS, GKVK Campus, Bangalore, p. 80.

Nagaraja, A., Kumar, B., Raguchander, T. *et al.* (2012) Impact of disease management practices on finger millet blast and grain yield. *Indian Phytopath.*, **65** (4), 356–359.

Nagarajan, K. and Saraswathi, V. (1971) Effect of systemic fungicides on the sugary disease organism. *Sorghum Newslett.*, **14**, 41.

Naidu, R.A., Harikrishnan, R., Manohar, S.K. *et al.* (1989) The occurrence of maize mosaic virus on sorghum in India. *Ann. Appl. Bio.*, **114**, 301–310.

Nakamura, K. (1982) Especializacao Fisiologic em *Colletotrichum graminicola* (Ces.) Wils. (Sensu Arx., 1957) Agelite Causal da Antracnose em Sorgho, in *PhD Thesis*, Univ Estadual Paulista, Jaboticabal, Brazil.

Nakayama, H., Nagamine, T. and Hayashi, N. (2005) Genetic variation of blast resistance in foxtail millet (*Setaria italica* (L.) P. Beauv) and its geographic distribution. *Genet. Resour. Crop Ev.*, **52**, 863–868.

Narayana, Y.D., Das, I.K., Bhagwat, V.R. *et al.* (2011) *Viral Disease of Sorghum in India*, Directorate of Sorghum Research, Rajendranagar, Hyderabad, Andhra Pradesh, India, 30 pp.

Nault, L.R. and Gordon, D.T. (1988) Multiplication of maize stripe virus in *Peregrinus maidis*. *Phytopathology*, **78**, 991–995.

Nelson, P.E., Toussoun, T.A. and Marasas, W.F.O. (1983) *Fusarium Species: An Illustrated Manual for Identification*, Pennsylvania State University Press, University Park.

Ngugi, H.K., King, S.B., Abayo, G.O. and Reddy, Y.V.R. (2002) Prevalence, incidence, and severity of sorghum diseases in Western Kenya. *Pl. Dis.*, **86**, 65–70.

Norred, W.P. (1993) Fumonisins – Mycotoxins produced by *Fusarium moniliforme*. *J. Toxicol. Environ. Health*, **38**, 309–328.

Pande, S., Bock, C.H., Bandyopadhyay, R. *et al.* (1997) *Downy Mildew of Sorghum. Information Bulletin No. 51*, International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh, India, p. 32.

Pande, S., Mughogho, L.K., Bandyopadhyay, R.B. and Karunakar, R.I. (1991) Variation in pathogenicity and cultural characteristics of sorghum isolates of *Colletotrichum graminicola* in India. *Pl. Dis.*, **75**, 778–783.

Pawar, M.N., Frederiksen, R.A., Mughogho, L.K. and Bonde, M.R. (1985) Survey of the virulence of *Peronosclerospora sorghi* isolates from India, Ethiopia, Nigeria, Texas (USA), Honduras, Brazil and Argentina. (Abstract). *Phytopathology*, **75**, 1374.

Payak, M.M. (1975) Downy mildews of maize in India. *Trop. Agric. Res. Series. (Tokyo)*, **8**, 13–18.

Perumal, R., Menz, M.A., Mehta, P.J. *et al.* (2009) Molecular mapping of *Cg1*, a gene for resistance to anthracnose (*Colletotrichum sublineolum*) in sorghum. *Euphytica*, **165**, 597–606.

Perumal, R., Nimmakayala, P., Erattaimuthu, S. *et al.* (2008) Simple sequence repeat markers useful for sorghum downy mildew (*Peronosclerospora sorghi*) and related species. *BMC Genet.*, **9**, 77.

Peterschmitt, M., Ratna, A.S., Sacks, W.R. *et al.* (1991) Occurrence of an isolate of maize stripe virus in India. *Ann. Appl. Bio.*, **118** (1), 57–70.

Prabhu, A.S., Filippi, M.C. and Castro, N. (1992) Pathogenic variation among isolates of *Pyricularia grisea* infecting rice, wheat, and grasses in Brazil. *Trop. Pest Manage.*, **38**, 367–371.

Prajapathi, V.P., Sabalpara, A.N. and Pawar, D.M. (2013) Assessment of yield loss due to finger millet blast caused by *Pyricularia grisea* (Cooke) Sacc. *Trends in Biosci.*, **6** (6), 876–878.

Prom, L.K., Perumal, R., Erattaimuthu, S.R. *et al.* (2012) Genetic diversity and pathotype determination of *Colletotrichum sublineolum* isolates causing anthracnose in sorghum. *Eur. J. Pl. Path.*, **133**, 671–685.

Puri, S. and Kumar, J. (2012) Characterization of leaf, neck and finger blast pathogen populations from *Eleusine coracana* and elucidating their interrelationships in *Eleusine-Magnaporthe* pathosystem. *Indian Phytopath.*, **65** (2), 133–141.

Pushpavathi, B., Thakur, R.P. and Chandrashekara Rao, K. (2006) Fertility and mating type frequency in Indian isolates of *Sclerospora graminicola*, the downy mildew pathogen of pearl millet. *Pl. Dis.*, **90**, 211–214.

Ramakrishnan, T.S. (1948) Ergot sclerotia on *Sorghum vulgare* Pers. *Curr. Sci.*, **17**, 218.

Ramteke, N.B., Mondhe, M.K., Gibhakate, P. and Jadhav, B.R. (2011) Biological management of leaf blast (*Pyricularia grisea*) of pearl millet. *J. Pl .Dis. Sci.*, **6** (2), 202–203.

Rao, A.N.S. (1990) Estimates of losses in finger millet (*Eleusine coracana*) due to blast disease (*Pyricularia grisea*). *J. Agric. Sci.*, **24**, 57–60.

Rao, V.P., Thakur, R.P. and Mathur, K. (1998) Morphological and pathogenic diversity among grain sorghum isolates of *Colletotrichum graminicola* in India. *Indian Phytopath.*, **51**, 64–74.

Rathod, K.S., Telang, S.M. and Rathod, R.M. (2004) Effect of chlorotic stripe stunt disease on fodder quality of forage cultivars. *J. Soil. Crop*, **14** (2), 351–353.

Revuru, S.S. and Garud, T.B. (1998) Effect of chlorotic stripe stunt disease on plant growth and grain yield of different sorghum cultivars. *J. Maha. Agric. Univ.*, **23**, 253–255.

Reynaud, B., Delatte, H., Peterschmitt, M. and Fargette, D. (2009) Effects of temperature increase on the epidemiology of three major vector-borne viruses. *Eur. J. Pl. Path.*, **123**, 269–280.

Rodriguez-Herrera, R., Waniska, R.W., Rooney, W.L. *et al.* (2006b) Antifungal proteins during sorghum grain development and grain mould resistance. *J. Phytopath.*, **154** (9), 565–571.

Ryley, M.J., Alcorn, J.L., Kochman, J.K. *et al.* (1996) *Ergot on Sorghum spp. in Australia. Aust. Pl. Path.*, **25**, 214.

Safeeulla, K.M. (1976) *Biology and Control of the Downy Mildews of Pearl Millet, Sorghum and Finger Millet*, University of Mysore, Mysore, Karnataka, India, p. 304.

Sangitrao, C.S. and Bade, G.H. (1979) Meteorological factors associated with honeydew development and sclerotial stage in sorghum ergot. *Sorghum Newslett.*, **22**, 107–108.

Sanmathi Kumar, R.P., Shanthala, L., Anilkumar, T.B. and Sudharsana, L. (2006) Phytotoxins from *Pyricularia grisea* and Their Effect on Finger Millet. *J. Pl. Biochem. Biotechnol.*, **15**, 63–66.

Sastry, J.G., Ramakrishna, W., Sivaramakrishnan, S. *et al.* (1995) DNA fingerprinting detects genetic variability in the pearl millet downy mildew pathogen (*Sclerospora graminicola*). *Theor. Appl. Genet.*, **91**, 856–861.

Shankara Rao, R., Rao, K.E.S., Singh, S.D. *et al.* (1987) Fungicidal control of downy mildew of pearl millet. *Ind. J. Pl. Prot.*, **15**, 146–151.

Sharma, R., Rao, V.P., Varshney, R.K. *et al.* (2010) Characterisation of pathogenic and molecular diversity in *Sclerospora graminicola*, the causal agent of pearl millet downy mildew. *Arch. Phytopath. Pl. Prot.*, **43**, 538–551.

Shetty, H.S., Mathur, S.B. and Neergaard, P. (1980) *Sclerospora graminicola* in pearl millet seeds and its transmission. *Trans. British Mycol. Soc.*, **74**, 127–134.

Singh, R.D.N. and Kaiser, S.A.K.M. (1991) Genetic analysis of resistance to charcoal rot of maize. *J. Mycopath. Res.*, **29**, 103–109.

Singh, S.D. and Bandyopadhyay, R. (2000) Grain mold, in *Compendium of Sorghum Diseases*, Second edn (eds R.A. Frederiksen and G.N. Odvody), APS Press, The American Phytopathological Society, St. Paul, MN, USA, pp. 38–40.

Singh, S.D. and de Milliano, W.A.J. (1989) First report of recovery of sorghum from downy mildew in Zimbabwe. *Pl. Dis.*, **73**, 1020.

Singh, S.D. and Gopinath, R. (1985) A seedling inoculation technique for detecting downy mildew resistance in pearl millet. *Pl. Dis.*, **69**, 582–584.

Singh, S.D., King, S.B. and Weraer, J. (1993) *Downy mildew disease of pearl millet. Information Bulletin No. 37. (In En. Summaries in Fr, Es.)*, International Crops Research Institute for the Semi-Arid Tropics Patancheru, Andhra Pradesh, India, p. 36.

Singh, S.D., Sathiah, P. and Rao, K.E.P. (1994) Sources of rust resistance in purple colored sorghum. *Int. Sorghum Millets Newslett.*, **35**, 100–101.

Singh, S.D. and Singh, G. (1987) Resistance to downy mildew in pearl millet hybrid NHB 3. *Indian Phytopath.*, **40** (2), 178–180.

Singh, Y. and Kumar, J. (2010) Study of genomic fingerprints profile of *Magnaporthe grisea* from finger millet (*Eleusine Coracona*) by random amplified polymorphic DNA-polymerase chain reaction (RAPD-PCR). *African J. Biotechnol.*, **9** (46), 7798–7804.

Sudisha, J., Ananda Kumar, S., Niranjana, S.R. *et al.* (2009) Cloning and development of pathotype-specific SCAR marker associated with *Sclerospora graminicola* isolates from pearl millet. *Aust. Pl. Pathol.*, **38**, 216–221.

Suh, J.P., Roh, J.H., Cho, Y.C. *et al.* (2009) The Pi40 gene for durable resistance to rice blast and molecular analysis of Pi40-advanced backcross breeding lines. *Phytopathology*, **99**, 243–250.

Sundaram, N.V. (1975) Ergot of bajra, in *Advances in Mycology and Plant Pathology*. New Delhi. India: Professor R.N. Tandon's Birthday Celebration Committee, pp. 155–160 (343 pp.).

Sutton, B.C. (1980) The Coelomycetes. Fungi Imperfecti with Pycnidia, in *Acervuli and Stroma*, Commonwealth Mycological Institute, Kew, Surrey, England, p. 696.

Takan, J.P., Chipili, J., Muthumeenakshi, S. *et al.* (2012) *Magnaporthe oryzae* populations adapted to finger millet and rice exhibit distinctive patterns of genetic diversity, sexuality and host interaction. *Mol. Biotechnol.*, **50** (2), 145–58.

Tapsoba, H. and Wilson, J.P. (1996) Pathogenic variation in *Puccinia substriata* var. *indica* in the southeastern United States and screening for resistance in pearl millet germplasm. *Pl. Dis.*, **80**, 395–397.

Thakur, R.P. and Kanwar, Z.S. (1978) Internal seed-borne infection and heat therapy in relation to downy mildew of *Pennisetum typhoides*. *Sci. Cult.*, **43**, 432–434.

Thakur, R.P., Rao, V.P. and King, S.B. (1989) Ergot susceptibility in relation to cytoplasmic male sterility in pearl millet. *Pl. Dis.*, **73**, 676–678.

Thakur, R.P., Rao, V.P. and Williams, R.J. (1984) The morphology and disease cycle of ergot caused by *Claviceps fusiformis* in pearl millet. *Phytopathology*, **74**, 201–205.

Thakur, R.P., Reddy, B.V.S., Indira, S. *et al.* (2006) *Sorghum Grain Mold*, Information Bulletin No. 72, International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh, India, p. 32.

Thakur, R.P., Reddy, B.V.S. and Mathur, K. (2007) *Screening Techniques for Sorghum Diseases*, Information Bulletin No. 76. ICRISAT, Patancheru, Andhra Pradesh, India, p. 92.

Thakur, R.P., Sharma, R. and Rao, V.P. (2011) *Screening Techniques for Pearl Millet Diseases*, Information Bulletin No. 89. International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh, India, p. 56.

Thomas, K.M., Ramakrishna, T.S. and Srinivasan, K.V. (1945) The occurrence of ergot in south India. *Proc. Indian Acad. Sci.*, **B21**, 93–100.

Thomas, M.D., Sissoko, I. and Sacco, M. (1995) Development of leaf anthracnose and its effect on yield and grain weight of sorghum in West Africa. *Pl. Dis.*, **80**, 151–153.

Todman, A.K., Pawar, D.R. and Joshi, M.H. (1994) Host reactions to finger millet blast (*Pyricularia grisea* Sacc.). *Mysore J. Agric. Sci.*, **28**, 45–46.

Tonapi, V., Ryley, M.J., Vic, G. *et al.* (2002) Influence of temperature and relative humidity on pollen traits and ergot severity in sorghum. *Int. Sorghum Millets Newslett.*, **43**, 74–76.

Tsukiboshi, T., Shimanuki, T. and Uematsu, T. (1999) *Claviceps sorghicola* sp. nov., a destructive ergot pathogen of sorghum in Japan. *Mycol. Res.*, **103** (11), 1403–1408.

Tuleen, D.M. and Frederiksen, R.A. (1977) Characteristics of resistance to *Exserohilum (Helminthosporium) turcicum* in *Sorghum bicolor*. *Pl. Dis. Report*, **61**, 657–661.

Upadhyaya, H.D., Wang, Y.-H., Sharma, R. and Sharma, S. (2013) Identification of genetic markers linked to anthracnose resistance in sorghum using association analysis. *Theor. Appl. Genet.*, **126**, 1649–1657.

Upasana, R., Chaudhary, D.P. and Srivastava, M. (2010) Downy mildew and its effect on quality of pearl millet hybrids. *Crop Impro.*, **37** (2), 206.

Viji, G., Gnanamanickam, S.S. and Levy, M. (2000) DNA polymorphisms of isolates of *Magnaporthe grisea* from India that is pathogenic to finger millet and rice. *Mycol. Res.*, **104** (2), 161–167.

Wilson, J.P. and Gates, R.N. (1993) Forage yield losses in hybrid pearl millet due to leaf blight caused primarily by *Pyricularia grisea*. *Phytopathology*, **83**, 739–743.

Wilson, J.P., Gates, R.N. and Hanna, W.W. (1991) Effect of rust on yield and digestibility of pearl millet forage. *Phytopathology*, **81**, 233–236.

12

Nutritional Qualities & Value Addition of Millets

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12.1 Introduction

Millets are a group of highly variable small-seeded grasses, widely grown around the world as cereal crops or grains for both human food and animal fodder. They do not form a taxonomic group, but rather a functional or agronomic one. Millets are important crops in the semi-arid tropics of Asia and Africa (especially in India, Nigeria and Niger), with 97% of millet production in developing countries. Millets are known as nutritious cereals and can be grown on marginal lands with less water. The crop is favoured due to its productivity and short growing season under dry, high temperature conditions. Millet was the main grain in China before rice. In North America and Europe, millet has been grown primarily for animal fodder, pasture grass and birdseed. Millet grows in stalks of 1–10 feet high, and ripens in 60–90 days. It grows in relatively infertile areas, is drought-resistant and matures in a short time; great for growing in less agriculturally developed areas. Millet ranks as the sixth most important grain in the world, sustains one-third of the world's population and is a significant part of the diet in northern China, Japan, Manchuria and various areas of the former Soviet Union, Africa, India and Egypt. China, India and Niger are the world's largest growers of millet today.

Millets include sorghum (*Sorghum bicolor* (L.) Moench), pearl millet (*Pennisetum glaucum* (L.) R. Br.), finger millet (*Eleusine coracana* (L.) Gaertn.), foxtail millet (*Setaria italica* (L.) Beauv.), kodo millet (*Paspalum scrobiculatum* (L.), little millet (*Panicum sumatrense*), proso millet (*Panicum miliaceum* (L.)) and barnyard millet (*Echinochloa colona* (L.) Link and *E. crusgalli* (L.) P.B.). The most widely grown millet is pearl millet, which is an important crop in India and parts of Africa. Finger millet, proso millet and foxtail millet are also important crop species. In the developed world, millets are less important. For example, in the United States, the only significant crop is proso millet, which is mostly grown for birdseed.

Presently, the consumption of traditional foods is limited mainly because of their longer processing methods as compared to the urban ready-to-eat or ready-to-cook foods. Information on the nutritional and biochemical status of millets is also insufficient, and these need to be studied in detail to create evidence-based awareness among the urban population. It is observed that although the nutritive value and potential health benefits of millet grains were found to be comparable to major cereals such as

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wheat, rice and maize, and although the processing technologies such as fermentation, soaking/malting and fortification/supplementation were found to improve their edible and nutritional characteristics, utilisation of millet grains as food is still mainly limited to populations in rural areas at the household level. This is due to the lack of innovative millet-processing technologies to provide easy-to-handle, ready-to-cook or ready-to-eat, and safe products and meals at a commercial scale that can be used to feed large populations in urban areas. Consumer-preferred food products such as breakfast cereals, pasta and noodles and baked products such as bread and biscuits are ideal foods to target the urban population. These foods are consumed internationally as well, irrespective of the nationality of the consumer. For a novel food product to be accepted, its nutritional information is important to convince the consumer.

However, with an increasing population and thus an increasing demand for food, feed and fuel, society will be pressed to increase agricultural production. Consumption of millets will be increased when there are technologies for processing available commercially in countries where millets are consumed. Diversification of food production must be encouraged both at the national and household levels in tandem with increasing yields. Providing more healthful and traditional whole-grain and multi-grain substitutes for refined carbohydrates can be one important aspect of therapeutic dietary modification and promoting utilisation of minor-grain foods to reduce the incidence of life-style diseases such as diabetes, cardiovascular diseases and cancer in the urban population.

12.2 Sorghum

The sorghum-cultivation area in India was more than 16 million ha in 1981, but it has gradually decreased to 7.8 million ha in 2007–2008 (still 20% of the world's sorghum area). Of this, 3.5 million ha was grown in the rainy (*kharif*) season and 4.3 million ha in the post-rainy (*rabi*) season. Production increased from 9 million t in the early 1970s to 12 million t in the early 1980s and maintained this level for over a decade until the early 1990s, followed by a steep decline to 7.3 million t. Sorghum grain yields in India have averaged 1170 kg/ha in the rainy season and 880 kg/ha in the post-rainy season in recent years.

With values ranging from 56 to 73%, the average starch content of sorghum is 69.5% (Subramanian and Jambunathan, 1988) (Table 12.1). About 70–80% of the sorghum starch is amylopectin and the remaining 20–30% is amylose (Deatherage *et al.,* 1955). Waxy or glutenous sorghum varieties are very low in amylose; their starch is practically 100% amylopectin (Ring *et al.,* 1982). But in sugary sorghum the amylose content of the starch is about 5–15% higher than in normal sorghum (Singh and Axtell, 1973). The total carbohydrate content of sugary sorghum is normal, however, since it contains exceptionally high levels of water-soluble polysaccharides (29.1%).

The digestibility of isolated starch of sorghum cultivars ranged from 33 to 48% as against the 53–58% for corn starches (Sikabbubba, 1989). The texture of the grain endosperm, the particle size of the flour and starch digestibility was found to be strongly correlated with each other. Starch in floury sorghum was found to be more digestible than that in corneous sorghum. Particles of ground floury sorghum were smaller than those of similarly ground corneous sorghum. The smaller particle size and correspondingly greater surface area facilitate the enzyme action and thus improve starch digestibility.

Table 12.1 Proximate principles and minerals of Millets and Cereals.[a]

Sl. No.	Millets and cereals	Protein (g)	Fat (g)	Minerals (g)	Crude fibre (g)	Carbohydrates (g)	Energy (Kcal)	Calcium (mg)	Phosphorous (mg)	Iron (mg)
1	Sorghum (Great millet)	10.4	1.9	1.6	1.6	72.6	349	25	222	4.1
2	Pearl millet	11.6	5	2.3	1.2	67.5	361	42	296	8
3	Finger millet	7.3	1.3	2.7	3.6	72	328	344	283	3.9
4	Foxtail millet	12.3	4.3	3.3	8	60.9	331	31	290	2.8
5	Proso millet	12.5	1.1	1.9	2.2	70.4	341	14	206	0.8
6	Little millet	7.7	4.7	1.5	7.6	67	341	17	220	9.3
8	Kodo millet	8.3	1.4	2.6	9	65.9	309	27	188	0.5
7	Barnyard millet	6.2	2.2	4.4	9.8	65.5	307	20	280	5
9	Wheat flour (whole)	12.1	1.7	2.7	1.9	69.4	341	48	355	4.9
10	Rice raw milled	6.8	0.5	0.6	0.2	78.2	345	10	160	0.7

a All values are per 100 gm of edible portion.

The chemical nature of the starch, particularly the amylose and amylopectin content, is yet another factor that affects its digestibility. The starch digestibility was reported to be higher in low-amylose, that is, waxy sorghum than in normal sorghum, corn and pearl millet grains (Hibberd *et al.,* 1982).

The second major component of sorghum and millet grains is protein. Both genetic and environmental factors affect the protein content of sorghum and millets (Table 12.1). In sorghum, the variability is large, probably because the crop is grown under diverse agro-climatic conditions which affect the grain composition (Burleson *et al.,* 1956; Waggle *et al.,* 1967; Deosthale *et al.,* 1972). Fluctuations in the protein content of the grain are generally accompanied by changes in the amino acid composition of the protein (Waggle and Deyoe, 1966).

The quality of a protein is primarily a function of its essential amino acid composition. To assess the protein quality, Block and Mitchell (1946) introduced the concept of an amino acid or chemical score, in which the amount of the essential amino acid that is in greatest deficit is expressed as a percentage of the amount present in a standard or reference protein. Egg and human milk proteins, for their very high biological value, have been considered as reference standards. Sorghum and millet proteins differed in their essential amino acid profile (Table 12.4). However, the most common feature was that lysine was always found to be the most limiting amino acid. The highest deficit of lysine was in the protein of barnyard millet (chemical score 31), closely followed by little millet (chemical score 33). Sorghum protein, with a chemical score of 37, did not differ very much in quality from the proteins of barnyard and little millet.

The primary function of dietary protein is to satisfy the body's needs for nitrogen and essential amino acids. According to the World Health Organization (WHO, 1985), the chemical score of a protein if calculated in relation to the essential amino acid requirement pattern as reference would be more realistic and indicative of the capacity of the protein to meet human requirements. Such data on chemical score relative to amino acid requirement for different age groups suggested that the inherent capacity of the existing millet varieties commonly consumed was not adequate to meet the growth requirements of infants and young children, though all of them except sorghum may be able to meet the maintenance requirements in adults.

Grain proteins are broadly classified into four fractions according to their solubility characteristics: albumin (water soluble), globulin (soluble in dilute salt solution), prolamin (soluble in alcohol) and glutelin (extractable in dilute alkali or acid solutions). In solubility fractionation studies with sorghum and pearl, finger and foxtail millets, five protein fractions were obtained. The levels of albumin plus globulin were higher in pearl millet varieties than in sorghum, while amounts of the cross-linked prolamin, β-prolamin, were higher in sorghum than in pearl millet.

12.3 Pearl Millet

India is the largest producer of pearl millet in Asia, both in terms of area (about 9 million ha) and production (8.3 million t), with an average productivity of 930 kg/ha during the past 3 years (Figure 12.1). From the early 1980s, the pearl millet area in India declined by 22%, but production increased by 36%, due to a 75% increase in productivity (from 530 kg/ha during 1981–1983 to 930 kg/ha during 2008–2010).

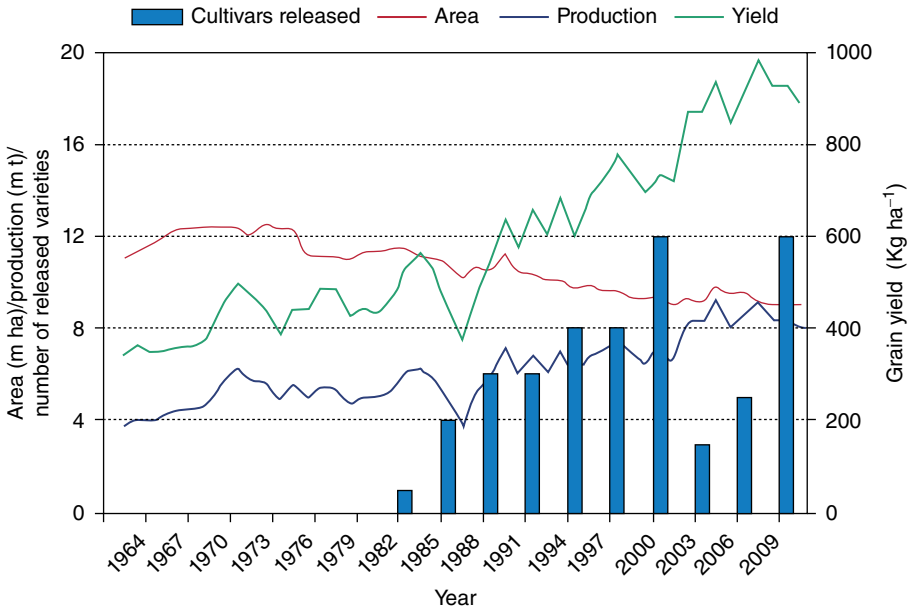

Figure 12.1 Three-year moving average for pearl millet area, production and grain yield; and number of varieties/hybrids released (3-year total) based on ICRISAT-bred material in India.

In different pearl millet genotypes, the starch content of the grain varied from 62.8 to 70.5% (Table 12.1), soluble sugar from 1.2 to 2.6% and amylose from 21.9 to 28.8% (Subramanian and Jambunathan, 1988). Lower values for starch (56.3–63.7%) and amylose (18.3–24.6%) have been found in some high-yielding Indian pearl millet varieties (Singh and Popli, 1973). Subramanian *et al.* (1981) found that the predominant component of total soluble sugar (2.16–2.78%) was sucrose (66%), followed by raffinose (28%). Other sugars detected in measurable amounts were stachyose, glucose and fructose. The proportion of sucrose in total sugar was lower in pearl millet than in sorghum.

The amylose content of these starches varied within a narrow range (22–24%). Variation in the water-binding capacity (83.6–99.5%) was probably due to differences in the proportions of amorphous and crystalline starch in the granule; amorphous starch has greater water absorption capacity than crystalline starch.

12.4 Finger Millet

In high-yielding varieties of finger millet analysed by Wankhede and colleagues (1979), mean starch content was 60.3 (59.5–61.25%) (Table 12.1). The swelling capacity and solubility in water at 90°C of the isolated starch of finger millet were lower than for sorghum and similar to those of other millet starches. The high peak viscosity and the increase in viscosity on cooling suggested a strong tendency of the starch to undergo retrogradation. The paste viscosity is reduced and the nutrient density, particularly energy density, is enhanced after malting of the grain, and, on this basis, weaning food containing 70 parts of malted finger millet and 30 parts of dehulled green gram has been developed (Malleshi and Desikachar, 1982).

12.4.1 Essential Amino Acid Composition (mg/g) and Chemical Score of Sorghum and Millet Proteins

Apart from a favourable essential amino acid profile, easy digestibility is an important attribute of a good-quality protein (Table 12.4). Chemical scores do not take into account the digestibility of protein or availability of amino acids. Biological methods based on measurement of growth and nitrogen retention assess the overall nutritional quality of the protein. These methods include determination of protein efficiency ratio (PER), net protein utilisation (NPU), biological value (BV) and true protein digestibility (TDP).

While millets are indigenous to many parts of the world, they most likely had an evolutionary origin in tropical Western Africa, as that is where the greatest numbers of both wild and cultivated forms exist. Millets have been important food staples in human history, particularly in Asia and Africa, and they have been in cultivation in East Asia for the last 10000 years (Arora *et al.,* 2011). Millets are not only adapted to poor, droughty and infertile soils, but they are also more reliable under these conditions than most other grain crops. This has, in part, made millet production popular, particularly in countries surrounding the Sahara Desert in Western Africa.

Millets, however, do respond to high fertility and moisture. On a per-hectare basis, millet grain can be produced with two to four times higher yields with the use of proper irrigation and sustainable soil supplements. Improved breeds of millets improve their disease resistance and can significantly enhance farm yield productivity. There has been a virtuous cycle of cooperation among the developing countries to improve millet yields.

12.5 Other Millets

Foxtail and proso millets have been reported to have both glutenous and non-glutenous endosperm types, while only the non-glutenous type of endosperm is reported to be present in finger and barnyard millets (Tomita *et al.,* 1981). The starch in two foxtail millet varieties was 100% amylopectin. Starches of foxtail, proso and barnyard millets were more digestible than maize starch in terms of *in vitro* amylolysis by pancreatic amylase. The glutenous starches were more digestible than non-glutenous types as in other cereal grains.

The increase in paste viscosity on cooling to 35 °C and the further rise after 1 hour's holding at that temperature indicated the strong tendency of these millet starches to undergo retrogradation. One of the prove varieties, namely big red prove, was exceptional in that its starch had higher water-binding capacity and gelatinisation temperature than that of five other varieties.

Millets are the most important drought-resistant crops in terms of world agriculture production. Also, millets have resistance to pests and diseases, short growing season, and productivity under drought conditions, compared to major cereals (Devi *et al.,* 2011). Therefore, millet grains are now receiving specific attention from these developing countries in terms of utilisation as food. (Bouis, 2000; Kaur *et al.,* 2012). The world total production of millet grains at last count was 762712 metric tonnes, and the top producer was India, with an annual production of 334500 t (43.85%) (FAO, 1965; Table 1). Millet grains, before consumption and for preparing food, are usually processed by commonly used traditional processing techniques including decortication, malting,

fermentation, roasting, flaking, and grinding to improve their edible, nutritional and sensory properties.

Therefore, with value-added strategies and appropriate processing technologies, the millet grains can find a place in the preparation of several value-added, health food-products, which may then result in high demand from large urban populations and non-traditional millet users. The presence of all the required nutrients in millets makes them suitable for large-scale utilisation in the manufacture of food products such as baby foods, snack foods and dietary food and, increasingly, more millet products have entered into the daily lives of people, including millet porridge, millet wine and millet nutrition powder from both grain and flour (Tables 12.2, 12.3, 12.4 and 12.5). Several traditional household food processing and preparation methods can also be used to enhance the bio-availability of micronutrients in plant-based diets. These include thermal processing, mechanical processing, soaking, fermentation and germination/malting. These procedures aim to increase the physicochemical accessibility of micronutrients (Tables 12.2, 12.3, 12.4), decrease the content of anti-nutrients, such as phytates or increase the content of compounds that improve bio-availability (Hotz and Gibson, 2007) (Table 12.6). Millets must also be accepted as functional food and nutraceuticals because they provide dietary fibres, proteins, energy, minerals (Table 12.3), vitamins and antioxidants required for human health (Table 12.2).

Pearl millet was found significantly rich in resistant starch, soluble and insoluble dietary fibres, minerals and antioxidants (Ragaee *et al.,* 2006). It contains about 92.5% dry matter, 2.1% ash, 2.8% crude fibre, 7.8% crude fat, 13.6% crude protein and 63.2% starch (Ali *et al.,* 2003). Also, foxtail millet protein characterisation showed that its protein concentrate is a potential functional food ingredient, and the essential amino acid pattern suggests possible use as a supplementary protein source to most cereals because it is rich in lysine (Mohamed *et al.,* 2009). Foxtail millet protein characterisation showed that its protein concentrate is a potential functional food ingredient, and the essential amino acid pattern suggests possible use as a supplementary protein source to most cereals because it is rich in lysine (Mohamed *et al.,* 2009).

Use of millet grains as replacement in wheat composite flours, complementary food, and food blends seems the best method that can be used for the preparation of nutritional, 'healthy' and safe, high-quality and shelf-stable food products at household and commercial scales to promote utilisation of millet grains. In addition, to produce high-quality products at a commercial scale for urban consumers, there is a need for innovative processing technologies for decortication, milling and other preparation treatments of millet grains. In return, a consistent supply of high-quality millet grains for industrial uses and development of millet cultivars with high essential amino acid content are needed. Evaluation of nutritive value and potential health benefits of millet grains and their fractions in animal and human models should be performed in future research studies to support efforts for promoting their utilisation as food. Fermentation also enhanced the crude protein and reduced fat and crude fibre after 16 h in fermented–cooked–fermented *rabadi* prepared in steel and earthen pots and cooked–fermented *rabadi* (a traditional fermented food) in earthen pots. Enhanced flavonoids were also observed in all samples after 16 h of fermentation (Gupta and Nagar, 2010). Therefore, malting generally improves the nutrient content and digestibility of foods, and it could be an appropriate food-based strategy to derive iron and other minerals maximally from food grains (Platel *et al.,* 2010). Germination and probiotic fermentation caused significant improvement in the contents of thiamine, niacin, total lysine, protein fractions,

Table 12.2 Vitamin content in Millets and Cereals.[a]

Sl. No.	Millets and cereals	Carotene (µg)	Thiamine (mg)	Riboflavin (mg)	Niacin (mg)	Total B6 (mg)	Folic acid (µg)		Vitamin C (mg)	Choline (mg)
							Free	Total		
1	Sorghum (Great millet)	47	0.37	0.13	3.1	0.21	14	20	0	—
2	Pearl millet	132	0.33	0.25	2.3	—	14.7	45.5	0	—
3	Finger millet	42	0.42	0.19	1.1	—	5.2	18.3	0	—
4	Foxtail millet	32	0.59	0.11	3.2	—	4.2	15	0	—
5	Proso millet	0	0.2	0.18	2.3	—			0	748
6	Little millet	0	0.3	0.09	3.2	—	2.2	9	0	—
7	Kodo millet	0	0.33	0.09	2	—	7.4	23.1	0	—
8	Barnyard millet	0	0.33	0.1	4.2	—	—	—	0	—
9	Wheat (whole)	64	0.45	0.17	5.5	0.57	142	36.6	0	—
10	Rice raw milled	0	0.06	0.06	1.9	—	4.1	8	0	—

a All values are per 100 gm of edible portion.

Table 12.3 Minerals and trace element composition in millets and cereals.[a]

Sl. No.	Millets and cereals	Mg	Sod	Pot	Cu	Mn	Mo	Zn	Cr	S	Cl
1	Sorghum (Great millet)	171	7.3	131	0.46	0.78	0.039	1.6	0.008	54	44
2	Pearl millet	137	10.9	307	1.06	1.15	0.069	3.1	0.023	147	39
3	Finger millet	137	11	408	0.47	5.49	0.102	2.3	0.028	160	44
4	Foxtail millet	81	4.6	250	1.4	0.6	0.07	2.4	0.03	171	37
5	Proso millet	153	8.2	113	1.6	0.6		1.4	0.02	157	19
6	Little millet	133	8.1	129	1	0.68	0.016	3.7	0.18	149	13
7	Kodo millet	147	4.6	144	1.6	1.1	—	0.7	0.02	136	11
8	Barnyard millet	82	—	—	0.6	0.96	—	3	0.09	—	_
9	Wheat (whole)	138	17.1	284	0.68	2.29	0.051	2.7	0.012	128	47
10	Rice milled 5%	90	—	—	0.14	0.59	0.058	1.4	0.004	—	—

a All values are mg per 100 gm of edible portion.
Sources: FAO, 1970; Indira and Naik, 1971.

Table 12.4 Essential amino acids (mg/G N)in Millets and Cereals.

Sl. No.	Millets and cereals	Approximate total *N* g/100 gm	Arginine	Histidine	Lysine	Tryptophan	Phenylalanine	Tyrosine	Methionine	Cystine	Threonine	Luecine	Isoleucine	Valine
1	Sorghum (Great millet)	1.7	240	160	150	70	300	180	100	90	210	880	270	340
2	Pearl millet	1.9	300	140	190	110	290	200	150	110	240	750	260	330
3	Finger millet	1.2	300	130	220	100	310	220	210	140	240	690	400	480
4	Foxtail millet	2	220	130	140	60	420	137*	180	100	190	1040	480	430
5	Proso millet	2	290	110	190	50	310	159*	160	172*	150	760	410	410
6	Little millet	1.2	250	120	110	60	330	—	180	90	190	760	370	350
7	Kodo millet	1.3	270	120	150	50	430	213*	180	110	200	650	360	410
8	Barnyard millet*		231	119	106	63	362	150	113	175	231	725	288	388
9	Wheat (whole)	1.9	290	130	170	70	280	180	90	140	180	410	220	280
10	Rice milled 5%	1.1	480	130	230	80	280	290	150	90	230	500	300	380

* Hulse *et al.* (1980) *Sorghum and the Millets: Their Composition and Nutritive Value.*

Table 12.5 Fat and fatty acids content in millets and cereals .

Sl. No.	Millets and cereals	Fat	Palmitic 16:0	Stearic 18:0	Arachidic 20:0	Behenic 22:0	Lignoceric 24:0	Total saturates	Palmitoliec 16:1	Oleic 18:1	Total Mono unsaturates	Linoleic 18:2 $n=6$	α-Linoleic 18:3 $n=3$	Total polyunsaturates
1	Sorghum (Great millet)	3.3	0.5	0.07	—	—	—	0.57	—	1	1	1.5	0.05	1.55
2	Pearl millet	5.5	1	0.24	—	—	—	1.24	—	1.2	1.2	2.2	0.13	2.33
3	Finger millet	1.5	0.3	0.02	—	—	—	0.32	—	0.7	0.7	0.3	0.05	0.35
4	Foxtail millet				—	—	—		—					
5	Proso millet				—	—	—		—					
6	Little millet				—	—	—		—					
7	Kodo millet				—	—	—		—					
8	Barnyard millet				—	—	—		—					
9	Wheat (whole)	2.9	0.4	0.1	—	—	—	0.5	—	0.3	0.3	1.1	0.17	1.27
10	Rice	1.7	0.4	0.05	—	—	—	0.45	—	0.4	0.4	0.5	0.01	0.51

Source: Hulse *et al.* (1980) *Sorghum and the Millets: Their Composition and Nutritive Value.*

Table 12.6 Oxalic acid and Phytin Phosphorous contents in Millets and Cereals.

Sl. No.	Millets and cereals	Oxalic acid mg/100 gm	Phytin P mg/100 gm	Phytin P as % of total P
1	Sorghum (Great millet)	10	172	77
2	Pearl millet	21	141	48
3	Finger millet	0	209	74
4	Foxtail millet	0	198	68
5	Proso millet	0	83	40
6	Little millet	0	57	26
7	Kodo millet	0	135	72
8	Barnyard millet			
9	Wheat (whole)	8	238	80
10	Rice (raw milled)	3	83	52

sugars, soluble dietary fibre and *in vitro* availability of Ca, Fe and Zn of food blends (Arora *et al.,* 2011).

Due to its importance in food preservation, fermentation is widely used throughout Africa, where modern food preservation methods are still not common. It helps to preserve many food products, provides a wide variety of flavours, and significantly improves the nutritional properties of the raw material. Fermented foods are also produced and consumed worldwide in terms of their importance for human food (Mugocha *et al.,* 2000; Gotcheva *et al.,* 2001).

A number of research studies have been carried out to investigate the possibility of producing ready-to-eat food products from pure-millet grains. For example, white proso and foxtail millets have been used in the formulation of a flaked whole-grain ready-to-eat breakfast cereal where the effects of dried honey or molasses as secondary sweeteners were also evaluated. Fortification of grain foods was found to be an effective strategy that can be used to overcome nutrient deficiencies. Supplementation of millet flour with soybean protein steadily decreased the In Vitro Protein Digestibility (IVPD) with an increase in the portion of soybean in the blend. Further, essential amino acids of millet flour were enriched on supplementation with soybean protein. Supplementation significantly increased lysine 1.5- to 2.4-fold. In addition, essential amino acid content remained higher in the cooked composite flours when compared with the cooked native millet flour (Ali *et al.,* 2010). It has also been found that supplementation of pearl millet with whey protein resulted in a significant increase in protein content compared to the control. In addition, sensory evaluation revealed higher acceptability for whey-protein-supplemented formulas compared to the control (Mallasy *et al.,* 2010). Therefore, it can be concluded that supplementation of millet grains with natural food products to enhance their nutritive value can be promising and highly cost-effective compared to fortification by chemical and synthetic nutrients.

In addition to their cultivating advantages, millets were found to have high nutritive value, comparable to that of major cereals such as wheat and rice (Parameswaran and Sadasivam, 1994). It has also been reported that millet proteins are good sources of essential amino acids except lysine and threonine, but are relatively high in methionine.

Millets are also rich sources of phytochemicals and micronutrients (Mal *et al.,* 2010; Singh *et al.,* 2012).

For example, pearl millet was found to be significantly rich in resistant starch, soluble and insoluble dietary fibres, minerals and antioxidants (Ragaee *et al.,* 2006). It contains about 92.5% dry matter, 2.1% ash, 2.8% crude fibre, 7.8% crude fat, 13.6% crude protein and 63.2% starch (Ali *et al.,* 2003). Also, foxtail millet protein characterisation showed that its protein concentrate is a potential functional food ingredient and the essential amino acid pattern suggests possible use as a supplementary protein source to most cereals because it is rich in lysine (Mohamed *et al.,* 2009). In addition, black finger millet contains 8.71 mg/g dry weight fatty acid and 8.47 g/g dry weight protein (Glew *et al.,* 2008). Kodo millet and little millet were also reported to have 37–38% of dietary fibre, which is the highest among cereals; and the fat has higher polyunsaturated fatty acids (Table 12.7) (Malleshi and Hadimani, 1993; Hegde and Chandra, 2005). The protein content of proso millet (11.6% of dry matter) was found to be comparable with that of wheat (Table 12.1), and the grain of proso millet was significantly richer in essential amino acids (leucine, isoleucine and methionine) than wheat protein (Kalinova and Moudry, 2006).

Several potential health benefits such as preventing cancer and cardiovascular diseases; reducing tumour incidence; lowering blood pressure, risk of heart disease, cholesterol and rate of fat absorption; delaying gastric emptying and supplying gastrointestinal bulk were reported for millets (Truswell, 2002; Gupta *et al.,* 2012). It has been reported that soluble- and insoluble-bound phenolic extracts of several varieties of millet (kodo, finger, foxtail, proso, pearl and little millets) whole grains are rich sources of phenolic compounds and show antioxidant, metal-chelating and reducing powers. However, the potential of whole millets as natural sources of antioxidants depends on the variety used (Chandrasekara and Shahidi, 2010). Much attention has been devoted to investigations of the nutraceutical and antioxidant properties of some major millet varieties, including finger millet, pearl millet, and foxtail millet. The reduction in some nutrients (minerals, fibres, and antioxidants) and antinutrients (phytates, tannin) could

Table 12.7 Dietary fibre content in millets and cereals.[a]

Sl. No	Millets and cereals	TDF (g)	IDF (g)	SDF (g)
1	Sorghum (Great millet)	9.7	8	1.7
2	Pearl millet	11.3	9.1	2.2
3	Finger millet	11.5	9.9	1.6
4	Foxtail millet			
5	Proso millet			
6	Little millet			
7	Kodo millet			
8	Barnyard millet			
9	Wheat	12.5	9.6	2.9
10	Rice	4.1	3.2	0.9

a All values are per 100 gm of edible portion. TDF = total dietary fibre; IDF = insoluble dietary fibre; SDF = soluble dietary fibre.

be attributed to the fact that they are mainly located in the peripheral parts of the grains (pericarp and aleurone layer); therefore, removing of the pericarp during decortication leads to reduce their contents (Hama *et al.,* 2011). Removing of the bran fraction by sieving, which is rich in nutrients, such as fibre, minerals and antioxidants, leads to decrease in the nutritive value and potential health benefits of grains, and so using whole-grain flour in human nutrition is suggested to be more beneficial for health promotion. It has been found that germination of proso millet grains increased the free amino acids and total sugars and decreased the dry weight and starch content. Increases in lysine, tryptophan and non-protein nitrogen were also noticed (Parameswaran and Sadasivam, 1994). Germination also appreciably improved the *in vitro* protein (14–26%) and starch (86–112%) digestibility in pearl millet, and the improvement by germination was significantly higher than by blanching (Archana and Kawatra, 2001).

12.6 Health Benefits of Millets

Millet provides a host of nutrients, has a sweet nutty flavour and is considered to be one of the most digestible and non-allergenic grains available. It is one of the few grains that are alkalising to the body. Most people have not even heard of millet, and much less understand the benefits of millet nutrition. And yet, millet is one of the best-kept secrets of our ancestors. Traced back to its origin in China, millet has been used throughout the ages and across many countries.

For centuries millet has been a prized crop in China, India, Greece, Egypt and Africa, used in everything from bread to couscous, and as cereal grain. Millet is even mentioned as a treasured crop in the Bible.

This tiny 'grain' is gluten-free and packed with vitamins and minerals. In fact, while it is often called a grain because of its grain-like appearance, millet is actually a seed. It is often used in birdseed mixture, but if you think it is just for the birds, you are missing out on the important benefits of millet nutrition. Millet is one of the four gluten-free grain-like seeds on the Body Ecology programme.

- Millet is alkaline and it digests easily.
- The Hunzas – who live in a remote area of the Himalayan foothills and are known for their excellent health and longevity – enjoy millet as a staple in their diet.
- Millet will hydrate your colon to keep you from being constipated.
- Millet acts as a probiotic, feeding micro flora in your inner ecosystem.
- The serotonin in millet is calming to your moods.
- Millet is a smart carb with lots of fibre and low simple sugars. Because of this, it has a relatively low glycaemic index and has been shown to produce lower blood sugar levels than wheat or rice. (Kumari and Sumathi, 2002).
- Magnesium in millet can help reduce the effects of migraines and heart attacks.
- Niacin (vitamin B3) in millet can help lower cholesterol.
- Millet consumption decreases triglycerides and C-reactive protein. Scientists in Seoul, South Korea, concluded that millet may be useful in preventing cardiovascular disease. (Lee *et al.,* 2010).
- All millet varieties show high antioxidant activity. A team of biochemists have analysed and confirmed this. (Chandrasekara and Shahidi, 2010).
- Millet is gluten-free and non-allergenic. A great grain for food-sensitive individuals.

- Millet's high protein content (15%) makes it a substantial addition to a vegetarian diet.
- Does not feed pathogenic yeast (candida).
- Phosphorus in millet helps with fat metabolism, body-tissue repair and creating energy (phosphorus is an essential component of adenosine tri phosphate or ATP, a precursor to the energy in your body).
- Millet can help lower risk of type 2 diabetes.
- Fibre from whole grains has been proven to protect against breast cancer.
- Whole grains have been shown to protect against childhood asthma.

12.7 Conclusion

Small quantities of millet grain are traded for use as flour and beer malt in both Africa and Asia. In areas where millet is competitive in terms of price and feed value, demand for millet grain for fish and poultry feed may grow. Pearl millet has the advantage of superior adaptation to high temperatures and infertile soils with low water-holding capacity. In specific areas where these constraints are important, millet grain will compete effectively as a livestock feed against other cereals that must be transported across long distances at considerable expense. Further, there will remain a market niche for millet trade as birdseed. In sum, millet will remain largely associated with the food security of drought-prone human populations. Correspondingly, productivity improvements will contribute most directly to the alleviation of poverty and food insecurity. The prospects for the expansion of market flows are reasonable if targeted within food-deficit areas. However, the prospects for commercial trade are limited, except in small specialty markets for flour, malt, feed grain and birdseed.

References

Ali, M.A.M., El Tinay, A.H. and Abdalla, A.H. (2003) Effect of fermentation on the in vitro protein digestibility of pearl millet. *Food Chem*, **80** (1), 51–54.

Ali, M.A.M., El Tinay, A.H., Mallasy, L.O. and Yagoub, A.E.A. (2010) Supplementation of pearl millet flour with soybean protein: effect of cooking on in vitro protein digestibility and essential amino acids composition. *Intl J Food Sci Technol*, **45**, 740–744.

Archana, S.S. and Kawatra, A. (2001) In vitro protein and starch digestibility of pearl millet (*Pennisetum glaucum* L.) as affected by processing techniques. *Nahrung Food*, **45** (1), 25–27.

Arora, S., Jood, S. and Khetarpaul, N. (2011) Effect of germination and probiotic fermentation on nutrient profile of pearl millet based food blends. *Br Food J*, **113** (4), 470–481.

Block, R.J. and Mitchell, M.M. (1946) The correlation of the amino acid composition of proteins with their nutritive value. *Nutr Abstr Rev*, **16**, 249–278.

Bouis, H.E. (2000) Enrichment of food staples through plant breeding: a new strategy for fighting micronutrient malnutrition. *Nutrition*, **16**, 701–704.

Burleson, C.A., Cowley, W.R. and Otey, G. (1956) Effect of nitrogen fertilization on yield and protein content of grain sorghum in the lower Rio Grande valley of Texas. *Agron J*, **48**, 524–525.

Chandrasekara, A. and Shahidi, F. (2010) Content of insoluble bound phenolics in millets and their contribution to antioxidant capacity. *J Agric Food Chem*, **58**, 6706–6714.

Deatherage, W.L., McMasters, M.M. and Rist, C.E. (1955) A partial survey of amylose content in starch from domestic and foreign varieties of corn, wheat and sorghum and from some other starch-bearing plants. *Trans Am Assoc Cereal Chem*, **13**, 31–42.

Deosthale, Y.G., Nagarajan, V. and Visweswar Rao, K. (1972) Some factors influencing the nutrient composition of sorghum grain. *Indian J Agric Sci*, **42**, 100–108.

Devi, P.B., Vijayabharathi, R., Sathyabama, S. *et al.* (2014) Health benefits of finger millet *(Eleusine coracana* L.) polyphenols and dietary fiber: a review. *J Food Sci Technol*, **51** (6), 1021–1040.

FAO (1965) Protein requirements. FAO Nutrition Meeting Report Series No. 37, Rome, Food and Agricultural Organization.

FAO (1970) Teneur des aliments en acides aminés et données biologique sur les protéines. Etudes nutritionnelles de la FAO. n° 24, Rome, Food and Agricultural Organization.

Glew, R.S., Chuang, L.T., Roberts, J.L. and Glew, R.H. (2008) Amino acid, fatty acid and mineral content of black finger millet (*Eleusine coracana*) cultivated on the Jos Plateau of Nigeria. *Food*, **2** (2), 115–118.

Gotcheva, V., Pandiella, S.S., Angelov, A. *et al.* (2001) Monitoring the fermentation of the traditional Bulgarian beverage boza. *Intl J Food Sci Technol*, **36**, 129–134.

Gupta, N., Srivastava, A.K. and Pandey, V.N. (2012) Biodiversity and nutraceutical quality of some Indian millets. *Proceedings of the National Academy of Sciences, India Section B: Biological Sci*, **82** (2), 265–273.

Gupta, V. and Nagar, R. (2010) Effect of cooking, fermentation, dehulling and utensils on antioxidants present in pearl millet rabadi – a traditional fermented food. *J Food Sci Technol*, **47** (1), 73–76.

Hama, F., Icard-Vernière, C., Guyot, J.P. *et al.* (2011) Changes in micro and macronutrient composition of pearl millet and white sorghum during in-field versus laboratory decortication. *J Cereal Sci*, **54**, 425–433.

Hegde, P.S. and Chandra, T.S. (2005) ESR spectroscopic study reveals higher free radical quenching potential in kodo millet (*Paspalum scrobiculatum*) compared to other millets. *Food Chem*, **92**, 177–182.

Hibberd, C.A., Wagner, D.G., Schemm, R.L. *et al.* (1982) Digestibility characteristics of isolated starch from sorghum and corn grain. *J Anim Sci*, **55**, 1490–1497.

Hotz, C. and Gibson, R.S. (2007) Traditional food-processing and preparation practices to enhance the bioavailability of micronutrients in plant-based diets. *J Nutr*, **37**, 1097–1100.

Hulse, J.H., Laing, E.M. and Pearson, O.E. (1980) *Sorghum and the Millets: Their Composition and Nutritive Value*, Academic Press, New York, pp. 1–997.

Indira, R. and Naik, M.S. (1971) Nutrient composition and protein quality of some minor millets. *Indian J Agric Sci*, **41**, 795–797.

Kalinova, J. and Moudry, J. (2006) Content and quality of protein in proso millet (*Panicum miliaceum L.*) varieties. *Plant Foods Hum Nutr*, **61**, 45–49.

Kaur, K.D., Jha, A., Sabikhi, L. and Singh, A.K. (2012) Significance of coarse cereals in health and nutrition: a review. *J Food Sci Technol,* **51** (8), 1429–1441.

Kumari, P.L. and Sumathi, S. (2002) Effect of consumption of finger millet on hyperglycemia in non-insulin dependent diabetes mellitus (NIDDM) subjects. *Plant Foods Hum Nutr*, **57**, 205–213.

Lee, S.H., Chung, I.M., Cha, Y.S., and Park, Y. (2010, April) Millet consumption decreased serum concentration of triglyceride and C-reactive protein but not oxidative status in hyperlipidemic rats. *Nutrition Research,* **30**(4), 290–296.

Mal, B., Padulosi, S. and Ravi, S.B. (2010) *Minor Millets in South Asia: Learnings from IFAD-NUS Project in India and Nepal*, Bioversity International, Maccarese, Rome, Italy, and M.S. Swaminathan Research Foundation, Chennai, India, pp. 1–185.

Mallasy, L.O., El Tinay, A.H., Elkhalifa *et al.* (2010) Effect of fermentation on biochemical and sensory characteristics of millet flour supplemented with whey protein. *Intl J Food Sci Technol*, **45**, 2387–2393.

Malleshi, N.G. and Hadimani, N.A. (1993) Nutritional and technological characteristics of small millets and preparation of value-added products from them, in *Advances in Small Millets* (eds K.W. Riley, S.C. Gupta, A. Seetharam and J.N. Mushonga), Oxford and IBH Publishing Co Pvt. Ltd., New Delhi, pp. 271–287.

Malleshi, N.G. and Desikachar, H.S.R. (1982) Formulation of a weaning food with low hot paste viscosity based on malted ragi (*Eleusine coracana*) and green gram (*Phaseolus radiatus*). *J Food Sci Technol*, **19**, 193–197.

Mohamed, T.K., Zhu, K., Issoufou, A. *et al.* (2009) Functionality, in vitro digestibility and physicochemical properties of two varieties of defatted foxtail millet protein concentrates. *Int J Mol Sci*, **10**, 5224–5238.

Mugocha, P.T., Taylor, J.R.N. and Bester, B.H. (2000) Fermentation of a composite finger millet-dairy beverage. *World J Microbiol Biotechnol*, **16**, 341–344.

Parameswaran, K. and Sadasivam, S. (1994) Changes in the carbohydrates and nitrogenous components during germination of proso millet (*Panicum miliaceum*). *Plant Foods Hum Nutr*, **45**, 97–102.

Platel, K., Eipeson, S.W. and Srinivasan, R. (2010) Bioaccessible mineral content of malted finger millet (*Eleusine coracana*), wheat (*Triticum aestivum*), and barley (*Hordeum vulgare*). *J Agric Food Chem*, **58**, 8100–8103.

Ragaee, S., Abdel-Aal, E.M. and Noaman, M. (2006) Antioxidant activity and nutrient composition of selected cereals for food use. *Food Chem*, **98** (1), 32–38.

Ring, S.H., Akingbala, J.O. and Rooney, L.W. (1982) Variation in amylose content among sorghums, in *Proceedings of the International Symposium on Sorghum Grain Quality* (eds L.W. Rooney and D.S. Murty),. Hyderabad, India, October 28–31, 1981, ICRISAT, Patancheru, India, p. 269–279.

Sikabbubba, R.,.M. (1989) The effect of alcohol soluble proteins an the digestibility of sorghum, in Masters Thesis, Kansas State University, Manhattan, Kansas, USA.

Singh, K.P., Mishra, A. and Mishra H.N. (2012). Fuzzy analysis of sensory attributes of bread prepared from millet based composite flours. *LWT Food Science and Technology*, **48**: 276–282.

Singh, R. and Axtell, J.D. (1973) Survey of world sorghum collection for opaque and sugary lines, in *Inheritance and Improvement of Protein Quality and Content in Sorghum*, Research Progress Report No. 10, Lafayette, Indiana, Etats-Unis, Department of Agronomy, Agricultural Experiment Station, Purdue University, Agence pour le développement international, Washington DC, USA, pp. l–18.

Singh, R. and Popli, S. (1973) Amylose content and amylolytic studies on high-yielding varieties of bajra (*Pennisetum typhoides*). *J Food Sci Technol*, **10**, 31–33.

Subramanian, V. and Jambunathan, R. (1988) *Potential for alternative uses of sorghum and pearl millet, in 4th Quadrennial Symposium on Sorghum and Millet, May 26–27, 1988*, Lausanne, Switzerland.

Subramanian, V., Jambunathan, R. and Suryaprakash, S. (1981) Sugars of pearl millet [Pennisetum americanum (L.) Leeke] grains. *Int J Food Sci Technol*, **45** (5), 1614–1615.

Tomita, Y., Sugimoto, Y., Sakamoto, S. and Fuwa, H. (1981) Some properties of starches of grain amaranth and several millets. *J Nutr Sci Vitaminol*, **27**, 471–484.

Truswell, A.S. (2002) Cereal grain and coronary heart disease. *Eur J Clin Nutr*, **56** (1), 1–4.

Waggle, D.H. and Deyoe, C.W. (1966) Relationship between protein level and amino acid composition of sorghum grain. *Feedstuffs*, **38**, 1819.

Waggle, D.H., Deyoe, C.W. and Smith, F.W. (1967) Effect of nitrogen fertilization on the amino acid composition and distribution in sorghum grain. *Crop Sci*, **7**, 367–368.

Wankhede, D.B., Shehnaj, A. and Raghavendra Rao, M.R. (1979) Carbohydrate composition of finger millet (*Eleusine coracana*) and foxtail millet (*Seturia italica*). *Plant Foods Hum Nutr*, **28**, 293–303.

WHO (1985) Energy and protein requirements: Report of a joint FAO/WHO/UNU expert consultation, in WHO Technical Report Series No. 724, Geneva, World Health Organization.

13

Molecular Markers for the Genetic Improvement of Millets

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13.1 Introduction

Millets are a group of small-seeded grasses belonging to the Poaceae family, which are widely cultivated, especially in the semi-arid regions of Asia and Africa. They are inherently drought-tolerant, quite resilient to the vagaries of agro-climatic changes and are grown under poor soil fertility with limited rainfall. Sorghum and pearl millet are considered as major millets since they are most widely grown for food, feed and fodder purposes. Minor millets or small millets are comprised of six other small-seeded grasses namely, finger millet, foxtail millet/Italian millet, kodo millet, proso/common millet, barnyard millet and little millet. The grains of most of the millets are rich in protein, fibre, calcium and minerals as compared to wheat and rice. Though India is the largest producer of millets in the world, there has been a drastic reduction in the area, beginning from 1961 (80% for small millets other than finger millet, 46% for finger millet, 59% for sorghum and 23% for pearl millet) (RESMISA, 2012). Due to productivity gains in some millets, the total production showed some increase despite the shrinkage in area. The productivity of small millets (other than finger millet) has remained more or less stagnant over the last two decades. Hence, there is a need for the genetic improvement of millets through the application of molecular breeding approaches.

Among millets, the sequencing of whole genomes of sorghum (Paterson *et al.,* 2009; Mace *et al.,* 2013) and foxtail millet (Zhang *et al.,* 2012; Bennetzen *et al.,* 2012) has led to the rapid development of DNA markers followed by quantitative trait loci (QTL) mapping (Doust *et al.,* 2004; 2005; Srinivas *et al.,* 2009a; Satish *et al.,* 2009; Murali Mohan *et al.,* 2010; Mauro-Herrera *et al.,* 2013). Even though the availability of simple sequence repeat (SSR) markers in pearl millet is limited, they have been used for the genetic diversity assessments (Budak *et al.,* 2003; Mariac *et al.,* 2006; Sumanth *et al.,* 2013) and QTL mapping (Poncet *et al.,* 2000; Yadav *et al.,* 2002; Kannan *et al.,* 2014). However, in other small millets, the availability of markers are very limited or not been reported. In this situation, sequencing of the complete genomes of these small millets is very much essential, which will help in the rapid development of SSR markers or single nucleotide polymorphisms (SNPs) through *in silico* approaches. The availability of markers will help in the construction of linkage maps and identification of QTL associated with important agronomic traits as well as tolerance to biotic and abiotic stresses

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that would accelerate breeding superior cultivars through marker-assisted breeding. This chapter discusses the advancements in the area of genetic diversity assessments, molecular marker development, genetic maps, QTL mapping and marker-assisted selection in various millets critically and also the future prospects.

13.2 Sorghum

13.2.1 Genetic Diversity

Assaying genetic diversity in crop germplasm and elite breeding material is an important aspect in plant breeding. Accurate measurement of levels and patterns of genetic diversity is invaluable for identifying diverse parents for making crosses, resulting in the development of superior cultivars. Characterisation, conservation and exploitation of crop plant germplasm maintained in gene banks is also a major challenge and this enables researchers to establish core and mini-core collections for better utilisation of crop genetic diversity, assessment of structure and marker-trait association studies and heterotic grouping of potential parental lines for hybrid breeding. Even though diverse data sets such as pedigree data, morphological data and protein/isozyme data have been deployed earlier for the assessment of genetic diversity in crop plants, DNA-based markers are extensively used nowadays due to the rapid and large-scale discovery of DNA markers with advancements in sequencing technologies. Different DNA marker systems have been employed globally in assessing the patterns of genetic diversity in sorghum germplasm as well as breeding lines. Initially, during the 1990s, restriction fragment length polymorphism (RFLP) was employed for this purpose. Subsequently, polymerase chain reaction (PCR)-based marker systems such as randomly amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), inter-simple sequence repeat (ISSR), SSR, diversity array technology (DArT)-based markers and currently SNP have been deployed to study molecular diversity in sorghum.

In earlier studies, RFLPs were successfully used for understanding the diversity among the derivatives of wild species, accessions from sub-species, races and sub-races (Aldrich and Doebly, 1992; Tao *et al.,* 1993; Deu *et al.,* 1994), which were generally consistent with the already reported classifications. RAPDs were employed for the assessment of genetic diversity among the accessions of different races and wild sorghum populations, but with inconsistent results (Menkir *et al.,* 1997; Ayana, Bekele *et al.,* 2000; Ayana, Bryngelsson *et al.*, 2000; Agrama and Tuinstra, 2003; Uptmoor *et al.,* 2003). Genetic relationship based on AFLP-SSR was highly related to morphological-SSR but that using morphological and AFLP markers alone did not correlate well (Geleta *et al.,* 2006). The availability of more number of SSR markers during the early 2000s led to several studies on genetic diversity in sorghum. SSRs were used for analysing the diversity among the landraces (Ghebru *et al.,* 2002; Casa *et al.,* 2005) and racial diversity (Agrama and Tuinstra, 2003; Deu *et al.,* 2008). A combination of SSR markers and morphological traits effectively differentiated closely related Maldandi accessions grown during post-rainy season in India (Rakshit *et al.,* 2012) and a low variability was observed among different accessions with a clear differentiation of parental lines of hybrids based on fertility groups (Ganapathy *et al.,* 2012). The grouping of genotypes based on race and geographic origin was reported by Madhusudhana *et al.* (2012), Ramu *et al.* (2013) and Billot *et al.* (2013). The potential of DArT markers in the clustering of sorghum genotypes was reported by Mace *et al.* (2008) and Bouchet *et al.* (2012).

A community resource for association mapping comprising of 377 accessions (major cultivated races and important American breeding lines) was constituted on the basis of the molecular characterisation with SSR markers (Casa *et al.,* 2008). Many research groups have used different sets of SSR markers for the assessment of genetic diversity in their crop material. With an aim of having a set of universal markers that can be used for analysing genetic diversity across the globe, reference sets of SSR markers were developed by different research groups (i) 38 SSR markers (Shehzad *et al.,* 2009), (ii) 48 SSR markers (Billot *et al.,* 2012) and (iii) a set of 40 EST-SSR (Ramu *et al.,* 2013). The second set of markers was used by Billot *et al.* (2013) to analyse the genetic diversity in Global Composite Germplasm Collection (GCGC) of sorghum.

13.2.1.1 Functional Diversity

The genetic diversity assessment using genomic SSR markers will not reveal the clear picture on the functional diversity among the genotypes since they are distributed randomly in the genome and not in the genic regions. However, the availability of a large number of expressed sequence tags (ESTs) in the public domain has helped in the identification of SSR markers commonly known as EST-SSR in sorghum (Srinivas *et al.,* 2008, 2009b; Ramu *et al.,* 2009). Assessment of the functional diversity among the reference set of germplasm lines developed by Billot *et al.* (2013) using 40 EST-SSR markers grouped the genotypes into eight clusters corresponding to the race within geographic origins (Ramu *et al.,* 2009). Even though previous studies could not group the accessions belonging to *bicolor* race distinctly, EST-SSRs could successfully group them into two major groups, highlighting the utility of these markers in clearly defining the functional groups.

13.2.1.2 Core and Reference Collections

Core collection constitutes 10% of the global germplasm that represents the complete diversity present in a crop species. Development of core collection was initiated using ICRISAT sorghum collection by Grenier *et al.* (2000), which led to the assembling of a core collection comprising 225 accessions by random sampling following logarithmic sampling strategy (Grenier *et al.,* 2001a; 2001b). A refined core collection comprising of 210 accessions was developed from this core set by Deu *et al.* (2006), and its genetic diversity was assessed through morphological traits and RFLP markers. Subsequently, a mini-core collection (242 accessions) explaining >90% genetic diversity was developed by Upadhyaya *et al.* (2007) based on 20 morpho-agronomic characters. A reference set (384 genotypes) was developed by Billot *et al.* (2013) from 3365 Global Composite Germplasm Collection (GCGC) of sorghum solely based on their molecular diversity, which was also evaluated using EST-SSR markers by Ramu *et al.* (2013). Apart from ICRISAT, a refined subset of Sudanese sorghum accessions providing unique information on relative heat tolerance was developed by Dahlberg *et al.* (2004). Similarly, a community resource comprising 377 sorghum accessions representing major cultivated races and important breeding lines from the United States along with their progenitors was developed by Casa *et al.* (2008), which was assessed for their population structure by genotyping (47 SSR markers) and phenotyping (eight morphological traits). This serves as a valuable resource for sorghum researchers to undertake association studies of various traits of interest.

13.2.2 Molecular Marker Resources

In the present era of genome sequencing, the whole genome sequence as well as the large-scale ESTs available in the public domain are the major sources for the development

of molecular markers such as SSRs, In-Dels, SNPs, intron length polymorphism (ILP), and so on, through *in silico* mining for targets associated with marker development. These molecular markers are the powerful tools for precision breeding through marker-assisted selection since they are useful for the construction of linkage maps, identification of QTL and their mapping leading to the identification of DNA markers tightly linked to the QTL for the traits of interest. In addition to this, the DNA markers are useful for the assessment of the extent of genetic diversity and population structure in germplasm collections, cultivar identification, genetic purity testing of hybrids and parental lines.

Due to their abundance, high polymorphic nature, codominance and amenability to high-throughput genotyping, SSRs are the markers of choice for the plant breeders for various genetics and mapping applications in sorghum. Prior to the availability of whole genome sequence of sorghum in 2009, a large number of SSR markers were developed by various research groups by following experimental or computational approaches. This led to the development of a large number of SSR markers, from genomic sequences (Brown *et al.,* 1996; Taramino *et al.,* 1997; Bhattramakki *et al.,* 2000; Kong *et al.,* 2000), cDNA sequences (Schloss *et al.,* 2002), EST sequences (Arun, 2006; Reddy *et al.,* 2008; Srinivas *et al.,* 2008; 2009b; Ramu *et al.,* 2009) and unigene sequences (Srinivas *et al.,* 2009a; Nagaraja Reddy *et al.,* 2012). With the availability of the whole genome sequence of sorghum (Paterson *et al.,* 2009), SSR markers were developed by the computational analysis of the whole genome resulting in the development of genome-wide SSR markers (Yonemaru *et al.,* 2009) and $(GATA)_n$ motif-based SSR markers (Jaikishan *et al.,* 2013).

Rapid and large-scale discovery of SNPs and InDels are made possible by the advances in sequencing technologies, availability of efficient computational tools and the availability of astonishing amounts of DNA sequence data, especially ESTs and whole genomes. About 40589 reliable SNPs were identified using the online SNP detection tool HaploSNPer (Singhal *et al.,* 2011), of which 3047 were In-Dels. Through short-read sequencing of eight diverse sorghum accessions, followed by their alignment with the reference genome, a total of 283000 SNPs were identified by Nelson *et al.* (2011). By employing genotyping-by-sequencing (GbS) for 971 accessions comprising the US Sorghum Association Panel, the mini core collection and the reference set of Generation Challenge Program, ~265000 SNPs were identified by Morris *et al.* (2013). Re-sequencing and alignment of two sweet (Keller and E-Tian) and one grain (Ji2731) sorghum inbred lines resulted in the identification of 1057018 SNPs and 99948 InDels of 1–10 bp in length (Zheng *et al.,* 2011). Similarly, Mace *et al.* (2013) identified 4946038 genome-wide SNPs after re-sequencing of the 44 sorghum genotypes representing all major races of cultivated *S. bicolor* in addition to its progenitors and *S. propinquum*. In addition, about 1982971 InDels were identified by the length ranging from 1 to 66 bp. Comparison of the genome sequences of two sorghum genotypes, Tx7000 and BTx642 with the reference genome of BTx623 led to the identification of 1.2 million SNPs and 120969 InDels distinguishing Tx7000 from BTx623, and 1.6 million SNPs and 152836 InDels distinguishing BTx642 from BTx623 (Evans *et al.,* 2013). By exploiting the polymorphic nature of introns, Yang *et al.* (2007) developed potential intron polymorphism (PIP) markers by targeting SNPs and InDels in the introns. A PIP database comprising of 57658 PIP markers representing 59 plant species was developed by them, of which 4314 markers are of sorghum. Using this PIP database, intron length polymorphism (ILP) markers were developed in sorghum through genome-wide analysis and a set of 200 markers were validated in 24 diverse sorghum genotypes. Among these markers, 172

Table 13.1 SSR markers and SNPs developed in sorghum.

Target sequence	No. of markers developed	Reference
SSR markers		
Genomic	206	Bhattramakki *et al.* (2000)
	38	Kong *et al.* (2000)
	15	Taramino *et al.* (1997)
	149	Brown *et al.* (1996)
cDNA-derived	74	Schloss *et al.* (2002)
Genomic sequence contigs	1758	Li *et al.* (2009)
Whole genome	5599	Yonemaru *et al.* (2009)
EST-derived	600	Ramu *et al.* (2009)
	520	Arun (2006)
	50	Srinivas *et al.* (2008)
	116	Srinivas *et al.* (2009a)
Unigene-derived	50	Srinivas *et al.* (2009b)
	1519	Nagaraja Reddy *et al.* (2012)
$(GATA)_n$ motif-based	110	Jaikishan *et al.* (2013)
Other	30	Mutegi *et al.* (2011); Billot *et al.* (2012)
SNPs		
EST	12421	Girma (2009)
	40589 reliable	Singhal *et al.* (2011)
Re-sequencing data	1057018	Zheng *et al.* (2011)
	4946038	Mace *et al.* (2013)
Eight genome equivalents to reference genome	283000	Nelson *et al.* (2011)
GbS data of 971 diverse sorghum accessions	265487	Morris *et al.* (2013)

SSR – simple sequence repeats; ESTs – expressed sequence tags; SNPs – single nucleotide polymorphisms; GbS – Genotyping-by-Sequencing.

gave sharp and robust amplicons and 48 of them were polymorphic (Jaikishan *et al.,* 2014). SSR markers and SNPs developed in sorghum till date is presented in Table 13.1.

13.2.3 Genetic Maps

Construction of linkage map is the first step on which further genetic analysis of a trait can be built upon, and DNA markers are extensively used for this purpose. The first linkage map was constructed using 36 RFLPs with a total length of 283 cM representing eight of the 10 linkage groups in sorghum (Hulbert *et al.,* 1990). Even though more RFLPs were added later resulting in increased map length and marker density (Binelli *et al.,* 1992; Berhan *et al.,* 1993; Chittenden *et al.,* 1994; Ragab *et al.,* 1994; Lin *et al.,* 1995; Dufour *et al.,* 1997; Tao *et al.,* 1998), they were not good enough in representing the complete genome. Complete sorghum linkage maps with increased map density and length was developed by Pereira *et al.* (1994) and Chittenden *et al.* (1994) using RFLP probes of maize and sorghum. Another linkage map comprising of 15 linkage groups

was constructed with the help of 38 sorghum and 33 maize genomic DNA probes spanning a map length of 633 cM (Ragab *et al.,* 1994). Five major RFLP-based linkage maps comprising of 1036 markers (Boivin *et al.,* 1999; Chittenden *et al.,* 1994; Pereira *et al.,* 1994; Ragab *et al.,* 1994; Xu *et al.,* 1994) were aligned and integrated with 10 linkage groups by Subudhi and Nguyen (2000), thereby helping in the assessment of accuracy of available maps and also the linkage of QTL markers in a particular genomic region.

The prominence of PCR-based markers such as RAPDs, AFLPs and SSRs during the 1990s had led to the development of linkage maps in sorghum with more number of markers. RAPDs were used to construct linkage maps initially (Tuinstra *et al.,* 1996; Agrama *et al.,* 2002; Knoll *et al.,* 2008), but, not preferred much due to its inherent problem of reproducibility across laboratories. Subsequently, AFLP markers were successfully used by various research groups for the saturation of linkage maps (McIntyre *et al.,* 2005; Murray *et al.,* 2008; Ritter *et al.,* 2008; Ramu *et al.,* 2009; Shiringani and Friedt, 2011). A limited number of SSR markers were initially used to map on the already available linkage maps (Taramino *et al.,* 1997; Tao *et al.,* 1998; 2000). Subsequently, 31 and 113 new SSR markers were added on the RFLP-based linkage map of Peng *et al.* (1999) by Kong *et al.* (2000) and Bhattramakki *et al.* (2000), respectively. A high-density framework linkage map was constructed using 323 RFLPs and 143 SSR (Bhattramakki *et al.,* 2000), which was further saturated by Menz *et al.* (2002) with 2926 markers (2454 AFLPs, 136 SSRs and 336 RFLPs from rice, barley, oat and maize cDNA and genomic clones) with an average marker distance of 0.5 cM. Another high-density map with a reduced distance between markers (0.4 cM) was developed by Bowers *et al.* (2003) using 2512 RFLP loci.

Even though many linkage maps were exclusively constructed using SSR markers, the SSR marker development is time-consuming, skill oriented and expensive. However, the growing number of cDNA/EST/unigene sequences in the public domain has made the job of SSR marker development easy, simple and rapid through the use of computational tools. Linkage maps based on EST-SSR (Ramu *et al.,* 2009; Srinivas *et al.,* 2009b) and unigene-based SSR (Srinivas *et al.,* 2009a; Nagaraja Reddy *et al.,* 2012) were developed, which have enormous potential in comparative genome mapping. Linkage mapping through high-throughput markers like DArT and SNPs are gaining importance due to the rapid advancements in marker discovery. DArT and non-DArT markers distributed across 10 chromosomes were used for the construction of linkage maps (Mace *et al.,* 2008; 2009). A linkage map of ultra-high density was constructed based on high-quality SNPs comprising of 3418 bin markers identified through re-sequencing of 244 RILs of the cross 654 × LTR108 (Zou *et al.,* 2012). The genetic maps constructed in sorghum during the last 10 years by various research groups are given in Table 13.2.

13.2.4 QTL Mapping

13.2.4.1 Phenology

Even though QTL mapping for maturity has led to the identification of six major effect genes (*Ma_1*, *Ma_2*, *Ma_3*, *Ma_4*, *Ma_5* and *Ma_6*) that govern the flowering time/maturity in sorghum (Quinby, 1967; Rooney and Aydin, 1999), only four genes (*Ma_1*, *Ma_3*, *Ma_4* and *Ma_5*) were mapped – *Ma_1* on LG 6 (Lin *et al.,* 1995; Klein *et al.,* 2008), *Ma_3* on LG 1 (Childs *et al.,* 1997), *Ma_4* on LG 10 (Hart *et al.,* 2001) and *Ma_5* on LG 2 (Kim, 2003). Several QTL/genomic regions associated with plant height have been reported (Lin *et al.,* 1995; Pereira and Lee, 1995; Rami *et al.,* 1998; Hart *et al.,* 2001; Klein *et al.,* 2001; Feltus *et al.,* 2006; Srinivas *et al.,* 2009a). Plant height in sorghum is governed by four

Table 13.2 Genetic linkage maps of sorghum constructed during the last 10 years.

Mapping population	Markers mapped	Reference
120 F_2 of 31945-2-2 × *S. arundinaceus*	169 RFLP, 30 RGA, 28 SSR, 86 AFLP	McIntyre *et al.* (2005)
218 F_2 of Malisor 84-7 × S34	92 RFLP, SSR	Deu *et al.* (2005)
119 RILs of BTx 623 × IS 3620C	336 RFLP, 136 SSR, 2454 AFLP	Brown *et al.* (2006)
207 F_{2-3} of Early Folger × N 32B	31 RFLP, 254 AFLP, 42 SSR	Bian *et al.* (2006)
137 RILs of BTx 623 × IS 3620C	177 RFLP and SSR	Feltus *et al.* (2006)
370 F_2 of BTx 623 × *S. propinquum*	96 RFLP, 36 SSR	
277 F_2 of Westland A × PI 550610	188 SSR	Wu *et al.* (2007)
153 RILs of Shan Qui Red × SRN 39	17 RFLP, 56 SSR, 67 RAPD	Knoll *et al.* (2008)
184 RILs of R 9188 × R 9403463-2-1	42 sorghum SSR, 10 sugarcane SSR, 247 AFLP	Ritter *et al.* (2008)
146 RILs of R 931945-2-2 × IS 8525	358 DArT, 47 SSR, 188AFLP	Mace *et al.* (2008)
176 F_{4-5} of Rio × BTx 623	191 AFLP, 68 SSR	Murray *et al.* (2008)
146 RILs of R 931945-2-2 × IS 8525	148 DArT, 36 SSR, 117 AFLP	Parh *et al.* (2008)
312 RILs of KS 115 × Macia	85 SSR, 27 InDel	Fernandez *et al.* (2008)
150 F_2 of B2 V4 × 1383-2	122 MSAP, 22 SSR	Duan *et al.* (2009)
168 RILs of 296B × IS 18551	100 SSR, 28 EST-SSR	Srinivas *et al.* (2009a)
168 RILs of 296B × IS 18551	100 SSR, 38 EST-SSR, 10 Unigene SSR	Srinivas *et al.* (2009b)
168 RILs of 296B × IS 18551	107 SSR, 38 EST-SSR, 10 Unigene SSR	Satish *et al.* (2009)
94 RILs of N 13 × E 36-1	14 RFLP, 125 AFLP, 45 genomic SSR, 55 EST-SSR, 3 RAPD	Ramu *et al.* (2009)
137 RILs of BTx 623 × IS 3620C	303 DArT, 259 RFLP, 226 SSR	Mace *et al.* (2009)
119 RILs of R 890592 × ICSV 745	234 DArT, 10 SSR, 244 RFLP	
146 RILs of R 931945-2-2 × IS 8525	357 DArT, 47SSR, 188 AFLP	
88 RILs of B 923296 × SC 170-6-8	170 DArT, 13 SSR	
94 RILs of BTx 642 × QL 12	117 DArT	
183 RILs of SAR 10 × SSM 249	627 DArT, 131 SSR, 47 RFLP	
Consensus map of above six populations	1190 DArT, 839 Non-DArT markers	
188 RILs of M 71 × SS 79	102 AFLP, 49 SSR, 6 EST-SSR	Shiringani *et al.* (2010)
141 RILs of B 923296 × SC 170-6-8	377 DArT	Mace *et al.* (2011)
90 RILs of BR 007 × SC 283	255 DArT, 83 SSR, 5 STS, 1 RFLP	Sabadin *et al.* (2012)

(*Continued*)

Table 13.2 (Continued)

Mapping population	Markers mapped	Reference
188 RILs of SS 79 × M7 1	102 AFLP, 49 SSR, 6 EST-SSR	Shiringani and Friedt (2011)
186 F_2 of Shihong 137 × L-Tian	118 SSR	Guan *et al.* (2011)
210 RILs of 27B × IS 2122	127 SSR, 21 genic-SSR	Aruna *et al.* (2011)
245 RILs of M 35-1 × B 35	228 SSR	Nagaraja Reddy *et al.* (2012, 2014)
244 RILs of 654 × LTR 108	3418 bin markers, SNP	Zou *et al.* (2012)
136 RILs of MS 138B × 74LH 3213	247 SSR	Takai *et al.* (2012)
161 RILs of BTx 623 × *S. propinquum*	141 SSR	Kong *et al.* (2013)
214 BC_1F_1 derived RILs of R931945-2-2 × *S. bicolor* subsp. *verticilliflorum*	467 DArT	Alam *et al.* (2014)
146 RILs of IS 8525/R 931945-2-2	357 DArT, 51 SSR	
141 RILs of B 923296/SC 170-6-8	337, major DArT	
214 BC_1F_4 of R 931945-2-2*2 × *S. bicolor* subsp. *verticilliflorum*	467, major DArT	

RFLP – restriction fragment length polymorphism; RAPD – random amplified polymorphic DNA; AFLP – amplified fragment length polymorphism; SSR – simple sequence repeats; EST-SSR – expressed sequence tags-derived simple sequence repeats; MSAP – methylation-sensitive amplified polymorphism; DArT – diversity Array Technology; RGA – resistance gene analogue.

major effect QTL (*Dw_1*, *Dw_2*, *Dw_3* and *Dw_4*) across different diverse backgrounds. The map position of *Dw_1* located on SBI-09 harbouring a major height gene SbHt9.1 (Pereira and Lee, 1995; Brown *et al.,* 2008) and the map positions of two of the most consistent QTL, *Dw_2* on SBI-06 and *Dw_3* on SBI-07 (Brown *et al.,* 2006; Feltus *et al.,* 2006; Klein *et al.,* 2008; Mace and Jordan, 2011) were reported by Mace and Jordan (2010). However, *Dw_4* is not mapped till date.

13.2.4.2 Grain Yield and Its Components

Over the last decade, few studies in sorghum have identified QTL for grain yield and its component traits (Hart *et al.,* 2001; Brown *et al.,* 2006; Ritter *et al.,* 2008; Srinivas *et al.,* 2009a; Nagaraja Reddy *et al.,* 2013). A total of eight QTL under different genetic backgrounds were identified on LG 2, 3, 6, 9 and 10, six of those are major effect QTL contributing >10% of phenotypic variance and three QTL on LG 10 are meta-QTL (Srinivas *et al.,* 2009a). Five major QTL associated with primary and secondary seed branches has been reported (Brown *et al.,* 2006; Pereira and Lee, 1995; Srinivas *et al.,* 2009a), followed by four meta-QTL for panicle seed branch length (Mace and Jordan, 2011). A set of seven and 13 major QTL for panicle width (Hart *et al.,* 2001) and panicle length (Srinivas *et al.,* 2009a) have been reported. Twenty-eight QTL were identified for seed weight, of which nine were meta-QTL, contributing 4.8–35% to the phenotypic variance of the trait (Rami *et al.,* 1998). One more major QTL contributing 14.8% to the phenotypic variation was linked to the SSR marker Xcup24 on SBI-01 (Tuinstra *et al.,* 1998; Srinivas *et al.,* 2009a).

13.2.4.3 Insect Resistance

The shoot fly – *Atherigona soccata* (Rondani) – is a major pest in sorghum, and the larva damages the central meristematic tissue in the seedlings up to 4 weeks after emergence, resulting in withering of the central shoot known as deadheart (Deeming, 1972). The component traits of resistance are complex and polygenically inherited (Halalli *et al.,* 1983) with predominantly additive effects. Among the three important components of resistance, viz., non-preference for oviposition, antibiosis and tolerance (Soto, 1974), the field resistance is primarily due to non-preference for oviposition followed by other component traits such as glossy leaves, leaf trichomes, seedling vigour, epicuticular wax and other biochemical factors. A total of 29 QTL for the component traits such as leaf glossiness, seedling vigour, oviposition, deadheart, adaxial and abaxial trichome density were identified by Satish *et al.* (2009) using a RIL population of the cross, 296B × IS18551. Interestingly, QTL for oviposition, deadhearts and trichome density are co-located on SBI-10. Some of the important QTL were validated in an alternate mapping population comprising of a RIL of the cross 27B × IS2122 (Aruna *et al.,* 2011).

Sorghum midge – *Stenodiplosis sorghicola* (Coquillett) – is widely distributed in Asia and other sorghum-growing countries. The most common resistance mechanism is ovipositional antixenosis (Henzell *et al.,* 1994) while antibiosis is also reported (Sharma, 1985). By employing a RIL population of the cross ICSV745 × 90562, Tao *et al.* (2003) identified two QTL (on SBI-03 and SBI-09) associated with antixenosis and one genomic region on SBI-07 associated with antibiosis. The QTL associated with antixenosis explained 12 and 15% of the total phenotypic variance for egg numbers/spikelet and that associated with antibiosis explained 34.5% of the total phenotypic variance for the difference of egg and pupal counts.

Green bug – *Schizaphis graminum* (Rondani) – causes considerable damage that is characterised by a dark red spot at the feeding site, surrounded by pale yellow discolouration. They are also vectors of viral pathogens (Harvey *et al.,* 1996) and a number of biotypes (C, E, I and K) have been identified. QTL mapping identified three loci on SBI-05, SBI-06 and SBI-07 conferring resistance to biotype I (Katsar *et al.,* 2002) and nine QTL associated with resistance and tolerance to the biotypes I and K (Agrama *et al.,* 2002). Three more QTL on SBI-01 and SBI-04 associated with biotype I–specific resistance were detected by Nagaraj *et al.* (2005) using chlorophyll loss as an indicator. Later, a major QTL conferring resistance against biotype I on SBI-09 was reported by Wu and Huang (2008). It is amply clear that resistance to green bug is associated with multiple genomic regions, some conferring biotype-specific resistance while other conferring biotype non-specific resistance.

13.2.4.4 Disease Resistance

Grain mould is a major disease in sorghum, especially in rainy season crop, caused by a complex of fungi, predominantly by *Fusarium moniliforme* and *Curvularia lunata*. The damage is characterised by a reduction in yield and seed quality due to the blackening of moulded grain caused by fungal growth, which affects the grain yield and quality, thereby fetching a lower price (Williams and Rao, 1981; Rooney and Serna-Saldivar, 1991). Resistance to grain mould is believed to be complex, governed by major and minor genes with additive and epistatic effects along with significant G × E interactions (Stenhouse *et al.,* 1998; Rodriguez-Herrera *et al.,* 2000). Five QTL for grain mould resistance were reported by Klein *et al.* (2001) with a phenotypic variance between 10 and 23% and their detection was dependent on environment. Two SNP loci linked to

grain mould resistance were identified by Upadhyaya *et al.* (2013a), of which one contained a nucleotide binding ARC and leucine rich repeat containing (NB-ARC-LRR) class of R-gene (Sb02g004900) exhibiting 57% similarity to *Rxo1*, a non-host-resistance gene of maize. However, the map positions did not match with the QTL reported earlier (Klein *et al.,* 2001), indicating the possibility of differential expression of resistance due to differences in the pathogen over diverse environments (Audilakshmi *et al.,* 2005; Little *et al.,* 2012).

Forage sorghum is quite susceptible to foliar diseases such as anthracnose, zonate leaf spot, target leaf spot, *Drechslera* leaf blight and rust, which affect the fodder quality by reducing the protein, zinc and *in vitro* dry matter digestibility (Rana *et al.,* 1999). A duplicate epistasis for resistance to zonate leaf spot (Grewal, 1988), a single dominant gene for anthracnose resistance, a single recessive gene for the resistance to leaf midrib anthracnose (Erpelding and Wang, 2007) and a polygenic control of resistance for these diseases were reported (Murali Mohan *et al.,* 2009). A major and consistent QTL for foliar disease resistance was identified on SBI-06 between the marker interval, Xtxp95-Xtxp57 with the contribution to phenotypic variance ranging between 32% (bacterial leaf blight, zonate leaf spot) and 55% (anthracnose) (Klein *et al.,* 2001). QTL linked to oval leaf spot resistance was also co-located in this region, which harbours QTL associated with resistance to several foliar diseases (Murali Mohan *et al.,* 2010). Eight SNP loci associated with anthracnose resistance across environments were identified by Upadhyaya *et al.* (2013b), two of which were co-located with the two major QTL (*QAnt3* and *QAnt2*) reported by Murali Mohan *et al.* (2010).

Rust is an important disease in sorghum caused by *Puccinia purpurea* Cooke since it reduces the quality and palatability of green fodder and also acts as a predisposing factor in other major diseases (Frederiksen and Rosenow, 1986). The genetics of rust resistance is considered as complex (Miller and Cruzado, 1969; Patil-Kulkarni *et al.,* 1972; Rana *et al.,* 1976) and was reported to be quantitative with the involvement of at least four loci (Tao *et al.,* 1998). Four major QTL were identified on SBI-01, SBI-02, SBI-03 and SBI-08 contributing 16–42% to the trait variation (Tao *et al.,* 1998). One more major QTL on SBI-08, assumed to be the *Pu* gene by Coleman and Dean (1961) and Miller and Cruzado (1969), was found to host a key rust R-gene homologue of *Rp1-D* from maize and sugarcane (McIntyre *et al.,* 2005). In a relatively recent study, Upadhyaya *et al.* (2013a) identified five SNP loci associated with rust resistance, two of them possessed resistance gene that are homologous to the rust resistance gene in maize (*Rp1-D*) and wheat (*Lr1*).

Charcoal rot, caused by the fungus *Macrophomina phaseolina*, occurs under moisture stress during post-flowering stage (Seetharama *et al.,* 1987), causing root and stalk rots leading to severe crop lodging and loss in grain yield and quality and quantity of stover. Genetics of charcoal rot resistance is complex, and both additive and non-additive gene actions have been reported (Indira *et al.,* 1983; Garud and Borikar, 1985; Rao *et al.,* 1993). Not much headway has been made in the detection and mapping of QTL associated with charcoal rot resistance. Nine consistent QTL have been identified for three morphological traits, viz., number of internodes crossed by the rot, length of infection and lodging (%) and biochemical traits (lignin and total phenols) that are associated with charcoal rot resistance (Reddy *et al.,* 2008; Patil *et al.,* 2012).

Ergot, also known as sugary disease is caused by *Claviceps africana*, which infects unfertilised ovaries of panicle during anthesis preventing fertilisation and seed set. A total of 18 QTL were identified for three component traits of ergot resistance (percentage

ergot infection, pollen quantity and pollen viability) (Parh *et al.,* 2008). Four major QTL were identified on SBI-01, SBI-06, SBI-08 and SBI-09 that are associated with percent ergot infection along with one major QTL each associated with pollen quantity (SBI-06) and pollen viability (SBI-07). Moreover, the major QTL on SBI-06 for percent ergot infection was co-located with those of grain mould, anthracnose, zonate leaf spot, and bacterial leaf spot resistance identified by Klein *et al.* (2001) and Murali Mohan *et al.* (2010). Similarly, three other regions that possess QTL for grain mould and rust resistance (SBI-07, SBI-10 and SBI-08) (Tao *et al.,* 1998; Klein *et al.,* 2001) also housed a QTL associated with ergot resistance (Parh *et al.,* 2008).

13.2.4.5 Resistance to Weed

Striga is a serious parasitic weed widely found in the sorghum fields in Africa and parts of Asia. *Striga* resistance is governed by a single recessive gene (*lgs*) associated with low *Striga* germination stimulant activity. Following a high-density mapping with 367 markers (DArT and SSRs) and an *in vitro* assay for estimating germination-stimulant activity towards *Striga asiatica* using 354 RIL population of the cross Shanqui Red (high stimulant) × SRN39 (low stimulant), the *lgs* gene was precisely tagged and mapped on SBI-05 between the SSR marker interval, SB3344 and SB3352 (Satish *et al.,* 2012).

13.2.4.6 Drought Tolerance

Drought tolerance is a complex and quantitatively inherited trait that is manifested by the involvement of morphological traits as well as physiological mechanisms. Among the physiological mechanisms, the mechanism of maintenance of photosynthesis through the persistent green leaf area during the grain filling, commonly referred as stay-green, play an important role in drought response. Even though many QTL were associated with stay-green trait across different genetic backgrounds, four major and consistent QTL (*Stg1* and *Stg2* on SBI-03; *Stg3* on SBI-02 and *Stg4* on SBI-05) were identified based on the comparisons of QTL reported by different research groups (Tuinstra *et al.,* 1997; Xu *et al.,* 2000; Subudhi *et al.,* 2000; Tao *et al.,* 2000). The probable contribution of roots in this trait due to the co-localisation of QTL for stay-green and root angle (Mace *et al.,* 2012) and the potential of stay-green QTL in improving transpiration efficiency and water extraction capacity (Vadez *et al.,* 2011), grain yield particularly under low-yield environments (Jordan *et al.,* 2012) and canopy development, leaf anatomy, root growth, water uptake and grain yield (Borrell, Mullet *et al.,* 2014; Borrell, Oosterom *et al.,* 2014) were reported. Recently, Nagaraja Reddy *et al.* (2014) suggested *Stg2, Stg3* and *StgB* as the key QTL suitable for the genetic improvement of terminal drought tolerance through MAS.

13.2.4.7 Cold Tolerance

Being a tropical crop, sorghum is affected by cool temperatures (≤15 °C), especially during the early growth stages leading to the production of more leaves (Hesketh *et al.,* 1969; Quinby, 1973), delayed floral initiation (Caddel and Weibel, 1971; Quinby, 1973) and male sterile panicles (Downes and Marshall, 1971; Singh, 1977). Even though the 'kaoliang' sorghum from China exhibits higher seedling emergence and vigour under cooler conditions (Qingshan and Dahlberg, 2001; Cisse and Ejeta, 2003), they also possess poor or undesirable agronomic traits (Knoll and Ejeta, 2008). Two QTL for germination – one on SBI-03 under both cold and optimal temperatures and the other on SBI-07 were identified, only under cold temperature. A major QTL exhibiting strong

associations with seedling emergence and vigour under early and late planting on SBI-01 and one minor QTL on SBI-02 for both early and late seedling emergence were identified (Knoll *et al.,* 2008). A total of 14 QTL were identified for important component traits of cold tolerance (germination at low and optimum temperature, field emergence and seedling vigour) using the new cold tolerance source, PI610727 (Burow *et al.,* 2011). The important major effect genes and QTL mapped in sorghum by various research groups are given in Table 13.3.

Table 13.3 Important major effect genes and QTL mapped in sorghum.

Character	QTL/marker	LG	R^2	Reference
Phenology				
Plant height	*Dw_1*	9	20	Pereira and Lee (1995)
	Dw_2	6	27	Ritter *et al.* (2008)
	Dw_3	7	29	Pereira and Lee (1995)
Maturity	*FlrAvgD1*	6	86	Lin *et al.* (1995)
	QDma-sbi01-2	1	15	Srinivas *et al.* (2009a)
	FlrF	6	36	Kebede *et al.* (2001)
Grain yield and components				
Grain yield	*AAG/CAA1*	2	18	Ritter *et al.* (2008)
	QGyl-sbi06	6	15	Srinivas *et al.* (2009a)
Kernal weight	*isu156/isu034*	10	16	Pereira *et al.* (1995)
	KW	1	19	Rami *et al.* (1998)
	QGwt.txs-G	10	14	Feltus *et al.* (2006)
Test weight	*100 seed weight*	4	16	Brown *et al.* (2006)
	TK	7	35	Rami *et al.* (1998)
	QWwt.txs.G	4	16	Feltus *et al.* (2006)
	QSwe-sbi01	1	15	Srinivas *et al.* (2009a)
Shoot fly resistance				
Glossiness	*QGs.dsr-5*	5	14	Satish *et al.* (2009)
Dead hearts	*QDh.dsr-10.3*	10	15	
Trichome density	*QTdu.dsr-10.2*	10	33	
	QTdl.dsr-10.2	10	23	
Midge resistance	*Antibiosis*	7	34	Tao *et al.* (2003)
	Antixenosis	9	15	
Green bug resistance				
Biotype I	*VIS_GBI8*	3	20	Nagaraj *et al.* (2005)
Biotype K	*SPA_K2*	5	16	
Biotype K	*Ssg6*	10	15	Katsar *et al.* (2002)
Anthracnose resistance	*QAnt*	6	40	Murali Mohan *et al.* (2010)
Zonate leaf spot resistance	*QZls*	6	17	
Target leaf spot resistance	*QTl*	6	45	Murali Mohan *et al.* (2010)

Table 13.3 (Continued)

Character	QTL/marker	LG	R^2	Reference
Rust resistance				
	BNL5.09	2	25	Tao *et al.* (1998)
	RZ323-ISU102	4	24	
	PSB47-TXS422	10	43	
	QRust	6	24	Murali Mohan *et al.* (2010)
Ergot resistance				
Infection %	*Sb4-32*	9	20	Parh *et al.* (2008)
Pollen viability	*AAGCCT6*	6	20	Parh *et al.* (2008)
Charcoal rot resistance				
Internodes crossed	*Xtxp297*	2	19	Reddy *et al.* (2008)
Lodging %	*Xtxp343*	4	15	Reddy *et al.* (2008)
***Striga* resistance**	*lgs*	5	NA	Satish *et al.* (2012)
Drought tolerance				
Stay-green	*Stg1*	3	20	Xu *et al.* (2000)
	Stg2	3	30	
	Stg3	2	16	
Cold tolerance				
Late emergence %	*PeriCol-OPK18*	1	21	Knoll *et al.* (2008)
Early vigour	*PeriCol-OPK18*	1	20	Knoll *et al.* (2008)
Late vigour	*PeriCol-OPK18*	1	28	Knoll *et al.* (2008)
Optimal germination	*UBC171-SbAGE01*	3	15	Knoll *et al.* (2008)
% Germination@12 °C	*Germ12-2.1*	2	20	Burow *et al.* (2011)
Field emergence	*Fearlygerm-9.2*	9	16	Burow *et al.* (2011)

QTL – quantitative trait loci; LG – linkage group; R^2 – % contribution to phenotypic variance.

13.2.5 Marker-Assisted Selection (MAS)

Availability of DNA markers, mapping populations for the traits of interest and refinements in phenotyping and statistical analysis has led to the identification and mapping of QTL associated with the important agronomic as well as biotic and abiotic stress tolerance along with the tightly linked DNA markers that can be employed in MAS. Selection of consistent major or an effective combination of minor QTL and tightly linked markers are important pre-requisites for the improvement of elite cultivars/parental lines of hybrids for the traits of interest through DNA marker–assisted molecular breeding. In sorghum, extensive QTL mapping studies have been done for drought tolerance (stay-green) and *Striga* resistance and tightly linked markers for the QTL of these traits are available for use with MAS.

Stay-green is a well-characterised trait associated with post-flowering drought tolerance and an initial evaluation of introgression lines (BC_3F_3/BC_1F_4) in the genetic background of R 16 possessing four stable QTL (*StgB, Stg1, Stg3* and *Stg4*) revealed higher chlorophyll levels in leaves at flowering and increases leaf area (%) during the later part of grain filling even though none of them exhibited stay-green on a par with B

35 (Kassahun *et al.,* 2010). An attempt to transfer three stay-green QTL on SBI-01, SBI-07 and SBI-10 from another donor line E36-1 to Ochuti, a farmer-favoured cultivar in Kenya through marker-assisted QTL introgression resulted in the transfer of a maximum of the latter two QTL with about 25% of the of the BC_1F_1 progenies possessed at least one QTL, depending on the number of plants screened (Ngugi *et al.,* 2013).

QTL associated with *Striga* resistance have been introgressed into the varieties preferred by the farmers in sub-Saharan Africa using a resistant variety N13 as a donor. A single QTL for *Striga* resistance to the farmer-preferred variety, Ochuti in Kenya (Osama, 2013), and five QTL from the same donor to farmer-preferred cultivars from Eritrea, Kenya, Mali and Sudan (Muth *et al.,* 2012) and another elite farmer preferred cultivar, Tabat (Gamar and Mohamed, 2013), were introgressed resulting in the identification of backcross derivatives exhibiting high levels of *Striga* resistance along with superior agronomic performance. Four agronomically superior and high-yielding *Striga*-resistant lines in the genetic background of the three farmer-preferred cultivars of sub-Saharan Africa, Tabat, AG-8 and Wad Ahmed developed by introgressing two or more major QTL (of the five QTL identified by Haussmann *et al.,* 2004) are the first products of MAS in sorghum released for cultivation (Mohamed *et al.,* 2014). Similarly, very recently, five QTL (QTL01, QTL02, QTL06, $QTL05_1$ and $QTL05_2$) associated with *Striga* resistance was transferred to the farmer-preferred variety Hugurtay and the introgression lines exhibited *Striga* resistance, which was a little less and yielding twofold as compared to N 13 (Yohannes *et al.,* 2015). Riding on the success of these MAS-based products in sorghum, there is immense potential for the introgression of effective QTL identified for grain yield and its components (Ritter *et al.,* 2008; Srinivas *et al.,* 2009a; Nagaraja Reddy *et al.,* 2013), shoot fly resistance (Satish *et al.,* 2009), resistance to foliar diseases (Murali Mohan *et al.,* 2010) and cold tolerance (Knoll *et al.,* 2008; Burow *et al.,* 2011).

13.3 Pearl Millet

13.3.1 Genetic Diversity

Genetic diversity is an important measure for the identification of diverse genotypes for further used in crop improvement programs. Characterisation of large number germplasm collections will also help in the better management of genetic resources of a crop species by the elimination of the duplicate accessions. Genetic diversity will also help in heterosis breeding as it can be hypothesised that for effective exploitation of heterosis. Even though phenotypic as well as isozyme/protein data were used earlier for assessing the genetic diversity in pearl millet, DNA-based markers were employed later resulting in a rapid and efficient assessment of genetic diversity among the parental lines. Different markers such as RFLPs (Gepts and Clegg, 1989; Bhattacharjee *et al.,* 2002), RAPDs (Chowdari, Davierwala*et al.,* 1998; Chowdari, Venkatachalam *et al.,* 1998; Govindaraj *et al.,* 2009), ISSRs (Kumar *et al.,* 2006; Yadav *et al.,* 2007), AFLPs (Busso *et al.,* 2000) and SSRs (Mariac *et al.,* 2006; Singh *et al.,* 2013) have been effectively used for determining the genetic diversity in pearl millet. The molecular markers can be used for germplasm classification, cultivar identification, selection of parental lines for hybridisation and to develop core and mini-core sets accommodating the total diversity.

Polymorphisms in the nuclear rDNA were revealed by Gepts and Clegg (1989) through RFLP analysis, mostly among wild pearl millet accessions, the majority of

which mapped to the non-transcribed spacer region. Molecular characterisation with SSR and RAPD revealed a greater extent of genetic diversity among the cultivars and landraces (Chowdari, Davierwala *et al.,* 1998) and genetic-distance based on $(GATA)_4$ microsatellite and RAPDs may be useful for the grouping of parents, but not for predicting heterotic combinations (Chowdari, Venkatachalam *et al.,* 1998). Similarly, RAPDs in combination with SSR indicated that the male-sterile lines 5054A, 5141A and 841A and the parental lines of popular hybrids such as 841A, PPMI 69, PPMI 301 D 23 were genetically diverse (Chandra-Shekara *et al.,* 2007). Assessment of genetic diversity using ISSR markers highlighted the presence of high levels of diversity among the genotypes comprising of three CMS lines, four restorers and five hybrids (Kumar *et al.,* 2006). The variability within and between landrace samples analysed using AFLP revealed the presence of their own group of ideotypes each in their own unique genetic backgrounds (Busso *et al.,* 2000).

Coefficients of genetic distance determined based on SSR marker polymorphism among germplasm lines were high (0.28–0.92), and the genotypes with potential traits are different from the cultivated gene pool (Budak *et al.,* 2003). A significantly lower number of alleles and lower gene diversity were observed by Mariac *et al.* (2006) in cultivated pearl millet accessions than wild accessions. An analysis using SSR markers by Sumanth *et al.* (2013) suggested that the diverse maintainer line ICMB 88004 can be used for the development of new male sterile line while the diverse restorer lines, viz., PT 6243, PT 6066, PT 6064, PT 6033 and PT 6029 can be used as potential pollinators for hybrid development. Recently, in a study by Manivannan *et al.* (2013), similarity indices based on peroxidase banding pattern revealed that the hybrids HHB 50, HHB 60, HHB 67 and HHB 146 entirely resembled their female parents MS 81A, MS 843A and ICMA 95222A. A high correlation ($r > 0.97$, $P < 0.05$) observed between molecular marker diversity and the genetic relationships among inbred lines might be helpful for formulating appropriate breeding strategies to achieve genetic enhancement in pearl millet (Thudi *et al.,* 2010).

13.3.1.1 Core and Reference Collections

A total of 22658 germplasm accessions of pearl millet is maintained by ICRISAT, which was collected from 50 countries across the globe (Upadhyaya, 2015). A core collection comprising of 2094 accessions (Upadhyaya *et al.,* 2009) selected from 20844 accessions for 22 traits (10% of the entire collection in genebank) and a mini core collection (Upadhyaya, Yadav *et al.,* 2011) comprising of 238 accessions (1.14% of the entire collection) are available at ICRISAT. In collaboration with GCP, ICRISAT has developed global composite collections (1021 accessions) in pearl millet, which were later genotyped using SSR markers to develop genotype-based reference set comprising of 300 accessions (Generation Challenge Program Project Abstracts, 2008). These collections have been found useful in selecting accessions with agronomic and nutritional traits, resistance to biotic and abiotic stresses and bioenergy traits for use in pearl millet improvement programmes. These collections are also useful for assessing genetic diversity, population structure, allelic diversity and also in association mapping.

13.3.2 Molecular Marker Resources

SSR markers are the widely used PCR-based markers for various genetics and mapping studies in pearl millet due to their abundance in the genome, highly polymorphic nature

and easy assay. Research groups have developed a large number of SSR markers conventionally through the development of BAC library and small-insert genomic library. Transcriptome projects have led to an enormous accumulation of ESTs and/or cDNA sequences for pearl millet, which were used as targets for the identification of SSR markers known as EST-SSR markers through the computational approach thereby making the SSR marker development rapid, easy and inexpensive. These markers were subsequently used for various genetic studies in pearl millet.

Twenty-five SSRs were isolated from bacterial artificial clones of pearl millet without any sub-cloning using 3′ anchored SSR primers and isolation of flanking sequences by suppression PCR (Qi *et al.,* 2001). PCR-based screening of a bacterial artificial chromosome (BAC) library constructed using nuclear DNA from pearl millet using five STS, led to the identification of six microsatellite markers (Allouis *et al.,* 2001). Similarly, screening of a small-insert partial genomic library with a $(CT)_{15}$ oligonucleotide probe resulted in the development of 18 SSR markers (Budak *et al.,* 2003), while 44 markers were developed from a $(CA)_n$-enriched small-insert genomic library (Qi *et al.,* 2004). A set of 90 new SSR markers was developed in pearl millet ESTs made available by the International Center for Genetic Engineering and Biotechnology (ICGEB), New Delhi, and University of Hyderabad, Hyderabad, India, resulting in 58 working SSR markers (Senthilvel *et al.,* 2008). SSCP-SNP, a new marker system was developed by predicting the intron–exon borders in pearl millet ESTs using annotated rice genomic sequences and designing primers. PCR amplification of precisely predicted introns in 299 homologues of single-copy rice genes followed by their analysis on SSCP gels revealed considerable polymorphism. SNPs accounted for about two-third of the variation while InDels accounted for one-third of the variation. This demonstrated the use of syntenic information to develop SSCP-SNP markers (Bertin *et al.,* 2005).

13.3.3 Genetic Maps

Linkage map is the basic framework that depicts the arrangement of molecular markers in different linkage groups based on the recombination frequency among the markers, which are essential for the mapping of QTL. The first RFLP linkage map in pearl millet was published by Liu *et al.* (1994). Using an inter-varietal F_2 population, a total of 181 loci was placed on a linkage map of seven linkage groups, with an average map distance of about 2 cM between loci. The linkage analysis was complicated initially since 83 loci were mapped to a single linkage group. However, a probable translocation breakpoint was identified in the middle of this large linkage group after analysis of a second cross. Comparative genetic maps constructed for the pearl millet genome with foxtail millet and rice by Devos *et al.* (2000) revealed greater genome rearrangements, and many of them probably would have taken place in pearl millet. Two duplications were reported in pearl millet: (i) between the distal segments of linkage groups 1 and 4 corresponding to the ancient duplication identified between chromosome arms 11S and 12S in rice and between chromosomes VII and VIII in foxtail millet, and (ii) observed in the same region, where the first duplication was observed in rice indicating its species specificity (Devos *et al.,* 2000).

An integrated consensus linkage map was developed from the genetic maps constructed for four different crosses using 353 RFLP and 65 SSR markers (Qi *et al.,* 2004). The mapping of 21 polymorphic SSR markers using existing mapping populations (ICMB 841-P3 × 863B-P2 and 81B-P8 × IPC 804) revealed that most EST-SSR markers

mapped to distal regions of linkage groups, often to previous gaps (Senthilvel *et al.,* 2008). An improved linkage map was constructed by integrating 258 DArT and 63 SSR marker data using a RIL population from cross H 77/833-2 9 and PRLT 2/89-33 with an average adjacent-marker interval length of 3.7 cM. (Supriya *et al.,* 2011). With an objective of developing a linkage map with more evenly distributed markers and greater marker coverage of the gaps in earlier maps, Pedraza-Garcia *et al.* (2010) constructed a map using 196 PCR-based DNA markers (66 SRAPs, 63 RAPDs, 27 ISSRs, 31 pearl millet, six sorghum and three maize SSRs) of nine linkage groups with an average genetic distance of 9.2 cM between markers. Linkage maps were also constructed by Rajaram *et al.* (2013) using 99 newly developed EST-SSR markers and previously mapped 17 EST-SSR, 53 genomic SSR and two STS markers. A consensus map of 174 loci (899 cM) was developed by integrating the individual linkage maps using MergeMap, which showed a well-conserved locus order for nearly all linkage groups.

13.3.4 QTL Mapping

Identification and deployment of QTL/genomic regions associated with important economically important traits, which are complex in nature, will help in the genetic enhancement of those traits through molecular breeding approaches. Molecular markers have been popularly used to identify genomic regions linked to traits of interest by conventional QTL mapping and association analysis. Linkage analysis using biparental mapping population was used for the identification and mapping of QTL of many complex traits. Many QTL for effective host plant resistance against pathogen isolates of *S. graminicola* have been identified (Jones *et al.,* 1995; Hash and Witcombe, 2001; Jones *et al.,* 2002), and some of these QTL have been introgressed to elite parental lines of popular hybrids through marker-assisted backcrossing.

13.3.4.1 Phenology and Morphological Traits

Phenology and morphological traits play an important role in plant development and domestication. Many morphological differences could be due to a small number of loci with relatively large effects, mainly on LG 2, LG 5, LG 6 and LG 7. QTL with large effects on plant height, number of spikes and weight of the spike were also mapped on LG 6 and LG 7 (Poncet *et al.,* 2000). Two regions of the genome on LG 6 and LG 7 controlled most of the key morphological differences, which is their central role both in the developmental control of spikelet structure and the domestication process (Poncet *et al.,* 2002). Significant associations were observed between polymorphisms of the pearl millet *PHYC* gene and flowering time, spike length and stem diameter (Saidou *et al.,* 2009). The D_1/d_1 plant height locus was mapped to LG 1, while the D_2/d_2 plant height locus and the *P/p* foliage colour locus were mapped to LG 4 (Azhaguvel *et al.,* 2003). The co-segregation of *ABCB1*, which encodes a P-glycoprotein involved in auxin transport with the d_2 phenotype, its differential expression in the tall (ICMP 451) and dwarf (Tift 23DB) inbreds, and the similar phenotype of stacked lower internodes in the sorghum dw_3 and pearl millet d_2 mutants suggested that *ABCB1* is a likely candidate for d_2 (Parvathaneni *et al.,* 2013).

13.3.4.1.1 Yield and Its Components

The genetic improvement of grain and stover yields along with their component traits is rather slow due to their complex inheritance and strong influence of genotype × environment interactions. Major genotype × season QTL were detected for flowering time (LG 4 and

LG 6), and mapped to the same intervals as a genotype × season QTL for several other yield contributing traits. All three QTL for grain yield had no genotype × season interaction, while those for stover yield (LG 2, LG 4 and LG 6) and grain yield (LG 4) were free of QTL × season interactions (Yadav *et al.,* 2003). QTL associated with flowering time were located on LG 6 and that of plant height on LG 4, LG 6 and LG 7. QTL on LG 6 were associated with stover yield, and those on LG 7 were associated with grain yield (Kannan *et al.,* 2014). QTL were identified for grain and stover yields (Yadav *et al.,* 2003; Kannan *et al.,* 2014) as well as yield components such as length of spikes, width of spikes, weight of the spike (Poncet *et al.,* 2000) and total number of spikes/plant (Poncet *et al.,* 2002).

13.3.4.1.2 Disease Resistance

Earlier studies on the genetics of downy mildew resistance revealed that resistance was governed by major dominant genes with non-additive action (Deswal and Govila, 1994; Singh and Talukdar, 1998; Hash *et al.,* 2003). The resistance generally exhibited a continuous variation during segregation (Singh *et al.,* 1980; Basavaraju *et al.,* 1981; Dass *et al.,* 1984), and hence it was considered as a quantitative trait. A number of QTL have been identified on different linkage groups (Hash *et al.,* 1999; Hash and Witcombe, 2001). One major QTL explaining up to 60% of phenotypic variance and a minor QTL contributing up to 16% of phenotypic variance were identified. Two more QTL were also detected (Jones *et al.,* 2002). DNA markers have been reported for 60 different putative downy mildew resistance QTL in pearl millet (Breese *et al.,* 2002; Hash and Witcombe, 2002). Even though many QTL were identified, many of them were specific to different pathotypes, suggesting the mechanism of pathotype-specific resistance.

The rust resistance gene *Rr1* from *P. glaucum* ssp. *monodii* was linked to the RAPD marker OP-G8350 (8.5 cM) on LG 3, those from Tift 89D2 and ICMP 83506 were located on LG 4 and that in ICMP 83506 was linked to the RFLP marker, Xpsm306 (10.0 cM). The resistance exhibited by Tift 89D2 was associated with RAPD markers OP-K19350 (8.8 cM) and OP-O8350 (19.6 cM). Only a single RAPD marker, OP-D11700 (5.6 cM) was associated with *Pyricularia* leaf spot resistance (Morgan *et al.,* 1998).

13.3.4.1.3 Drought Tolerance with Emphasis on Yield

Several QTL were associated with drought tolerance in terms of both grain and stover yields and its components, the important one being a QTL mapped on LG 2 explaining up to 23% of the phenotypic variation (Yadav *et al.,* 2002). Harvest index and panicle harvest index were co-mapped with grain yield, suggesting that increased drought tolerance and yield was achieved by increased partitioning of dry matter from stover to the grains (Yadav *et al.,* 2004). The drought tolerance QTL-based hybrids developed with test cross pollinators bred from mapped F_2-derived F_4 lines from a population H 77/833-2 × PRLT 2/89-33 were significantly, but modestly, higher yielding in a series of both absolute and partial terminal stress environments thereby confirming the effectiveness of this on LG 2 (Bidinger *et al.,* 2005). Eighteen genes and two hypothetical proteins were co-mapped in the drought tolerance-QTL interval (LG 2), and many of them have significant association with QTL for grain yield, flowering time and leaf rolling under drought stress conditions (Sehgal *et al.,* 2012). The important QTL mapping studies in pearl millet and their conclusions are presented in Table 13.4.

Table 13.4 Important major effect genes and QTL mapped in pearl millet.

Trait	QTL/locus	LG	R^2	Reference
Plant height	*hmax6*	6	25.3[a]	Poncet *et al.* (2000)
	hmax7	7	16.1	
	D_1/d_1	1	NA	Azhaguvel *et al.* (2003)
	D_2/d_2	4	NA	
	PH Xpsmp2085_175	4	NA	Kannan *et al.* (2014)
	PH Xpsmp2224_157	7	NA	
Yield and its components				
Grain yield		1	20	Yadav *et al.* (2003)
		1	15	
		2	15	
		3	15	
		4	15	
	GY Xpsmp2224_159	7	NA	Kannan *et al.* (2014)
Stover yield		2	19	Yadav *et al.* (2003)
		4	19	
		6	19	
	SDMY Xpsmp2220_115	5	NA	Kannan *et al.* (2014)
	SDMY Xpsmp2224_157	7	NA	
	SDMY Xpsmp2233_262	5	NA	
	SDMY Xpsmp2248_162	6	NA	
	SDMY Xpsmp2248_166	6	NA	
Length of the spikes	*los1*	1	13.2	Poncet *et al.* (2000)
	los2	2	35.9	
	los7	7	55.7[b]	
Width of the spikes	*wis5*	5	15.4	Poncet *et al.* (2000)
	wis7	7	62.0	
Total number of spikes/plant	*ns2*	2	15.2	Poncet *et al.* (2002)
	ns6	6	37.0	
	ns7	7	12.9	
Weight of the spike	*wes2*	2	60.9	Poncet *et al.* (2000)
	wes5	5	22.5	
	wes6	6	77.1[c]	
Downy mildew resistance		1	60	Jones *et al.* (2002)
		2	16	
Rust resistance	*Rr1*	3	NA	Morgan *et al.* (1998)
	Rust res. (ICMP 83506)	4	NA	

(*Continued*)

Table 13.4 (Continued)

Trait	QTL/locus	LG	R^2	Reference
Drought tolerance index of grain and stover yield determining traits				
Grain yield	*gy3*	5	15.6	Yadav *et al.* (2004)
Panicle number	*pn2*	2	15.3	Yadav *et al.* (2002)
100-grain mass	*hgm2*	2	16.1	
	hgm6	6	11.6	
Panicle grain number	*pgn1*	1	10.3	
Grain yield	*gy1*	1	13.3	
	gy2	2	23.0	
Stover yield	*sy2*	2	13.2	
	sy4	4	10.6	
	sy6	6	18.1	
Biomass yield	*bmy2*	2	16.2	
	bmy6	6	10.7	
Harvest index	*hi2*	2	18.0	

QTL – quantitative trait loci; LG – linkage group; R^2 – % contribution to phenotypic variance; [a]cumulative of *hmax6* and *hmax7*; [b]cumulative of *los1*, los2 and *wes7*; [c]cumulative of *wes2*, *wes5* and *wes6.*

13.3.5 Marker-Assisted Selection (MAS)

Even though conventional breeding approaches will continue to make valuable contributions to the genetic improvement of important traits in pearl millet, the efficiency of such concerted efforts can be increased considerably through the supplementation of marker-assisted selection approaches. A number QTL and associated markers have been identified for downy mildew resistance (Hash *et al.,* 1999; Hash and Witcombe, 2001; Jones *et al.,* 2002; Breese *et al.,* 2002; Hash and Witcombe, 2002). Several QTL have been introgressed to elite inbred parental lines of the popular hybrid HHB 67 through RFLP-based marker-assisted backcross breeding (Thakur *et al.,* 2008). Validation of major drought tolerance QTL in the LG 2 target region was done by using NILs of H 77/833-2 introgressed with various putative QTL regions from PRLT 2/89-33 (donor) by marker-assisted backcrossing (Serraj *et al.,* 2005). BC_4F_3 progeny from selected BC_4F_2 plants homozygous for different segments of the LG 2 target region were crossed to five different seed parents. Evaluation of the resultant hybrids under a range of moisture regimes revealed that the hybrids exhibited a large variation in the expression of yield components and yield response to the moisture regimes, with a consistent yield advantage in hybrids.

HHB 67 is a public-bred hybrid developed and released by Haryana Agricultural University in 1995–1996, which was widely adapted by farmers in Haryana and Rajasthan, especially under rainfed farming systems. After more than 10 years of its successful cultivation, the hybrid was constantly affected by downy mildew disease, which can destroy 30% of the grain yield. A major effect QTL for terminal drought tolerance on LG 2, explaining over 30% of the yield variation under terminal drought was introgressed to the male parent (H77/833-2) through marker-assisted QTL introgression

and several genes for downy mildew resistance were introgressed from ICML 22 to the female parent (843A/B) by conventional breeding to create the new hybrid HHB 67-improved (843A × ICMR 01029), ICMR 01029 being the male introgression line. This is the first product developed through marker-assisted breeding in crop plants (Hash *et al.,* 2006). Evaluation of 16 hybrids of drought-tolerant QTL introgression lines obtained from ICRISAT in India for their drought tolerance in Guinea Savannah zone of Ghana resulted in the identification of two hybrids (843A × H77/833-2 and 843A × PRLT 2/89-33) with the highest 100-seed weight and a hybrid (863B × H77/833-2) with excellent in plant height, fresh and dry stover weights, ear head length, ear head diameter, 100-seed weight, head yield and grain yield. This indicated the utility of MAS in breeding high-yielding cultivars with drought tolerance (Demuyakor *et al.,* 2013).

13.4 Finger Millet

13.4.1 Genetic Diversity

The assessment of genetic diversity among the germplasm accessions, landraces, improved varieties and accessions collected from different geographical locations was performed by using different systems of DNA markers such as RFLP (Muza *et al.,* 1995; Salimath *et al.,* 1995), RAPD (Hilu 1995; Das *et al.,* 2007), ISSR (Salimath *et al.,* 1995; Prabhu and Meenakshi Ganesan, 2013), SSR (Dida *et al.,* 2008; Manyasa *et al.,* 2014) and gene-based markers (Panwar, Nath *et al.,* 2010; Panwar, Saini *et al.,* 2010). Various studies on the genetic diversity assessment in finger millet has used a different number of SSR markers for analysing the genotypes. The use of optimum number of genotypes is important for the rapid assessment of genetic diversity by saving time as well as resources. In this regard, De Villiers *et al.* (2015) very recently concluded that dendrograms constructed using 52 markers and a sub-set of 20 markers were similar, indicating that the sub-set of 20 markers is enough to capture the genetic diversity.

Genetic diversity analysis of 22 accessions belonging to five species of *Eleusine* using three marker systems (RFLP, RAPD and ISSR) by Salimath *et al.* (1995) revealed that two accessions of *E. floccifolia* exhibited a high level of diversity as compared to *E. coracana*. Moreover, *E. floccifolia* along with *E. compressa* are most divergent than *E. coracana*, *E. indica* and *E. tristachya*. Another study by Hilu (1995) using RAPD indicated that genotypes belonging to subspecies *africana* revealed more affinity to *E. indica*, failing to group closely with that of *E. coracana*. Using SSR marker, Dida *et al.* (2008) grouped *E. coracana* germplasm into three distinct subpopulations, corresponding to subsp. *africana*, subsp. *coracana* (African origin) and subsp. *coracana* (Asian origin) with a few lines inter-mixed between the two origins. Another study involving SSR markers indicated that the cultivated varieties exhibited the lowest diversity in comparison to the highest diversity exhibited by the wild species along with several desirable alleles (Nethra *et al.,* 2014). The utility of EST-SSR markers in the assessment of genetic diversity among finger millet accessions was also reported (Bheema Lingeswara Reddy *et al.,* 2012).

Classification of accessions in relation to their geographical origin was also reported in some studies. By using RAPD, SSR and cytochrome P450 gene-based markers, the accessions from different geographical regions of India and Africa were grouped into distinct clusters, while the latter two marker systems were found to be useful for the

assessment of genetic diversity (Panwar, Saini *et al.,* 2010). Analysis of landraces and improved varieties by Bezaweletaw (2011) classified them into nine clusters with the absence of a clear-cut grouping in relation to the origin of their respective region. In a study by Arya *et al.* (2013), south Indian accessions were grouped together with African lowland types, while north Indian accessions were grouped with that of African highlands. Recently, Manyasa *et al.* (2014) reported that within-country diversity was more than between-country diversity with highest diversity among Kenyan accessions and the least diversity among Ugandan accessions.

Few studies were performed with an objective of classification of germplasm accessions based on their cytotypes, calcium content, resistance or susceptibility to blast and also for the identification of diverse lines for further use in breeding programmes. RFLP patterns could classify the genotypes from Africa and India into three cytotype groups (Muza *et al.,* 1995). By employing a combination of markers (RAPD, SSR, cytochrome P450 gene-based markers), Panwar, Nath *et al.* (2010) classified the genotypes on the basis of calcium content, viz., high (300–450 mg/100 g), medium (200–300 mg/100 g) and low (100–200 mg/100 g). The genotypes GEC 182 and CO 12 were identified as ideal parents for the hybridisation programme since they are distantly related and contrasting for days to flowering and grain weight (Kalyana Babu *et al.,* 2007). Similarly, the genotypes VL 149, KOPN 338, KOPN 929 and KOPN 161 were identified by Karad *et al.* (2013) as the most diverse genotypes, which can be crossed with elite genotype to develop new breeding lines. SSR polymorphisms in orthologs of important genes related to grain amino acid composition (*Opaque2*) and calcium content (calcium transporters, calmodulin) were used in the characterisation of germplasm accessions that differed in their seed protein and calcium content (Nirgude *et al.,* 2014; Kumar *et al.,* 2014). Eight out of the 15 new EST-SSR markers tested by Kalyana Babu *et al.* (2014a) discriminated the genotypes based on resistance and susceptibility to blast disease and the marker FMBLEST5 could clearly classify them into resistant and susceptible types.

13.4.1.1 Core and Reference Collections

Core and mini core collections or genotype-based reference sets are helpful in the selection of germplasm with superior agronomical traits for future crop breeding programmes (Glaszmann *et al.,* 2010). The core collection in finger millet (Upadhyaya *et al.,* 2006) was constituted comprising of about 10% (622) of the accessions of the entire collection (5949), while the mini core (Upadhyaya *et al.,* 2010) was constituted with 1.34% (80) of the entire collection representing the diversity of the entire collection. In addition, a genotype-based reference set comprising of 300 accessions was developed by genotyping of the global composite collections of finger millet developed by ICRISAT in collaboration with the Generation Challenge Program (GCP) using SSR markers (Generation Challenge Program Project Abstracts, 2008). These collections act as an invaluable resource for discovering new sources of variation for agronomic and nutritional traits, resistance to biotic and abiotic stresses as well as bioenergy traits. They are also useful as a diversity panel for assessing population structure, genetic diversity, allelic richness and for association mapping (Upadhyaya, 2015).

13.4.2 Molecular Marker Resources

Availability of whole genomes as well as ESTs, along with the advancements in computational software, led to the swift development of DNA markers, particularly SSR

markers in sorghum and foxtail millet. However, the progress is very limited in the case of finger millet due to the non-availability of complete genome sequence and the presence of very limited ESTs in the public database. The first set of 82 SSR markers was developed by Dida *et al.* (2007) by using methylation-sensitive restriction enzymes. Recently, another set of 92 SSR markers was developed through the *in silico* analysis of sequence data obtained after enrichment and 454 GS-FLX sequencing of the finger millet genotypes KNE 755 and KNE 796 by Musia (2013). These markers add to the existing resource of 82 SSRs and are useful for genetic diversity assessment, linkage map construction, QTL mapping and MAS. In addition, SSR markers can be developed from the ESTs generated through EST projects, which are available in the public domain through *in-silico* mining of SSRs. EST-SSR markers were developed for finger millet from 1740 ESTs available in the public domain by Arya *et al.* (2009). A set of 31 SSR markers was synthesised based on di, tri, tetra and penta-nucleotide repeat sequences. Of the 31 SSR markers tested, 17 yielded clear and robust amplicons, and nine were found polymorphic when analysed in 11 elite germplasm accessions of Indian and African origin. Another set of 132 EST-SSR markers were developed through the *in silico* mining of 1927 ESTs of finger millet available in the NCBI database (Bheema Lingeswar Reddy *et al.,* 2012). Of these, 30 SSR markers were used for variety identification and genetic diversity assessment of 15 accessions. Very recently, about 545 EST-SSR markers were developed from the 1956 ESTs of finger millet (Kalyana Babu *et al.,* 2014a). One more set of 58 genic SSR markers were developed from the ESTs blast-related genes like NBS-LRR regions from finger millet and sequences of various rice blast resistance genes (Kalyana Babu *et al.,* 2014b).

The Bio-resources Innovations Network for Eastern Africa Development (Bio-Innovate) program, hosted and managed by the International Livestock Research Institute (ILRI) and co-located with the Biosciences Eastern and Central Africa (BecA)-ILRI hub in Nairobi, has partnered with the African Orphan Crop Consortium for an initiative on the genome sequencing of finger millet. This initiative is being coordinated by the ICRISAT regional team based at Nairobi in partnership with BecA Hub, University of California, University of Georgia and the Swedish University of Agricultural Sciences. The project involves whole genome sequencing of the finger millet genotype, KNE796 and re-sequencing of 35 blast-resistant, five blast-susceptible, 35 drought-tolerant, five drought-susceptible accessions and 20 wild accessions of finger millet (http://bioinnovate-africa.org/about-us/news/item/162-finger-millet-genomics-project-to-provide-researchers-with-better-tools-for-variety-production; http://hpc.ilri.cgiar.org/beca/training/AdvancedBFX2014_2/course/fingermilletProject.pdf). This will help in the rapid development of a large number of SSR, InDel and SNP markers in finger millet through *in silico* approaches.

13.4.3 Genetic Maps, QTL Mapping and Marker-Assisted Selection (MAS)

Even though finger millet is a highly nutritious crop, only limited progress has been made with respect to molecular marker development, linkage map construction and QTL mapping. A set of RFLP, AFLP and SSR markers were used for the construction of the first genetic map of finger millet by Dida *et al.* (2008), which spans 721 cM and 787 on A and B genomes, respectively, and at least partially cover all 18 chromosomes. A comparative genome analysis between finger millet and rice by Srinivasachary *et al.* (2007) revealed that six of the nine finger millet groups were homoeologous to a single

rice chromosome each, and the remaining three groups were orthologous to two rice chromosomes. Gene orders were highly conserved between rice and finger millet, and only 10% of markers were mapped to non-syntenic positions, with the majority of them located in the distal end of chromosomes, suggesting a possible correlation between recombination and evolution that was observed earlier in wheat.

The majority of the agronomically important traits is complex and governed by QTL. Hence, the genetic improvement of these traits can be achieved through marker-assisted breeding once these QTL are identified and mapped. Linkage analysis and association mapping are the two most commonly employed tools for dissecting complex traits. However, the association mapping is advantageous since it requires natural population, achieves high-resolution mapping, involves more number of alleles and take less time. Association mapping 15 agro-morphological traits with SSRs resulted in identification of markers associated QTL of four traits – the locus UGEP81 with the QTL for basal tiller number, two SSR loci UGEP77 and UGEP90 with the QTL for days to 50% flowering and the SSR marker, FM9 with flag leaf width and plant height (Kalyana Babu *et al.,* 2014c). Four QTL for finger blast and one QTL for neck blast resistance were identified through association mapping (Kalyana Babu *et al.,* 2014b). The QTL for finger blast was associated with the markers RM262, FMBLEST32 and UGEP81, while the QTL for neck blast was associated with UGEP18. Interestingly, three common QTL for blast resistance were found by using GLM and MLM approaches. The above-mentioned QTL along with associated markers can be used for fine mapping and for the development of blast-resistant genotypes that are agronomically superior through marker-assisted QTL introgression.

13.5 Foxtail Millet

13.5.1 Genetic Diversity

Assessment of genetic diversity and population structure of landraces and germplasm accessions is critical for genetic resource management, trait mapping and crop breeding. Earlier, the presence of high levels of diversity among the landraces was demonstrated through the phenotypic analysis on morphological characteristics (Li and Wu, 1996; Reddy *et al.,* 2006) followed by the utility of isozymes for this purpose (Jusuf and Pernes, 1985). The advent of DNA-based markers led to the use of RFLP and other multi-locus markers such as RAPD, ISSR and AFLP, especially for the assessment of genetic diversity in landrace collections as well as germplasm accessions. RFLP analysis by Fukunaga and Kato (2002) revealed that Chinese landraces were highly diverse than those from East and Southeast Asia, Afghanistan, India, Central Asia and Europe. In another study by Fukunaga *et al.* (2002), the landraces were grouped into five major clusters, Clusters I and II comprised of landraces from East Asia, Cluster III from subtropical and tropical regions in Asia, Cluster IV from East Asia, Nepal and Myanmar and Cluster V from central and western regions of Eurasia. A study by Li *et al.* (1998) involving RAPD analysis suggested that foxtail millet is closer to green foxtail millet than other *Setaria* species, with a considerable variation in *S. italica* and *S. glauca*. Schontz and Rether (1999) identified three genetic groups among 37 lines representing Eurasian diversity, one corresponding to central European origin and two corresponding to Asian origin. AFLP analysis by Le Thierry d'Ennequin *et al.* (2000) grouped the

accessions from Eastern Europe and Africa into two separate clusters and China as the centre of domestication was supported by the high diversity among Chinese accessions.

With the development of SSR markers by various research groups (Jia, Shi *et al.,* 2007; Jia, Zhang *et al.*, 2009; Gupta *et al.,* 2012), several studies on the genetic diversity assessment have been published in foxtail millet during the last 10 years. Most of the reports involving Chinese accessions/landraces revealed a clustering of genotypes in accordance with their eco-geographical distribution (Jia, Zhang *et al.,* 2009; Jia, Tan *et al.*, 2009; Hirano *et al.,* 2011; Wang *et al.,* 2012; Diao, 2014; Liu *et al.,* 2014), except the studies by Kim *et al.* (2012), Jia, Shi *et al.* (2013) and Liu *et al.* (2011), where it was reported that the lack of correspondence between clustering and eco-geographical distribution in China revealed a partially mixed distribution. Similarly, the landraces from Taiwan were classified into three groups corresponding to the geographical regions, viz., northern, central and southern Taiwan (Lin *et al.,* 2012). SSR analysis by Zhao *et al.* (2012) classified the accessions into six clusters, and all Korean accessions were grouped in a separate cluster, revealing their distinctness from other introduced accessions. A fair correlation of genetic diversity with racial classification was observed and *indica* race exhibited greater diversity from *maxima* and *moharia* races (Vetriventhan *et al.,* 2012).

13.5.1.1 Core and Reference collections

Development of core collections representing >90% of the total genetic diversity of the germplasm collections is a pre-requisite for the identification of suitable accessions for the traits of interest. A core collection in foxtail millet comprising of 155 accessions was reported by Upadhyaya *et al.* (2008). A mini core collection of the 35 accessions was constituted from the core collection and further analysis resulted in the identification of superior accessions for early maturity, grain yield, seed protein, calcium, iron and zinc (Upadhyaya, Ravishankar *et al.,* 2011). In addition, a genotype-based reference set comprising of 200 accessions was developed by genotyping of the global composite collections of finger millet (452 accessions) developed by ICRISAT in collaboration with the Generation Challenge Program (GCP) using SSR markers (Generation Challenge Program Project Abstracts, 2008). Apart from ICRISAT, two core collections comprising of 107 and 152 accessions of foxtail millet was developed (Lata, Bhutty *et al.,* 2011; Lata, Jha *et al.*, 2011), which are being used by the same group for determining population structure and allele mining of important agronomic and abiotic stress-related traits. Another core collection of 128 accessions was developed in China from 3356 germplasm accessions collected from three major ecological regions, namely, North, Northwest and Northeast (Liu *et al.,* 2011), and its SSR genotyping indicated the presence of a high level of genetic diversity.

13.5.2 Molecular Marker Resources

Prior to the whole genome sequencing of foxtail millet simultaneously by two independent groups (Zhang *et al.,* 2012; Bennetzen *et al.,* 2012), ESTs developed from various functional genomics projects are considered as the important targets for the development of SSR markers. This was demonstrated by Jia, Shi *et al.* (2007) by the development of 26 SSR markers from 1213 foxtail millet ESTs, which was followed by the development of 100 polymorphic SSR markers from two genomic libraries enriched

for $(GA)_n$ and $(CA)_n$ repeat motifs (Jia, Zhang *et al.,* 2009). Another set of 45 polymorphic SSR markers was developed from RAPD-enriched library by Heng *et al.* (2011), and their utility in genetic diversity and cross-species transferability was demonstrated. A new set of 172 genomic SSR markers was developed from a $(CA)_n$, $(AAC)_n$ and $(ATG)_n$ enriched genomic library constructed using a drought- and salt-tolerant foxtail millet cultivar (Prasad) (Gupta *et al.,* 2012). They developed 78 more SSR markers from a $(GA/CT)_n$ microsatellite-enriched genomic library (Gupta *et al.,* 2013). A total of 447 EST-SSR markers were developed from 66027 ESTs of foxtail millet available in the NCBI EST database, which were successfully validated in green foxtail and other millets, cereals and bioenergy grasses (Kumari *et al.,* 2013). These markers are useful for various genotyping applications, QTL mapping, establishing phylogenetic relationships and transferability to other grass species.

The availability of high-throughput, advanced sequencing technologies and high-quality complete genome sequence of foxtail millet (Zhang *et al.,* 2012; Bennetzen *et al.,* 2012) offers an excellent opportunity for the development of DNA markers such as SSRs and SNPs in a large-scale. A total of 28342 SSRs was identified by the genome-wide analysis, and a high-density physical map was generated (Pandey *et al.,* 2013). Similarly, Zhang *et al.* (2014) identified a total of 5020 SSRs and designed primers for 788 SSRs based on the comparison of sequences between foxtail millet and green foxtail, of which 733 were polymorphic, and a physical map was constructed. A set of 9576 and 7056 potential SSR markers were developed from 42754 transcripts of green foxtail generated by reference-based assembly with foxtail millet and 60751 transcripts generated by the *de novo* assembly, respectively (Xu *et al.,* 2013). About 2584083 SNPs were identified by Jia, Huang *et al.* (2013) through the sequencing of 916 diverse genotypes and a haplotype map of foxtail millet was constructed using 845787 common SNPs. In the same way, a total of 762082 SNPs, 26802 InDels of 1–5 bp in length, and 10109 SVs between Shi-Li-Xiang and Yugu1; 915434 SNPs, 28546 InDels and 12968 SVs between Shi-Li-Xiang and Zhang gu were identified by Bai *et al.* (2013) through re-sequencing. By targeting the InDels specific to introns, Gupta *et al.* (2011) identified 98 potential intron length polymorphism (ILP) markers from the EST sequences of dehydration- and salinity-stressed suppression subtractive hybridisation (SSH) libraries constructed by Lata *et al.* (2010) and Puranik *et al.* (2011). Later, a set of 5123 ILP markers was developed by Muthamilarasan *et al.* (2013) by the genome-wide analysis. The genome-wide analysis of the foxtail millet genome sequence also led to the development of 176 miRNA-based markers (Yadav, Muthamilarasan *et al.,* 2014) and 20278 transposable elements-based markers (Yadav, Bonthala *et al.,* 2014). The details of various DNA-based markers developed in foxtail millet are given in Table 13.5.

13.5.3 Genetic Maps

Genetic linkage maps are essential for the mapping of major genes and QTL in foxtail millet and comparative genome mapping with related millets and cereals. The first linkage map in foxtail millet was constructed in an inter-varietal cross of foxtail millet (Longgu 25 × Pagoda Flower Green) with the help of 160 RFLP marker loci by Wang *et al.* (1998) comprising of nine linkage groups. The comparison of this map to an inter-specific map constructed using the cross, *S. italica* × *S. viridis*, revealed greater conservation of marker order and genetic distances between the loci. This laid the foundation for further genetic analysis of important traits and comparative genomic studies. Using

Table 13.5 DNA-based markers developed in foxtail millet.

Target sequence	No. of markers developed	Reference
SSR markers		
Genomic	100	Jia, Zhang *et al.* (2009)
	45	Heng *et al.* (2011)
	172	Gupta *et al.* (2012)
	78	Gupta *et al.* (2013)
ESTs	26	Jia, Shi *et al.* (2007)
	447	Kumari *et al.* (2013)
Whole genome sequence	28342	Pandey *et al.* (2013)
	733	Zhang *et al.* (2014)
RNA-seq data	9576	Xu *et al.* (2013)
	7056	
SNPs		
Re-sequencing data	762082	Bai *et al.* (2013)
	915434	
	2584083	Jia, Huang *et al.* (2013)
InDels		
Re-sequencing data	26802	Bai *et al.* (2013)
	28546	
ILP markers		
ESTs	98	Gupta *et al.* (2011)
Whole genome sequence	5123	Muthamilarasan *et al.* (2013)
miRNA-based markers		
Whole genome sequence	176	Yadav, Muthamilarasan *et al.* (2014)
TE-based markers		
Whole genome sequence	20278	Yadav, Bonthala *et al.* (2014)

SSR – simple sequence repeats; ESTs – expressed sequence tags; SNP – single nucleotide polymorphism; InDel – insertion-deletion; ILP – intron length polymorphism; miRNA – microRNA; TE – transposable element.

this as a framework map, Doust *et al.* (2004; 2005) mapped QTL for vegetative branching and inflorescence architecture. Moreover, a comparative mapping among foxtail millet, rice and pearl millet by Devos *et al.* (1998; 2000) revealed that the presence of some homologous chromosomal fragments between these genomes, highlighting their close relationships among the crops of Poaceae. In the recent past, a linkage map of length 1654 cM spanning nine chromosomes was constructed by Jia, Zhang *et al.* (2009) based on 81 new SSR markers with 20 RFLP anchored markers using an F_2 population of the cross B100 (cultivated *S. italica*) × A10 (wild *S. viridis*). Approximately 1000 SNPs were identified from sequencing pools of RILs developed from the cross B100 (*S. italica*)× A10 (*S. virdis*), and these SNPs were used for the construction of a genetic linkage map with evenly mapping SNPs on the nine chromosomes of foxtail millet (http://www.plantbio.uga.edu/media/2010_grad_symposium(1).pdf). By employing 1733 markers from foxtail millet (SSR, STS, SNP and SV) and pearl millet (ACGM and SSR),

a genetic linkage map with nine linkage groups spanning 2082.5 cM was constructed using an F_2 mapping population of the cross Gao 146A × K 103, which contained 192 different kinds of markers and 33 new markers (Wang *et al.,* 2014).

The assembling of reference genomes of foxtail millet and green foxtail during the year 2012, independently by two Zhang *et al.* (2012) and Bennetzen *et al.* (2012) paved way for the construction of high-resolution genetic linkage maps due to the identification of several thousands of SNPs and other DNA sequence variations. A genetic linkage map was constructed using the cross Zhang gu × A2, in which 751 markers were mapped including 118 SNPs and 641 SVs (Zhang *et al.,* 2012). The sequencing of RILs from the cross B100 (*S. italica*) × A10 (*S. viridis*) resulted in the identification of 3149093 SNPs, of which 992 were scored for segregation and used for map construction (Bennetzen *et al.,* 2012). Later, Pandey *et al.* (2013) identified 28342 SSRs from the whole genome sequence and generated a high-density physical map with the SSRs mapping across nine chromosomes of foxtail millet. Recently, a physical map was constructed using the 733 polymorphic SSR markers developed based on the comparison of foxtail millet and green foxtail genome (Zhang *et al.,* 2014). A haplotype map was constructed based on 845787 common SNPs selected from a total of 2584083 SNPs obtained from the sequencing of 916 diverse foxtail millet varieties (Jia, Huang *et al.,* 2013).

13.5.4 QTL Mapping

Unlike major millets such as sorghum and pearl millet, there are very limited studies on the mapping of QTL/genomic regions associated with various agronomic and stress tolerance traits in foxtail millet. With the availability of whole genome sequence of foxtail millet, a large number of DNA markers have been developed in the last 2 years. This will hasten the pace of QTL mapping in this crop. In a pioneering study, Doust *et al.* (2004) identified a total of four QTL (one each on chromosomes I and V and two on chromosome III) associated with the basal branching and four QTL (one each on chr. VI and IX and two on chr. V) associated with axillary branching. They also implicated the roles of auxin and gibberellins pathway genes along with many transcription factors in controlling branching. An investigation on the genetic control of flowering in *Setaria* spp. by Mauro-Herrera *et al.* (2013) revealed the co-localisation of QTL governing flowering time over a range of photoperiods. A comparison of these QTL with that of sorghum and maize suggested a combined role of conserved and lineage-specific genes in governing flowering time in all grasses. Investigation of the genic male sterility using a highly male-sterile line (Gao 146A) indicated that the trait was controlled by a single recessive gene (*ms1*). By analysing the F_2 population of the cross Gao146A × K103, this gene was mapped on chromosome VI (Wang *et al.,* 2013), which was linked to b234 SSR marker, which is 16.7 cM away from the gene.

In a salt-tolerant line under high salinity, up-regulation of the transcripts of hydrogen peroxide scavenging enzymes, particularly phospholipid hydroperoxide glutathione peroxidase (PHGPX), ascorbate peroxidase and catalase 1 was observed. Moreover, a 25 kD PHGPX protein was induced prominently at high salinity level (250 mmol/L), clearly indicating the vital role of this protein in the defence against salt-induced oxidative damage (Sreenivasulu *et al.,* 2004). In $F_{(2:3)}$ progeny of a cross between the green millet (weedy) and foxtail millet (domesticated) the number of branches varies with genotype and density of planting, with significant GxE interactions. Based on the map location and phenotypic effect, the genes teosinte branched1 (*tb1*) and barren stalk1 (*bs1*) were identified as the likely candidate genes underlying the QTL (Doust and Kellogg, 2006). A differential

accumulation of proline was observed in two finger millet cultivars analysed under salt stress, with more accumulation in Prasad (tolerant) as compared to Lepakshi (susceptible) and the proline accumulation was positively correlated with the increased glutamine synthetase (GS) and pyrroline-5-carboxylate (P5C) reductase activities (Preston and Kellogg, 2006). Aldose reductase activity was increased under increasing levels of salinity stress, exhibiting a positive correlation with increased levels of sorbitol, an osmoprotectant involved in maintaining osmotic balance. Glutathione-S-transferase activity was higher in the tolerant cultivar that showed a low 4-hydroxynon-2-enal content, suggesting a possible mechanism for detoxification of 4-hydroxynon-2-enal by glutathione-S-transferase and aldose reductase under stressful conditions (Veeranagamallaiah *et al.,* 2009). A significant up-regulation of *SiDREB2* gene was observed under dehydration and salinity stress and a synonymous SNP (A/T) was detected at the 558th position of the gene in a core set of 45 foxtail millet accessions, which was targeted for the development of allele-specific marker (Lata, Bhutty *et al.,* 2011).

Waxy grains are characterised by less or no amylose, which normally constitute ≥20% of the total starch in the endosperm of non-waxy grains. Analysis of structural variation in the waxy gene revealed a correlation of RFLP type with phenotype – types I and II to non-waxy, types III and VI to low-amylose and types IV, V and VII to waxy phenotypes. These differences are due to insertions in the gene, indicating multiple, independent insertions in the waxy gene resulted in the loss-of-function waxy phenotypes (Fukunaga *et al.,* 2002). Analysis of the F_2 mapping population of Yugu1 × SLX by Bai *et al.* (2013) revealed that waxy grain is governed by a single recessive gene, which was mapped on chromosome 4. By using the SV markers in the F_2 mapping population, the waxy trait was mapped between sca4-SV36 and sca4-SV43. Among the 23 predicted genes, the potential gene Si006103m (starch synthase encoding granule-bound starch synthase 1) was sequenced in SLX and Yugu1 that revealed the insertion of a TSI-2 transposon (5258 bp) into the first intron in SLX while the remaining nucleotides were almost identical to Yugu1. Recently, a linkage disequilibrium analysis of 184 accessions collected from diverse geographical regions using 50 SSR markers revealed a considerable association of eight SSR markers with nine agronomic traits ($R^2 = 18\%$), of which the SSR markers b129, p75, b225 and p61 were associated with grain yield, grain weight, inflorescence compactness and grain weight, respectively (Gupta *et al.,* 2014). Association of some of the genes such as *SiPf40*, *Si69*, *SiPLDα1*, *SiNAC* and *ACCase* with lateral shoot growth, aluminium tolerance, drought tolerance, drought and salinity tolerance and herbicide tolerance, respectively, was confirmed by transgene expression or silencing approaches. The details of important major genes and QTL identified in foxtail millet are given in Table 13.6. These major genes/QTL together with their linked markers offer excellent opportunity for the genetic improvement of these traits through marker-assisted breeding.

13.6 Other Small Millets

Among the small millets, very limited information is available on the development of molecular markers, genetic diversity assessment using DNA markers, linkage maps and QTL mapping for kodo-, proso-, barnyard- and little millet. Therefore, concerted efforts on whole genome and EST sequencing are essential for the rapid development of DNA-based markers in this group of crops. Furthermore, a comparative genomics approach can be used effectively to develop orthologous markers based on the sequence

Table 13.6 Important major genes and QTL mapped in foxtail millet.

Trait	QTL/gene	LG	Reference
Phenology and morphology			
Flowering time	*QTL 4.1*	4	Mauro-Herrera *et al.* (2013)
Vegetative branching	*tb1* and *ba1*	7	Doust and Kellogg (2006)
Grass spikelet	*FUL1* and *FUL2*	1	Preston and Kellogg (2006)
Basal branching		1	Doust *et al.* (2004)
		3	
		5	
Axillary branching		5	
		6	
		9	
Lateral branching and tillering	*SiPf40*	4	Liu *et al.* (2009)
Genic male sterility	*ms1*	6	Wang *et al.* (2013)
Grain amylase content	GBSS 1	1	Fukunaga *et al.* (2002)
	waxy-slx	4	Bai *et al.* (2013)
Stress tolerance			
Salinity tolerance	*PHGPX*	2	Sreenivasulu *et al.* (2004)
	GS and *P5C*	2	Veeranagamallaiah *et al.* (2007)
	Aldose reductase	6	Veeranagamallaiah *et al.* (2009)
Drought tolerance	*SiOPR1*	1	Zhang *et al.* (2007)
	SiPLDα1	1	Peng *et al.* (2010)
	SiDREB2	2	Lata, Bhutty *et al.* (2011); Lata and Prasad (2012)
Salinity and drought tolerance	*SiNAC*	2	Puranik *et al.* (2011)
	SiWD40	4	Mishra *et al.* (2012)
Herbicide tolerance	*psbA*	2	Jia, Yuan *et al.* (2007)
	Acetyl-coA carboxylase	3	Dong *et al.* (2011)
Aluminium tolerance	*Si69*	2	Zhao *et al.* (2009)
Rust resistance	*Rust1*		Zhao *et al.* (2010)

QTL – quantitative trait loci; LG – linkage group; R^2 – % contribution to phenotypic variance.

information of other millets. The molecular marker research in these millets is discussed together due to the availability of limited reports in this area.

13.6.1 Genetic Diversity

Among the above-mentioned small millets, proso millet leads in the genetic diversity assessment studies. The genetic diversity determined using AFLP identified the black seeded Colorado-Weld County and Wyoming-Platte County as the most distinct based on the dissimilarity. About six weed biotypes exhibiting some cultivated phenotypes were

grouped along with domesticated ones while the three typical wild phenotypes formed another group (Karam *et al.,* 2004). Similarly, AFLP was effective in grouping the American proso millet biotypes in two clusters, but without a clear-cut separation of hybrid biotypes from wild biotypes (Karam *et al.,* 2006). Analysis of genetic diversity of 118 accessions of broomcorn millet (proso millet) using SSR markers from rice, wheat, oat and barley revealed a moderate level of diversity. The cluster analysis classified the accessions into five groups, which was consistent with ecological growing areas. The study also revealed the highest level of diversity in the accessions from Loess Plateau, the probable site of origin of proso millet (Hu *et al.,* 2009). Analysis of genetic diversity among 98 landrace accessions collected across Eurasia using SSR markers by Hunt *et al.* (2011) revealed a distinct grouping of accessions into eastern and western genetic groups with an approximate boundary in northwestern China. These two genepools were further subdivided into clusters, each representing a clear geographic pattern. Assessment of genetic diversity among 50 accessions of proso millet by Cho *et al.* (2010) using 25 polymorphic SSR markers revealed the presence of greater diversity with a mean genetic similarity coefficient of 0.3711. The newly developed SSR markers could be used as efficient molecular resources for assessing genetic diversity, understanding population structure, and breeding of proso millet.

Barnyard millet is differentiated into two species, viz., *Echinochloa esculenta* – Japanese barnyard millet and *Echinochloa frumentacea* – Indian barnyard millet (Yabuno, 1987; Wanous, 1990). Very few genetic diversity studies with a limited number of samples were reported for Japanese barnyard millet involving isozymes, RAPD, SSR and chloroplast DNA markers (Hilu, 1994; Nakayama *et al.,* 1999; Yamaguchi *et al.,* 2005; Nozawa *et al.,* 2006). RAPD analysis in Indian barnyard millet by Hilu (1994) suggested that the sequence diversity is significantly higher than its Japanese counterpart, possibly due to multiple domestication events across India. The genetic diversity among the accessions of *Echinochloa crus-galli* (barnyard grass) and *E. frumentacea* assessed through RAPD analysis by Prabha *et al.* (2012) classified the accessions in two groups with clear separation of inter- and intra-species diversity. Molecular characterisation of the core collection of barnyard millet using whole-genome genotyping-by-sequencing recently by Wallace *et al.* (2015) led to the identification of several thousand SNPs, which, when employed in population structure analysis revealed four population clusters for *E. colona* accessions and three clusters for *E. crus-galli*. Even though the clusters match with phylogenetic relationships, they do not correspond racial classification or morphology-based clustering.

Assessment of genetic diversity and patterns of geographic variation among kodo millet and *Paspalum polystachyum* collections using RAPD markers classified the accessions into three major groups, one comprising of African accessions, and other two comprising of Indian accessions. The accessions of North African kodo millet and *P. polystachyum* were genetically diverse, while Australian kodo millet exhibited closeness to the African types (M'Ribu and Hilu, 1996). Way back in 2001, RFLP analysis of the chloroplast DNA, the trnS-psbC gene region was used to identify seven millet species (Parani *et al.,* 2001) when the HaeIII-MspI enzyme combination was used. The molecular research in little millet is very limited and demands concerted efforts for the large-scale development of molecular markers, which will be useful for the construction of genetic maps leading to QTL mapping and MAS.

13.6.1.1 Core collections

Core collections were also developed in barnyard-, kodo-, little- and proso millet. The core collection in these small millets comprises of 106 accessions in proso millet, 89

Table 13.7 Core collections of small millets.

Crop	No. of accessions	Reference
Finger millet	622	Upadhyaya *et al.* (2006)
Foxtail millet	155	Upadhyaya *et al.* (2008)
	152	Lata, Bhutty *et al.* (2011); Lata, Jha *et al.* (2011)
	128	Liu *et al.* (2011)
Proso millet	106	Upadhyaya, Sharma *et al.* (2011)
Barnyard millet	89	Upadhyaya *et al.* (2014)
Kodo millet	75	Upadhyaya *et al.* (2014)
Little millet	56	Upadhyaya *et al.* (2014)

accessions in barnyard millet, 75 accessions in kodo millet and 56 accessions in little millet (Table 13.7), which constituted about 10% of the accessions of the entire collection of this group of crops in genebank. These collections are the rich sources of allelic diversity and also include donors for important agronomic, nutritional as well as biotic and abiotic stress tolerances. These are also useful resources for studying the population structure and association mapping studies.

13.6.2 Molecular Marker Resources, Mapping and Marker-Assisted Selection

The development of molecular markers is at infancy in barnyard-, kodo-, little- and proso millet. Hence, only a few hundreds of SSR markers have been developed in the case of proso millet and SSR marker development was not reported in barnyard-, kodo-, little millet. More number of markers have to be developed by the concerted efforts, which can be useful for the construction of linkage maps, QTL mapping and MAS. Very few DNA markers have been employed in the characterisation of molecular diversity and phylogeny (M'Ribu and Hilu, 1996; Kushwaha *et al.,* 2015). Genetic maps are not available for kodo millet due to the non-availability of SSR or SNP markers in addition to the persistent cross-hybridisation with wild relatives.

Twenty-five polymorphic SSR markers were developed by Cho *et al.* (2010) using a SSR-enriched genomic DNA library of proso millet. With the lack of DNA sequence information, a large number of DNA markers can be developed in proso millet with the help of available sequence information in related grasses (Hu *et al.,* 2009; Rajput *et al.,* 2014). This was demonstrated by the testing of 548 switchgrass SSR markers reported by Wang *et al.* (2011) and Liu *et al.* (2012) on eight proso millet genotypes, of which only 339 SSR markers were amplified, revealing a transferability of 62% to proso millet. These markers will be useful for the construction of linkage maps, QTL mapping and other marker-assisted breeding efforts in proso millet.

13.7 Progress of Molecular Marker Research in Millets

Among the various millets, sorghum and pearl millet, predominantly grown in semi-arid tropic regions of the world, were given preference for the molecular marker research. In both these crops, studies on the genetic diversity assessments using

molecular markers were initiated as early as 1990s and many reports were published over the years. The first genetic map in sorghum was constructed during the early 1990s, while it was constructed during mid 1990s for pearl millet. The genetic diversity studies were initiated in other millets during mid 1990s. QTL mapping was initiated in pearl millet during mid 1990s, while it was done during early 2000 in sorghum. SSR marker development in sorghum and pearl millet was initiated during early 2000. In foxtail millet and finger millet, the first set of SSR markers was developed during 2007 (Jia, Shi *et al.,* 2007; Dida *et al.,* 2007). The development of markers picked the rapid pace in sorghum and foxtail millet after the sequencing of their genomes in 2009 (Paterson *et al.,* 2009) and 2012 (Zhang *et al.,* 2012; Bennetzen *et al.,* 2012), respectively. In the case of pearl millet, the draft genome sequence is in progress by International Pearl Millet Genome Sequencing Consortium (IPMGSC) for the inbred line Tift23D_2B_1 through whole genome shotgun sequencing (WGS) along with the re-sequencing of >500 pearl millet germplasm lines. The first version of genome assembly capturing 1.5 Gb based on WGS data has been defined while the final version is being developed by integrating WGS data, BAC sequence data, and the consensus genetic map (Varshney, 2014). The finger millet genome sequencing initiative effort is being organised by Bio-Innovate Program in partnership with the African Orphan Crop Consortium (http://hpc.ilri.cgiar.org/beca/training/AdvancedBFX2014_2/course/fingermilletProject.pdf). These genome sequencing projects will help in the large-scale development of DNA markers in pearl millet and finger millet in a short time through computational approaches, which will be further employed for the construction of genetic maps, QTL mapping and MAS. The identification of QTL in sorghum and pearl millet for yield as well as biotic and abiotic stress tolerance traits and the availability of tightly linked DNA markers has led to the development of superior cultivars for specific traits through marker-assisted backcross breeding (Kassahun *et al.,* 2010; Ngugi *et al.,* 2013; Mohamed *et al.,* 2014; Yohannes *et al.,* 2015). In the present era of rapid genome sequencing, the genomes of millets other than sorghum, pearl millet and foxtail millet will be the targets for sequencing in the near future, which will lead to the rapid development of DNA markers useful for the construction of genetic maps, QTL mapping and MAS. The progress of DNA marker research in millets is represented pictorially in Figure 13.1.

13.8 Future Prospects

The millets are valued for their nutritional status and health benefits, low-input agriculture and resilience to extreme climatic conditions, especially drought. Even though an enormous amount of research on molecular markers has been accomplished in sorghum, pearl millet and foxtail millet, there is an immense need for the rapid development of molecular markers to enhance the construction of linkage maps and the mapping of QTL for agronomically important traits as well as tolerance to biotic and abiotic stresses, especially in small millets. In the current era of rapid sequencing of genomes, these crops have better opportunities for marker development since the complete genomes can be sequenced in very less time. The genome sequence will be the target for the rapid identification of SSRs, InDels and SNPs, which can be utilised for the identification and mapping of QTL through association studies since development of a biparental mapping population is a difficult task in many of the small millets. However, in sorghum, pearl millet and foxtail millet, where a lot of information is

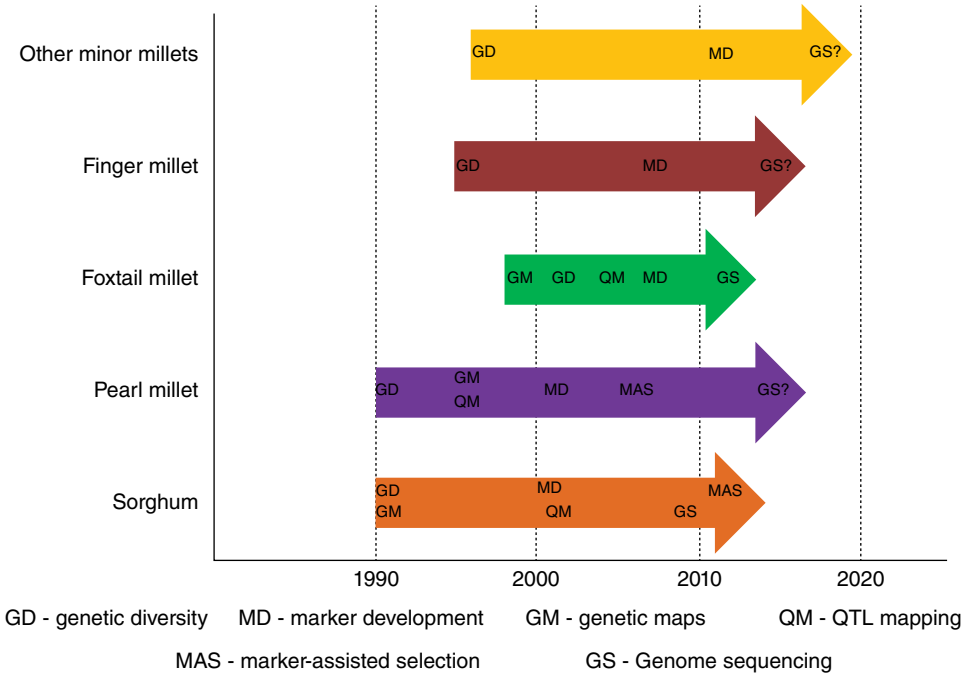

Figure 13.1 Progress of molecular marker research in millets.

available on DNA markers, genetic maps and QTL mapping, deployment of effective QTL for important target traits through marker-assisted selection should be given top priority. Therefore, in the situation of limiting natural resources and climate change, these crops offer immense promise to achieve better nutrition and health security.

References

Agrama, H., Widle, G., Reese, J. *et al.* (2002) Genetic mapping of QTL associated with greenbug resistance and tolerance in *Sorghum bicolor*. *Theor. Appl. Genet.*, **104**, 1373–1378.

Agrama, H.A. and Tuinstra, M.R. (2003) Phylogenetic diversity and relationships among sorghum accessions using SSRs and RAPDs. *Afr. J. Biotechnol.*, **10**, 334–340.

Alam, M.M., Mace, E.S., van Oosterom, E.J. *et al.* (2014) QTL analysis in multiple sorghum populations facilitates the dissection of the genetic and physiological control of tillering. *Theor. Appl. Genet.*, **127** (10), 2253–2266.

Aldrich, P.R. and Doebley, J. (1992) Restriction fragment variation in the nucleus and chloroplast genomes of cultivated and wild *Sorghum bicolor*. *Theor. Appl. Genet.*, **85**, 293–302.

Allouis, S., Qi, X., Lindup, S. *et al.* (2001) Construction of a BAC library of pearl millet, *Pennisetum glaucum*. *Theor. Appl. Genet.*, **102**, 1200–1205.

Arun, S.S. (2006) *In silico* EST data mining for elucidation of repeats biology and functional annotation in sorghum [*Sorghum bicolor* (L.) Moench.], in *M.Sc. thesis*, University of Agricultural Sciences, Dharwad.

Aruna, C., Bhagwat, V.R., Madhusudhana, R. *et al.* (2011) Identification and validation of genomic regions that affect shoot fly resistance in sorghum [*Sorghum bicolor* (L.) Moench]. *Theor. Appl. Genet.*, **122**, 1617–1630.

Arya, L., Verma, M., Gupta, V.K. and Karihaloo, J.L. (2009) Development of EST SSRs in finger millet (*Eleusine coracana* ssp *coracana*) and their transferability to pearl millet (*Pennisetum glaucum*). *J. Plant Biochem. Biotechnol.*, **18** (1), 97–100.

Arya, L., Verma, M., Gupta, V.K. and Seetharam, A. (2013) Use of genomic and genic SSR markers for assessing genetic diversity and population structure in Indian and African finger millet [*Eleusine coracana* (L.) Gaertn.] germplasm. *Plant Syst. Evol.*, **299**, 1395–1401.

Audilakshmi, S., Stenhouse, J.W. and Reddy, T.P. (2005) Genetic analysis of grain mold resistance in white seed sorghum genotypes. *Euphytica*, **145**, 95–101.

Ayana, A., Bekele, E. and Bryngelsson, T. (2000) Genetic variation in wild sorghum (*Sorghum bicolor* ssp. *verticilliflorum* L. Moench) germplasm from Ethiopia assessed by random amplified polymorphic DNA (RAPD). *Hereditas*, **132**, 249–254.

Ayana, A., Bryngelsson, T. and Bekele, E. (2000) Genetic variation of Ethiopian and Eritrean sorghum (*Sorghum bicolor* L. Moench) germplasm assessed by random amplified polymorphic DNA (RAPD). *Genetic Resour. Crop Evol.*, **47**, 471–482.

Azhaguvel, P., Hash, C.T., Rangasamy, P. and Sharma, A. (2003) Mapping the d_1 and d_2 dwarfing genes and purple foliage color locus *P* in pearl millet. *J. Hered.*, **94**, 155–159.

Bai, H., Cao, Y., Quan, J. *et al.* (2013) Identifying the genome-wide sequence variations and developing new molecular markers for genetics research by re-sequencing a landrace cultivar of foxtail millet. *PLoS ONE,* **8**(9), e73514, 12.

Basavaraju, R., Safeeulla, K.M. and Murty, B.R. (1981) Genetic variance and heritability for resistance to downy mildew in pearl millet. *Indian J. Genet.*, **41**, 137–143.

Bennetzen, J.L., Schmutz, J., Wang, H. *et al.* (2012) Reference genome sequence of the model plant *Setaria*. *Nat. Biotechnol.*, **30**, 555–561.

Berhan, A.M., Hulbert, S., Butler, L. and Bennetzen, J. (1993) Structure and evolution of the genomes of *Sorghum bicolor* and *Zea mays*. *Theor. Appl. Genet.*, **86**, 598–604.

Bertin, I., Zhu, J.H. and Gale, M.D. (2005) SSCP-SNP in pearl millet – a new marker system for comparative genetics. *Theor. Appl. Genet.*, **110**, 1467–1472.

Bezaweletaw, K. (2011) Genetic diversity of finger millet [*Eleusine coracana* (L.) Gaertn] landraces characterized by random amplified polymorphic DNA analysis. *Innov. Syst. Design Engineer.*, **2** (4), 207–217.

Bhattacharjee, R., Bramel, P.J., Hash, C.T. *et al.* (2002) Assessment of genetic diversity within and between pearl millet landraces. *Theor. Appl. Genet.*, **105**, 666–673.

Bhattramakki, D., Dong, J., Chhabra, A.K. and Hart, G.E. (2000) An integrated SSR and RFLP linkage map of *Sorghum bicolor* (L.) Moench. *Genome*, **43**, 988–1002.

Bheema Lingeswara Reddy, I.N., Lakshmi Narasu, M. and Sivaramakrishnan, S. (2012) Identification and characterization of EST-SSRs in finger millet (*Eleusine coracana* (L.) Gaertn.). *J. Crop Sci. Biotech.*, **15** (1), 9–16.

Bian, Y.L., Yazaki, S., Inoue, M. and Cai, H.W. (2006) QTL for sugar content of stalk in sweet sorghum (*Sorghum bicolor* L. Moench). *Agri. Sci. China*, **5**, 736–744.

Bidinger, F.R., Serraj, R., Rizvi, S.M.H. *et al.* (2005) Field evaluation of drought tolerance QTL effects on phenotype and adaptation in pearl millet [*Pennisetum glaucum* (L.) R. Br.] topcross hybrids. *Field Crops Res.*, **94**, 14–32.

Billot, C., Rivallan, R., Sall, M.N. *et al.* (2012) A reference microsatellite kit to assess for genetic diversity of *Sorghum bicolor* (Poaceae). *Am. J. Bot.*, **99**, e245–260.

Billot, C., Ramu, P., Bouchet, S. *et al.* (2013) Massive sorghum collection genotyped with SSR markers to enhance use of global genetic resources. *PLoS ONE,* **8**, e59714, 16.

Binelli, G., Gianfranceschi, L., Pe, M. *et al.* (1992) Similarity of maize and sorghum genomes as revealed by maize RFLP probes. *Theor. Appl. Genet.*, **84**, 10–16.

Boivin, K., Deu, M., Rami, J.F. *et al.* (1999) Towards a saturated sorghum map using RFLP and AFLP markers. *Theor. Appl. Genet.*, **98**, 320–328.

Borrell, A.K., Mullet, J.E., George-Jaeggli, B. *et al.* (2014) Drought adaptation of stay-green sorghum is associated with canopy development, leaf anatomy, root growth, and water uptake. *J. Exp. Bot.*, **65**, 6251–6263.

Borrell, A.K., Oosterom, E.J., Mullet, J.E. *et al.* (2014) Stay-green alleles individually enhance grain yield in sorghum under drought by modifying canopy development and water uptake patterns. *New Phytol.*, **203**, 817–830.

Bouchet, S., Pot, D., Deu, M. *et al.* (2012) Genetic structure, linkage disequilibrium and signature of selection in sorghum: Lessons from physically anchored DArT markers. *PLoS ONE*, **7**, e33470, 15.

Bowers, J.E., Abbey, C., Anderson, S. *et al.* (2003) A high-density genetic recombination map of sequence-tagged sites for sorghum, as a framework for comparative structural and evolutionary genomics of tropical grains and grasses. *Genetics*, **165**, 367–386.

Breese, W.A., Hash, C.T., Devos, K.M. and Howarth, C.J. (2002) Pearl millet genomics – an overview with respect to breeding for resistance to downy mildew, in *Sorghum and Millets Diseases* (ed. J.F. Leslie), Iowa State Press, Ames, Iowa, USA, pp. 243–246.

Brown, S.M., Hopkins, M.S., Mitchell, S.E. *et al.* (1996) Multiple methods for the identification of polymorphic simple sequence repeats in sorghum [*Sorghum bicolor* (L.) Moench]. *Theor. Appl. Genet.*, **93**, 190–198.

Brown, P.J., Klein, P.E., Bortiri, E. *et al.* (2006) Inheritance of inflorescence architecture in sorghum. *Theor. Appl. Genet.*, **113**, 931–942.

Brown, P.J., Rooney, W.L., Franks, C. and Kresovich, S. (2008) Efficient mapping of plant height quantitative trait loci in a sorghum association population with introgressed dwarfing genes. *Genetics*, **180**, 629–637.

Budak, H., Pedraza, F., Cregan, P.B. *et al.* (2003) Development and utilization of SSRs to estimate the degree of genetic relationships in a collection of pearl millet germplasm. *Crop Sci.*, **43**, 2284–2290.

Burow, G., Burke, J.J., Xin, Z. and Franks, C.D. (2011) Genetic dissection of early-season cold tolerance in sorghum [*Sorghum bicolor* (L.) Moench]. *Mol. Breed.*, **28**, 391–402.

Busso, C.S., Devos, K.M., Ross, G. *et al.* (2000) Genetic diversity within and among landraces of pearl millet (*Pennisetum glaucum*) under farmer management in West Africa. *Genet. Resour. Crop Evol.*, **47**, 561–568.

Caddel, J.L. and Weibel, D.E. (1971) Effect of photoperiod and temperature on the development of sorghum. *Agron. J.*, **63**, 799–803.

Casa, A.M., Mitchell, S.E., Hamblin, M.T. *et al.* (2005) Diversity and selection in sorghum: simultaneous analyses using simple sequence repeats. *Theor. Appl. Genet.*, **111**, 23–30.

Casa, A.M., Pressoir, G., Brown, P.J. *et al.* (2008) Community resources and strategies for association mapping in sorghum. *Crop Sci.*, **48**, 30–40.

Chandra-Shekara, A.C., Prasanna, B.M., Bhat, S.R. and Singh, B.B. (2007) Genetic diversity analysis of elite pearl millet inbred lines using RAPD and SSR markers. *J. Plant Biochem. Biotech.*, **16** (1), 23–28.

Childs, K.L., Miller, F.R., Cordonnier-Pratt, M.M. *et al.* (1997) The sorghum photoperiod sensitive gene, Ma_3, encodes a phytochrome B. *Plant Physiol.*, **113**, 611–619.

Chittenden, L., Schertz, K., Lin, Y. *et al.* (1994) A detailed RFLP map of *Sorghum bicolor* × *S. propinquum*, suitable for high-density mapping, suggests ancestral duplication of sorghum chromosomes or chromosomal segments. *Theor. Appl. Genet.*, **87**, 925–933.

Cho, Y.I., Chung, J.W., Lee, G.A. *et al.* (2010) Development and characterization of twenty-five new polymorphic microsatellite markers in proso millet (*Panicum miliaceum* L.). *Genes & Genomics*, **32** (3), 267–273.

Chowdari, K.V., Davierwala, A.P., Gupta, V.S. *et al.* (1998) Genotype identification and assessment of genetic relationships in pearl millet [*Pennisetum glaucum* (L.) R. Br] using microsatellites and RAPDs. *Theor. Appl. Genet.*, **97**, 154–162.

Chowdari, K.V., Venkatachalam, S.R., Davierwala, A.P. *et al.* (1998) Hybrid performance and genetic distance as revealed by the $(GATA)_4$ microsatellite and RAPD markers in pearl millet. *Theor. Appl. Genet.*, **97**, 163–169.

Cisse, N.D. and Ejeta, G. (2003) Genetic variation and relationships among seedling vigor traits in sorghum. *Crop Sci.*, **43**, 824–828.

Coleman, O.H. and Dean, J.L. (1961) The inheritance of resistance to rust in sorgo. *Crop Sci.*, **1**, 152–154.

Dahlberg, J.A., Burke, J.J. and Rosenow, D.T. (2004) Development of sorghum core collection: Refinement and evaluation of a subset from Sudan. *Econ. Bot.*, **58**, 556–557.

Das, S., Mishra, R.C., Rout, G.R. and Aparajita, S. (2007) Genetic variability and relationships among thirty genotypes of finger millet [*Eleusine coracana* L. Gaertn.] using RAPD markers. *Z. Naturforsch.*, **62c**, 116–122.

Dass, S., Kapoor, R.L., Paroda, R.S. and Jatasra, D.S. (1984) Gene effects for downy mildew (*Sclerospora graminicola*) resistance in pearl millet. *Indian J. Genet.*, **44**, 280–285.

De Villiers, S.M., Michael, V.N., Manyasa, E.O. *et al.* (2015) Compilation of an informative microsatellite set for genetic characterisation of East African finger millet (*Eleusine coracana*). *Electronic J. Biotech.,* (10.1016/j.ejbt.2014.12.001) *Electronic J. Biotech.*, **18**(2), 77–82.

Deeming, J.C. (1972) A review of the taxonomy of African shoot flies of sorghum. *Samaru Res. Bull.*, **236**, 24.

Demuyakor, B., Galyuon, I., Kyereh, S. and Ahmed, M. (2013) Evaluation of agronomic performance of drought-tolerant QTL introgression hybrids of millet [*Pennisetum glaucum* (L.) R. Br.] in the Guinea Savannah zone of Ghana. *Int. J. Agric. Sci.*, **5** (1), 354–358.

Deswal, D.P. and Govila, O.P. (1994) Genetics of resistance to downy mildew (*Sclerospora graminicola*) in pearl millet (*Pennisetum glaucum*). *Indian J. Agric. Sci.*, **64**, 661–663.

Deu, M., Gonzalez-de-Leon, D., Glazsmann, J.C. *et al.* (1994) RFLP diversity in cultivated sorghum in relation to racial differentiation. *Theor. Appl. Genet.*, **88**, 838–844.

Deu, M., Ratnadass, A., Hamada, M.A. *et al.* (2005) Quantitative trait loci for head-bug resistance in sorghum. *Afr. J. Biotechnol.*, **4**, 247–250.

Deu, M., Rattunde, F. and Chantereau, J. (2006) A global view of genetic diversity in cultivated sorghums using core collection. *Genome*, **49**, 168–180.

Deu, M., Sagnard, F., Chantereau, J. *et al.* (2008) Niger- wide assessment of *in situ* sorghum genetic diversity with microsatellite markers. *Theor. Appl. Genet.*, **116**, 903–913.

Devos, K.M., Wang, Z.M., Beales, J. *et al.* (1998) Comparative genetic maps of foxtail millet (*Setaria italica*) and rice (*Oryza sativa*). *Theor. Appl. Genet.*, **96**, 63–68.

Devos, K.M., Pittaway, T.S., Reynolds, A. and Gale, M.D. (2000) Comparative mapping reveals a complex relationship between the pearl millet genome and those of foxtail millet and rice. *Theor. Appl. Genet.*, **100**, 190–198.

Diao. X.M. (2014) Genetic diversity and genome-wide association analysis of major characters of foxtail millet, an emerging model for the Panicoideae grasses and C_4 photosynthesis. XXII International Plant and Animal Genome Conference, January 11–15, 2014, San Diego, CA.

Dida, M.M., Srinivasachary, Ramakrishnan, S. *et al.* (2007) The genetic map of finger millet, *Eleusine coracana*. *Theor. Appl. Genet.*, **114**, 321–332.

Dida, M.M., Wanyera, N., Harrison Dunn, M.L. *et al.* (2008) Population structure and diversity in finger millet (*Eleusine coracana*) germplasm. *Trop. Plant Biol.*, **1** (2), 131–141.

Dong, Z., Zhao, H., He, J. *et al.* (2011) Overexpression of a foxtail millet Acetyl-CoA carboxylase gene in maize increases sethoxydim resistance and oil content. *Afr. J. Biotechnol.*, **10**, 3986–3995.

Doust, A.N., Devos, K.M., Gadberry, M.D. *et al.* (2004) Genetic control of branching in foxtail millet. *Proc. Natl. Acad. Sci. USA*, **101** (24), 9045–9050.

Doust, A.N., Devos, K.M., Gadberry, M.D. *et al.* (2005) The genetic basis for inflorescence variation between foxtail and green millet (Poaceae). *Genetics*, **169**, 1659–1672.

Doust, A.N. and Kellogg, E.A. (2006) Effect of genotype and environment on branching in weedy green millet (*Setaria viridis*) and domesticated foxtail millet (*Setaria italica*) (Poaceae). *Mol. Ecol.*, **15**, 1335–1349.

Downes, R.W. and Marshall, D.R. (1971) Low temperature induced male sterility in *Sorghum bicolor*. *Aust. J. Exp. Agric. Anim. Husb.*, **11**, 352–356.

Duan, Y., Qian, J., Sun, Y. *et al.* (2009) Construction of methylation linkage map based on MSAP and SSR markers in *Sorghum bicolor* (L.). *IUBMB Life*, **61**, 663–669.

Dufour, P., Deu, M., Grivet, L. *et al.* (1997) Construction of a composite sorghum genome map and comparison with sugarcane, a related complex polyploïd. *Theor. Appl. Genet.*, **94**, 409–418.

Erpelding, J.E. and Wang, M.L. (2007) Response to anthracnose infection for a random selection of sorghum germplasm. *Plant Pathol. J.*, **6**, 127–133.

Evans, J., McCormick, R.F., Morishige, D. *et al.* (2013) Extensive variation in the density and distribution of DNA polymorphism in sorghum genomes. *PLoS ONE,* **8**(11), e79192, 13.

Feltus, F.A., Hart, G.E., Schertz, K.F. *et al.* (2006) Alignment of genetic maps and QTL between inter-and intra-specific sorghum populations. *Theor. Appl. Genet.*, **112**, 1295–1305.

Fernandez, M.G.S., Hamblin, M.T., Li, L. *et al.* (2008) Quantitative trait loci analysis of endosperm color and carotenoid content in sorghum grain. *Crop Sci.*, **48**, 1732–1743.

Frederiksen, R. and Rosenow, D. (1986) Controlling sorghum diseases, in *Compendium of Sorghum Diseases* (ed. R.A. Frederiksen), American Phytopathological Society in cooperation with Dept. of Plant Pathology and Microbiology, Texas A&M University, pp. 65–67.

Fukunaga, K. and Kato, K. (2002) Mitochondrial DNA variation in foxtail millet. *Setaria italica (L.) P. Beauv. Euphytica*, **129**, 7–13.

Fukunaga, K., Kawase, M. and Kato, K. (2002) Structural variation in the Waxy gene and differentiation in foxtail millet [*Setaria italica* (L.) P. Beauv.]: implications for multiple origins of the waxy phenotype. *Mol. Genet. Genomics*, **268** (2), 214–222.

Gamar, Y.A. and Mohamed, A.H. (2013) Introgression of Striga resistance genes into a Sudanese sorghum cultivar, Tabat, using marker assisted selection (MAS). *Greener J. Agric. Sci.*, **3** (7), 550–556.

Ganapathy, K.N., Gomashe, S.S., Rakshit, S. *et al.* (2012) Genetic diversity revealed utility of SSR markers in classifying parental lines and elite genotypes of sorghum (*Sorghum bicolor* L. Moench). *Aust. J. Crop Sci.*, **6**, 1486–1493.

Garud, T.B. and Borikar, S.T. (1985) Genetics of charcoal rot resistance in sorghum. *Sorghum Newsl.*, **28**, 87.

Geleta, N., Labuschangne, M.T., Chris, D. and Viljoen, C.D. (2006) Genetic diversity analysis in sorghum germplasm as estimated by AFLP, SSR and morpho-agronomical markers. *Biodivers. Conserv.*, **15**, 3251–3265.

Generation Challenge Program Project Abstracts (2008) Generation Challenge Program: Cultivating plant diversity for the resource poor. *Abstract.,* pp. 47–50 and 64–66.

Gepts, P. and Clegg, M.T. (1989) Genetic diversity in pearl millet [*Pennisetum glaucum* (L.) R. Br.] at the DNA sequence level. *J. Hered.*, **80**, 203–208.

Ghebru, B., Schmidt, R.J. and Bennetzen, J.L. (2002) Genetic diversity of Eritrean sorghum landraces assessed with simple sequence repeat (SSR) markers. *Theor. Appl. Genet.*, **105**, 229–236.

Girma, Y. (2009) Mining genomic resources for SNP and SNP-CAPS markers and divergence for drought tolerance in sorghum [*Sorghum bicolor* (L.) Moench]. M.Sc. (Ag) Thesis submitted to the University of Agricultural Sciences, Dharwad, India.

Glaszmann, J.C., Kilian, B., Upadhyaya, H.D. and Varshney, R.K. (2010) Accessing genetic diversity for crop improvement. *Curr. Opin. Plant Biol.*, **13**, 167–173.

Govindaraj, M., Selvi, B., Arun Prabhu, D. and Rajarathinam, S. (2009) Genetic diversity analysis of pearl millet [*Pennisetum glaucum* (L.) R. Br.] accessions using molecular markers. *Afr. J. Biotechnol.*, **8** (22), 6046–6052.

Grenier, C., Bramel-Cox, P.J., Noirot, M. *et al.* (2000) Assessment of genetic diversity in three subsets constituted from the ICRISAT sorghum collection using random vs. non-random sampling procedures. A. Using morpho-agronomical and passport data. *Theor. Appl. Genet.*, **101**, 190–196.

Grenier, C., Hamon, P. and Bramel-Cox, P.J. (2001a) Core collection of sorghum: I. Stratification based on eco- geographical data. *Crop Sci.*, **41**, 234–240.

Grenier, C., Hamon, P. and Bramel-Cox, P.J. (2001b) Core collection of sorghum: II. *Comparison of three random sampling strategies. Crop Sci.*, **41**, 241–246.

Grewal, R.P.S. (1988) Genetic basis of resistance to zonate leaf spot disease in forage sorghum. *Theor. Appl. Genet.*, **76**, 550–554.

Guan, Y.A., Wang, H.L., Qin, L. *et al.* (2011) QTL mapping of bio-energy related traits in sorghum. *Euphytica*, **182**, 431–440.

Gupta, S., Kumari, K., Das, J. *et al.* (2011) Development and utilization of novel intron length polymorphic markers in foxtail millet [*Setaria italica* (L.) P. Beauv.]. *Genome*, **54**, 586–602.

Gupta, S., Kumari, K., Sahu, P.P. *et al.* (2012) Sequence based novel genomic microsatellite markers for robust genotyping purposes in foxtail millet [*Setaria italica* (L.) P. Beauv.]. *Plant Cell Rep.*, **31**, 323–337.

Gupta, S., Kumari, K., Muthamilarasan, M. *et al.* (2013) Development and utilization of novel SSRs in foxtail millet [*Setaria italica* (L.) P. Beauv.]. *Plant Breed.*, **132**, 367–374.

Gupta, S., Kumari, K., Muthamilarasan, M. *et al.* (2014) Population structure and association mapping of yield contributing agronomic traits in foxtail millet. *Plant Cell Rep.*, **33**, 881–893.

Halalli, M., Gowda, B., Kulkarni, K. and Goud, J. (1983) Evaluation of advanced generation progenies for resistance to shootfly in sorghum. *Indian J. Genet.*, **43**, 291–293.

Hart, G.E., Schertz, K.F., Peng, Y. and Syed, N.H. (2001) Genetic mapping of *Sorghum bicolor* (L.) Moench QTL that control variation in tillering and other morphological characters. *Theor. Appl. Genet.*, **103**, 1232–1242.

Harvey, T., Seifers, D. and Kofoid, K. (1996) Effect of sorghum hybrid and imidacloprid seed treatment on infestations by corn leaf aphid and greenbug (Homoptera: Aphididae) and the spread of sugarcane mosaic virus strain MDMV-B. *J. Agric. Entomol.*, **13**, 9–15.

Hash, C.T., Singh, S.D., Thakur, R.P. and Talukdar, B.S. (1999) Breeding for disease resistance, in *Pearl Millet Breeding* (eds I.S. Khairwal, K.N. Rai, D.J. Andrews and G. Harinarayana), Oxford & IBH, New Delhi, India, pp. 337–379.

Hash, C.T. and Witcombe, J.R. (2001) Pearl millet molecular marker research. *Int. Sorgh. Millets Newslett.*, **42**, 8–15.

Hash, C.T. and Witcombe, J.R. (2002) Gene management and breeding for downy mildew resistance, in *Sorghum and Millets Diseases* (ed. J.E. Leslie), Iowa State Press, Ames, Iowa, USA, pp. 27–36.

Hash, C.T., Sharma, A., Kolesnikova-Allen, M.A. *et al.* (2003) Marker-assisted breeding to improve pearl millet hybrid HHB 67: Lab to field, in Abstracts and Final Program, In the Wake of the Double Helix: From the Green Revolution to the Gene Revolution, May 27–31, 2003, Bologna, Italy.

Hash, C.T., Sharma, A., Kolesnikova-Allen, M.A. *et al.* (2006) Teamwork delivers biotechnology products to Indian small-holder crop-livestock producers: Pearl millet hybrid "HHB 67 Improved" enters seed delivery pipeline. *SAT eJournal*, **2** (1), 1–3.

Haussmann, B.I.G., Hess, D.E., Omanya, G.O. *et al.* (2004) Genomic regions influencing resistance to the parasitic weed *Striga hermonthica* in two recombinant inbred populations of sorghum. *Theor. Appl. Genet.*, **109**, 1005–1016.

Heng, L., Chih, C., Song, C. and Chang, K. (2011) Development of simple sequence repeats (SSR) markers in *Setaria italica* (Poaceae) and cross-amplification in related species. *Int. J. Mol. Sci.*, **12**, 7835–7845.

Henzell, R., Franzmann, B. and Brengman, R. (1994) Sorghum midge resistance research in Australia. Sorghum Improvement Conference of North America, USA; University of Georgia, USA; International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh, India.

Hesketh, J., Chase, S. and Nanda, D. (1969) Environmental and genetic modification of leaf number in maize, sorghum, and Hungarian millet. *Crop Sci.*, **9**, 460–463.

Hilu, K.W. (1994) Evidence from RAPD markers in the evolution of *Echinochloa* millets (Poaceae). *Plant Syst. Evol.*, **189**, 247–257.

Hilu, K.W. (1995) Evolution of finger millet: evidence from random amplified polymorphic DNA. *Genome*, **38** (2), 232–238.

Hirano, R., Naito, K., Fukunaga, K. *et al.* (2011) Genetic structure of landraces in foxtail millet [*Setaria italica* (L.) Beauv.] revealed with transposon display and interpretation to crop evolution of foxtail millet. *Genome*, **54** (6), 498–506.

Hu, X., Wang, J., Lu, P. and Zhang, H. (2009) Assessment of genetic diversity in broomcorn millet (*Panicum miliaceum* L.) using SSR markers. *J. Genet. Genomics*, **36** (8), 491–500.

Hulbert, S.H., Richter, T.E., Axtell, J.D. and Bennetzen, J.L. (1990) Genetic mapping and characterization of sorghum and related crops by means of maize DNA probes. *Proc Natl Acad Sci USA*, **87**, 4251–4255.

Hunt, H.V., Campana, M.G., Lawes, M.C. *et al.* (2011) Genetic diversity and phylogeography of broomcorn millet (*Panicum miliaceum* L.) across Eurasia. *Mol. Ecol.*, **20**, 4756–4771.

Indira, S., Rana, B. and Rao, N. (1983) Genetics of host plant resistance to charcoal rot in sorghum. *Indian J. Genet.*, **43**, 472–477.

Jaikishan, I., Paik, G.R., Madhusudhana, R. *et al.* (2013) Development of microsatellite markers targeting $(GATA)_n$ motifs in sorghum [*Sorghum bicolor* (L.) Moench]. *Mol. Breed.*, **31**, 223–231.

Jaikishan, I., Rajendrakumar, P., Madhusudhana, R. *et al.* (2014) *In silico* identification of potential introns and development of PCR-based markers targeting intron length polymorphism in sorghum [*Sorghum bicolor* (L.) Moench), in *Abstracts* (eds M. Khetmalas, A. Pandey, P. Gunasekaran *et al.*), International Conference on Advances in Biotechnology and Bioinformatics ICABB 2013 and X Convention of the Biotech Research Society, India, p. C11.

Jia, X.P., Shi, Y.S., Song, Y.C. *et al.* (2007) Development of EST-SSR in foxtail millet (*Setaria italica*). *Genet. Resour. Crop Evol.*, **54**, 233–236.

Jia, X., Yuan, J., Shi, Y. *et al.* (2007) A ser-Gly substitution in plastid-encoded photosystem II D1 protein is responsible for atrazine resistance in foxtail millet (*Setaria italica*). *Plant Growth Regul.*, **52**, 81–89.

Jia, X.P., Zhang, Z.B., Liu, Y.H. *et al.* (2009) Development and genetic mapping of SSR markers in foxtail millet [*Setaria italica* (L.) Beauv.]. *Theor. Appl. Genet.*, **118** (4), 821–829.

Jia, X.P., Tan, X.J., Li, Y.X. *et al.* (2009) A study on the genetic diversity of foxtail millet cultivars by SSR markers. *Acta Agriculturae Universitatis Jiangxiensis*, **31** (4), 633–638.

Jia, G., Shi, S., Wang, C. *et al.* (2013) Molecular diversity and population structure of Chinese green foxtail [*Setaria viridis* (L.) Beauv.] revealed by microsatellite analysis. *J. Exp. Bot.*, **64**, 3645–3656.

Jia, G., Huang, X., Zhi, H. *et al.* (2013) A haplotype map of genomic variations and genome-wide association studies of agronomic traits in foxtail millet (*Setaria italica*). *Nat. Genet.*, **45**, 957–961.

Jones, E.S., Liu, C.J., Gale, M.D. *et al.* (1995) Mapping quantitative trait loci for downy mildew resistance in pearl millet. *Theor. Appl. Genet.*, **91**, 448–456.

Jones, E.S., Breese, W.A., Liu, C.J. *et al.* (2002) Mapping quantitative trait loci for resistance to downy mildew in pearl millet: Field and glasshouse screens detect the same QTL. *Crop Sci.*, **42**, 1316–1323.

Jordan, D., Hunt, C., Cruickshank, A. *et al.* (2012) The relationship between the stay-green trait and grain yield in elite sorghum hybrids grown in a range of environments. *Crop Sci.*, **52**, 1153–1161.

Jusuf, M. and Pernes, J. (1985) Genetic variability of foxtail millet (*Setaria italica* (L.) P. Beauv): Electrophoretic study of five isoenzyme systems. *Theor. Appl. Genet.*, **71**, 385–391.

Kalyana Babu, B., Senthil, N., Michael Gomez, S. *et al.* (2007) Assessment of genetic diversity among finger millet [*Eleusine coracana* (L.) Gaertn.] accessions using molecular markers. *Genet. Resour. Crop Evol.*, **54**, 399–404.

Kalyana Babu, B., Pandey, D., Agrawal, P.K. *et al.* (2014a) *In-silico* mining, type and frequency analysis of genic microsatellites of finger millet (*Eleusine coracana* (L.) Gaertn.): A comparative genomic analysis of NBS-LRR regions of finger millet with rice. *Mol. Biol. Rep.*, **41**, 3081–3090.

Kalyana Babu, B., Pandey, D., Agrawal, P.K. *et al.* (2014b) Comparative genomics and association mapping approaches for blast resistant genes in finger millet using SSRs. *PLoS ONE* **9**(6), e99182, 12.

Kalyana Babu, B., Agrawal, P.K., Pandey, D. *et al.* (2014c) Association mapping of agro-morphological characters among the global collection of finger millet genotypes using genomic SSR markers. *Mol Biol Rep* **41**, 5287–5297.

Kannan, B., Senthilvel, S., Raj, A.G.B. *et al.* (2014) Association analysis of SSR markers with phenology, grain, and stover-yield related traits in pearl millet [*Pennisetum glaucum* (L.) R. Br.]. *Scientific World J.,* **2014** (10.1155/2014/562327).

Karad, S.R., Patil, J.V. and Kale, A.A. (2013) Study of genetic diversity in finger millet (*Elesuine coracana* L.) genotypes using RAPD markers. *Int. J. Int Sci. Inn. Tech. Sec. A*, **2** (4), 31–36.

Karam, D., Westra, P., Nissen, S.J. *et al.* (2004) Genetic diversity among Proso millet (*Panicum miliaceum*) biotypes assessed by AFLP technique. *Planta Daninha, Viçosa-MG*, **22** (2), 167–174.

Karam, D., Westra, P., Niessen, S.J. *et al.* (2006) Assessment of silver-stained AFLP markers for studying DNA polymorphism in proso millet (*Panicum miliaceum* L.). *Rev. Bras. Bot.*, **29** (4), 609–615.

Kassahun, B., Bidinger, F., Hash, C. and Kuruvinashetti, M. (2010) Stay-green expression in early generation sorghum [*Sorghum bicolor* (L.) Moench] QTL introgression lines. *Euphytica*, **172**, 351–362.

Katsar, C.S., Paterson, A.H., Teetes, G.L. and Peterson, G.C. (2002) Molecular analysis of sorghum resistance to the greenbug (Homoptera: Aphididae). *J. Econ. Entomol.*, **95**, 448–457.

Kebede, H., Subudhi, P.K., Rosenow, D.T. and Nguyen, H.T. (2001) Quantitative trait loci influencing drought tolerance in grain sorghum (*Sorghum bicolor* L. Moench). *Theor. Appl. Genet.*, **103**, 266–276.

Kim, J. (2003) Genomic analysis of sorghum by fluorescence in situ hybridization, in *Ph.D. thesis*, Texas A&M University, TX.

Kim, E.J., Sa, K.J., Park, K.C. and Lee, J.K. (2012) Study of genetic diversity and relationships among accessions of foxtail millet [Setaria italica (L.) P. Beauv.] in Korea, China, and Pakistan using SSR markers. *Genes & Genom.*, **34** (5), 529–538.

Klein, R., Rodriguez-Herrera, R., Schlueter, J. *et al.* (2001) Identification of genomic regions that affect grain-mould incidence and other traits of agronomic importance in sorghum. *Theor. Appl. Genet.*, **102**, 307–319.

Klein, R.R., Mullet, J.E., Jordan, D.R. *et al.* (2008) The effect of tropical sorghum conversion and inbred development on genome diversity as revealed by high-resolution genotyping. *Crop Sci.,* **48** (Supplement), S12–S26.

Knoll, J. and Ejeta, G. (2008) Marker-assisted selection for early-season cold tolerance in sorghum: QTL validation across populations and environments. *Theor. Appl. Genet.*, **116**, 541–553.

Knoll, J., Gunaratna, N. and Ejeta, G. (2008) QTL analysis of early-season cold tolerance in sorghum. *Theor. Appl. Genet.*, **116**, 577–587.

Kong, L., Dong, J. and Hart, G. (2000) Characteristics, linkage-map positions, and allelic differentiation of *Sorghum bicolor* (L.) Moench DNA simple-sequence repeats (SSRs). *Theor. Appl. Genet.*, **101**, 438–448.

Kong, W., Jin, H., Franks, C.D. *et al.* (2013) Genetic analysis of recombinant inbred lines for *Sorghum bicolor* × *Sorghum propinquum*, in *G3 (Bethesda)*, **3** (1), 101–108.

Kumar, A., Arya, L., Kumar, V. and Sharma, S. (2006) Inter-simple sequence repeat (ISSR) analysis of cytoplasmic male sterile, male fertile lines and hybrids of pearl millet [*Pennisetum glaucum* (L.) R.Br.]. *Indian J. Crop Sci.*, **1** (1–2), 117–119.

Kumar, A., Mirza, N., Charan, T. *et al.* (2014) Isolation, characterization and immunolocalization of a seed dominant CaM from finger millet (*Eleusine coracana* L. Gartn.) for studying its functional role in differential accumulation of calcium in developing grains. *Appl. Biochem. Biotechnol.*, **172**, 2955–2973.

Kumari, K., Muthamilarasan, M., Misra, G. *et al.* (2013) Development of eSSR-markers in *Setaria italica* and their applicability in studying genetic diversity, cross-transferability and comparative mapping in millet and non-millet species. *PLoS ONE,* **8**, e67742, 15.

Kushwaha, H., Jillo, K.W., Singh, V.K. *et al.* (2015) Assessment of genetic diversity among cereals and millets based on PCR amplification using Dof (DNA binding with One Finger) transcription factor gene-specific primers. *Plant Syst. Evol.*, **301**, 833–840.

Lata, C., Sahu, P.P. and Prasad, M. (2010) Comparative transcriptome analysis of differentially expressed genes in foxtail millet (*Setaria italica* L.) during dehydration stress. *Biochem. Biophy. Res. Commun.*, **393**, 720–727.

Lata, C., Bhutty, S., Bahadur, R.P. *et al.* (2011) Association of an SNP in a novel DREB2-like gene *SiDREB2* with stress tolerance in foxtail millet [*Setaria italica* (L.)]. *J. Exp. Bot.*, **62**, 3387–3401.

Lata, C., Jha, S., Dixit, V. *et al.* (2011) Differential antioxidative responses to dehydration-induced oxidative stress in core set of foxtail millet cultivars [*Setaria italica* (L.)]. *Protoplasma*, **248**, 817–828.

Lata, C. and Prasad, M. (2012) Validation of an allele-specific marker associated with dehydration stress tolerance in a core set of foxtail millet accessions. *Plant Breed.,* **132** (5), 496–499.

Le Thierry d'Ennequin, M., Panaud, O., Toupance, B. and Sarr, A. (2000) Assessment of genetic relationships between *Setaria italica* and its wild relative *S. viridis* using AFLP markers. *Theor. Appl. Genet.*, **100**, 1061–1066.

Li, Y. and Wu, S.Z. (1996) Traditional maintenance and multiplication of foxtail millet (*Setaria italica* (L) P. Beauv.) landraces in China. *Euphytica*, **87**, 33–38.

Li, Y., Jia, J., Wang, Y. and Wu, S. (1998) Intraspecific and interspecific variation in *Setaria* revealed by RAPD analysis. *Genetic Resour. Crop Evol.*, **45**, 279–285.

Li, M., Yuyama, N., Luo, L. *et al.* (2009) *In silico* mapping of 1758 new SSR markers developed from public genomic sequences for sorghum. *Mol. Breed.*, **24**, 41–47.

Lin, Y.R., Schertz, K.F. and Paterson, A.H. (1995) Comparative analysis of QTL affecting plant height and maturity across the Poaceae, in reference to an interspecific sorghum population. *Genetics*, **141**, 391–411.

Lin, H.S., Chiang, C.Y., Chang, S.B. *et al.* (2012) Genetic diversity in the foxtail millet (*Setaria italica*) germplasm as determined by agronomic traits and microsatellite markers. *Aust. J. Crop Sci.*, **6** (2), 342–349.

Little, C.R., Perumal, R., Tesso, T. *et al.* (2012) Sorghum pathology and biotechnology – A fungal disease perspective: Part I. Grain mold, head smut, and ergot. *Eur. J. Plant Sci. Biotechnol.*, **6**, 10–30.

Liu, C.J., Witcombe, J.R., Pittaway, T.S. *et al.* (1994) An RFLP-based genetic map of pearl millet (*Pennisetum glaucum*). *Theor. Appl. Genet.*, **89**, 481–487.

Liu, Y., Feng, X., Xu, Y. *et al.* (2009) Overexpression of millet ZIP-like gene (*SiPf40*) affects lateral bud outgrowth in tobacco and millet. *Plant Physiol. Biochem.*, **47**, 1051–1060.

Liu, Z.L., Bai, G.H., Zhang, D.D. *et al.* (2011) Genetic diversity and population structure of elite foxtail millet [*Setaria italica* (L.) Beauv.] germplasm in China. *Crop Sci.*, **51** (4), 1655–1663.

Liu, L., Wu, Y., Wang, Y. and Samuels, T. (2012) A high-density simple sequence repeat-based genetic linkage map of switchgrass. *G3 (Bethesda)*, **2** (3), 357–370.

Liu, Z., Zhang, T., Li, C. and Bai, G.H. (2014) Genetic diversity and classification of cytoplasm of Chinese elite foxtail millet [*Setaria italica* (L.) P. Beauv.] germplasm. *Crop Sci.*, **54**, 659–666.

Mace, E.S., Xia, L., Jordan, D.R. *et al.* (2008) DArT markers: diversity analyses and mapping in *Sorghum bicolor*. *BMC Genomics*, **9**, 26.

Mace, E.S., Rami, J.F., Bouchet, S. *et al.* (2009) A consensus genetic map of sorghum that integrates multiple component maps and high-throughput Diversity Array Technology (DArT) markers. *BMC Plant Biol.*, **9**, 13.

Mace, E.S. and Jordan, D.R. (2010) Location of major effect genes in sorghum (*Sorghum bicolor* (L.) Moench). *Theor. Appl. Genet.*, **121**, 1339–1356.

Mace, E.S. and Jordan, D.R. (2011) Integrating sorghum whole genome sequence information with a compendium of sorghum QTL studies reveals uneven distribution of QTL and of gene-rich regions with significant implications for crop improvement. *Theor. Appl. Genet.*, **123**, 169–191.

Mace, E.S., Singh, V., Van Oosterom, E.J. *et al.* (2012) QTL for nodal root angle in sorghum (*Sorghum bicolor* L. Moench) co-locate with QTL for traits associated with drought adaptation. *Theor. Appl. Genet.*, **124**, 97–109.

Mace, E.S., Tai, S., Gilding, E.K. *et al.* (2013) Whole-genome sequencing reveals untapped genetic potential in Africa's indigenous cereal crop sorghum. *Nat. Commun.*, **4**, 2320.

Madhusudhana, R., Balakrishna, D., Rajendrakumar, P. *et al.* (2012) Molecular characterization and assessment of genetic diversity of sorghum inbred lines. *Afr. J. Biotechnol.*, **11**, 15626–15635.

Manivannan, A., Nimbal, S. and Chhabra, A.K. (2013) Peroxidase isozyme characterization of elite genotypes of pearl millet [*Pennisetum glaucum* (L.) R. Br.]. *Afr. J. Agric. Res.*, **8** (28), 3662–3667.

Manyasa, E.O., Tongoona, P., Shanahan, P. *et al.* (2014) Genetic diversity in East African finger millet (*Eleusine coracana* L. Gaertn) landraces based on SSR markers and some qualitative traits. *Plant Genet. Resour.*, **13** (1), 45–55.

Mariac, C., Luong, V., Kapran, I. *et al.* (2006) Diversity of wild and cultivated pearl millet accessions (*Pennisetum glaucum* [L.] R. Br.) in Niger assessed by microsatellite markers. *Theor. Appl. Genet.*, **114**, 49–58.

Mauro-Herrera, M., Wang, X., Barbier, H. *et al.* (2013) Genetic control and comparative genomic analysis of flowering time in *Setaria* (Poaceae). *G3*, **3**, 283–295.

McIntyre, C.L., Casu, R., Drenth, J. *et al.* (2005) Resistance gene analogues in sugarcane and sorghum and their association with quantitative trait loci for rust resistance. *Genome*, **48**, 391–400.

Menkir, A., Golsbrough, P. and Ejeta, G. (1997) RAPD-based assessment of genetic diversity in cultivated races of sorghum. *Crop Sci.*, **37**, 564–569.

Menz, M., Klein, R., Mullet, J. *et al.* (2002) A high-density genetic map of *Sorghum bicolor* (L.) Moench based on 2926 AFLP®, RFLP and SSR markers. *Plant Mol. Biol.*, **48**, 483–499.

Miller, F.R. and Cruzado, H.J. (1969) Allelic interactions at the Pu locus in *Sorghum bicolor* (L.) Moench. *Crop Sci.*, **9**, 336–338.

Mishra, A.K., Puranik, S., Bahadur, R.P. and Prasad, M. (2012) The DNA binding activity of an AP2 protein is involved in transcriptional regulation of a stress-responsive gene, *SiWD40*, in foxtail millet. *Genomics*, **100** (4), 252–263.

Mohamed, A., Ali, R., Elhassan, O. *et al.* (2014) First products of DNA marker-assisted selection in sorghum released for cultivation by farmers in sub-Saharan Africa. *J. Plant Sci. Mol. Breed.*, **3**, 2050–2389.

Morgan, R.N., Wilson, J.P., Hanna, W.W. and Ozais-Akins, P. (1998) Molecular markers for rust and pyricularia leaf spot disease resistance in pearl millet. *Theor. Appl. Genet.*, **96**, 413–420.

Morris, G.P., Ramu, P., Deshpande, S.P. *et al.* (2013) Population genomic and genome-wide association studies of agroclimatic traits in sorghum. *Proc Natl Acad Sci USA*, **110**, 453–458.

M'Ribu, H.K. and Hilu, K.W. (1996) Application of random amplified polymorphic DNA to study genetic diversity in *Paspalum scrobiculatum* L. (Kodo millet, Poaceae). *Genet. Resour. Crop Evol.*, **43** (3), 203–210.

Murali Mohan, S., Madhusudhana, R., Mathur, K. *et al.* (2009) Co-localization of quantitative trait loci for foliar disease resistance in sorghum. *Plant Breed.*, **128**, 532–535.

Murali Mohan, S., Madhusudhana, R., Mathur, K. *et al.* (2010) Identification of quantitative trait loci associated with resistance to foliar diseases in sorghum [*Sorghum bicolor* (L.) Moench]. *Euphytica*, **176**, 199–211.

Murray, S.C., Sharma, A., Rooney, W.L. *et al.* (2008) Genetic improvement of sorghum as a biofuel feedstock: I. QTL for stem sugar and grain nonstructural carbohydrates. *Crop Sci.*, **48**, 2165–2179.

Musia, G.D. (2013) Identification of microsatellite markers for finger millet (*Eleusine coracana*) by analysis of Roche 454 GS-FLX Titanium sequence data, in *M.Sc. Thesis*, School of Pure and Applied Sciences, Kenyatta University, Nairobi.

Mutegi, E., Sagnard, F., Semagn, K. *et al.* (2011) Genetic structure and relationships within and between cultivated and wild sorghum [*Sorghum bicolor* (L.) Moench] in Kenya as revealed by microsatellite markers. *Theor. Appl. Genet.*, **122**, 989–1004.

Muth, P., Elhassan, O., Mohammed, A. *et al.* (2012) Effect of marker-assisted backcrossing to introgress resistance to Striga hermonthica into African sorghum varieties. Conference on "Resilience of agricultural systems against crises", Tropentag, September 19–21, 2012, Gottingen-Kassel/Witzenhausen.

Muthamilarasan, M., Venkata Suresh, B., Pandey, G. *et al.* (2013) Development of 5123 intron-length polymorphic markers for large-scale genotyping applications in foxtail millet. *DNA Res.*, **21**, 41–52.

Muza, F.R., Lee, D.J., Andrews, D.J. and Gupta, S.C. (1995) Mitochondrial variation in finger millet (*Eleusine coracana Gaertn.*). *Euphytica*, **81** (2), 199–205.

Nagaraj, N., Reese, J.C., Tuinstra, M.R. *et al.* (2005) Molecular mapping of sorghum genes expressing tolerance to damage by greenbug (Homoptera: Aphididae). *J. Econ. Entomol.*, **98**, 595–602.

Nagaraja Reddy, R., Madhusudhana, R., Mohan, S.M. *et al.* (2012) Characterization, development and mapping of Unigene-derived microsatellite markers in sorghum [*Sorghum bicolor* (L.) Moench]. *Mol. Breed.*, **29**, 543–564.

Nagaraja Reddy, R., Madhusudhana, R., Murali Mohan, S. *et al.* (2013) Mapping QTL for grain yield and other agronomic traits in post-rainy sorghum [*Sorghum bicolor* (L.) Moench]. *Theor. Appl. Genet.*, **126**, 1921–1939.

Nagaraja Reddy, R.R., Madhusudhana, R., Murali Mohan, S. *et al.* (2014) Detection and validation of stay-green QTL in post-rainy sorghum involving widely adapted cultivar, M35-1 and a popular stay-green genotype B35. *BMC Genomics*, **15** (1), 909.

Nakayama, Y., Umemoto, S. and Yamaguchi, H. (1999) Identification of polyploidy groups in the genus *Echinochloa* by isozyme analysis. *J. Weed Sci. Technol.*, **44**, 205–217.

Nelson, J.C., Wang, S., Wu, Y. *et al.* (2011) Single nucleotide polymorphism discovery by high-throughput sequencing in sorghum. *BMC Genomics*, **12**, 352.

Nethra, N., Gowda, R., Rajendra Prasad, S. *et al.* (2014) Utilization of SSRs to estimate the degree of genetic relationships in finger millet (*Eleusine coracana* L. Gaertn.) genotypes and subspecies. *SABRAO J. Breed. Genet.*, **46** (1), 136–149.

Ngugi, K., Kimani, W., Kiambi, D. and Mutitu, E.W. (2013) Improving drought tolerance in *Sorghum bicolor* L. Moench: Marker-assisted transfer of the stay-green quantitative trait loci (QTL) from a characterized donor source into a local farmer variety. *Int. J. Scientific Res. Knowledge*, **1** (6), 154–162.

Nirgude, M., Babu, B.K., Shambhavi, Y. *et al.* (2014) Development and molecular characterization of genic molecular markers for grain protein and calcium content in finger millet (*Eleusine coracana* (L.) Gaertn.). *Mol. Biol. Rep.*, **41**, 1189–1200.

Nozawa, S., Takahashi, M., Nakai, H. and Sato, Y.I. (2006) Difference in SSR variations between Japanese barnyard millet (*Echinochloa esculenta*) and its wild relative *E. crusgalli*. *Breed. Sci.*, **56**, 335–340.

Osama, K.S. (2013) Marker assisted introgression of Striga resistance into farmer preferred sorghum variety (Ochuti), in M.Sc. Thesis, College of Agriculture and Veterinary Sciences, University of Nairobi.

Pandey, G., Misra, G., Kumari, K. *et al.* (2013) Genome-wide development and use of microsatellite markers for large-scale genotyping applications in foxtail millet [*Setaria italica* (L.)]. *DNA Res.*, **20**, 197–207.

Panwar, P., Nath, M., Yadav, V.K. and Kumar, A. (2010) Comparative evaluation of genetic diversity using RAPD, SSR and ctyochrome P450 gene based markers with respect to calcium content in finger millet (*Eleusine coracana* Gaertn.). *J. Genet.*, **89** (2), 121–133.

Panwar, P., Saini, R.K., Sharma, N. *et al.* (2010) Efficacy of RAPD, SSR and Cytochrome P450 gene based markers in accessing genetic variability amongst finger millet (*Eleusine coracana*) accessions. *Mol. Biol. Rep.*, **37** (8), 4075–4082.

Parani, M., Rajesh, K., Lakshmi, M. *et al.* (2001) Species identification in seven small millet species using polymerase chain reaction-restriction fragment length polymorphism of trnS-psbC gene region. *Genome*, **44**, 495–499.

Parh, D.K., Jordan, D.R., Aitken, E.A.B. *et al.* (2008) QTL analysis of ergot resistance in sorghum. *Theor. Appl. Genet.*, **117**, 369–382.

Parvathaneni, R.K., Jakkula, V., Padi, F.K. *et al.* (2013) Fine-mapping and identification of a candidate gene underlying the d_2 dwarfing phenotype in pearl millet, *Cenchrus americanus* (L.) Morrone. *Genes Genomes Genetics*, **3**, 563–572.

Paterson, A.H., Bowers, J.E., Bruggmann, R. *et al.* (2009) The *Sorghum bicolor* genome and the diversification of grasses. *Nature*, **457**, 551–556.

Patil, A., Fakrudin, B., Salimath, P.M. and Rajkumar (2012) Genome-wide molecular mapping and QTL analysis, validated across locations and years for charcoal rot disease incidence traits in *Sorghum bicolor* (L.) Moench. *Indian J. Genet.*, **72**, 296–302.

Patil-Kulkarni, B.G., Puttarudrappa, A., Kajjari, N.B. and Goud, J.V. (1972) Breeding for rust resistance in sorghum. *Indian Phytopathol.*, **25**, 166–168.

Pedraza-Garcia, F., Specht, J.E. and Dweikat, I. (2010) A new PCR-based linkage map in pearl millet. *Crop Sci.*, **50**, 1754–1760.

Peng, Y., Schertz, K., Cartinhour, S. and Hart, G. (1999) Comparative genome mapping of *Sorghum bicolor* (L.) Moench using an RFLP map constructed in a population of recombinant inbred lines. *Plant Breed.*, **118**, 225–235.

Peng, Y., Zhang, J., Cao, G. *et al.* (2010) Overexpression of a *PLDa1* gene from *Setaria italica* enhances the sensitivity of *Arabidopsis* to abscisic acid and improves its drought tolerance. *Plant Cell Rep.*, **29**, 793–802.

Pereira, M., Lee, M., Bramel-Cox, P. *et al.* (1994) Construction of an RFLP map in sorghum and comparative mapping in maize. *Genome*, **37**, 236–243.

Pereira, M.G. and Lee, M. (1995) Identification of genomic regions affecting plant height in sorghum and maize. *Theor. Appl. Genet.*, **90**, 380–388.

Pereira, M.G., Ahnert, D., Lee, M. and Klier, K. (1995) Genetic mapping of quantitative trait loci for panicle characteristics and seed weight in sorghum. *Rev. Brasil Genet.*, **18**, 249–257.

Poncet, V., Lamy, F., Devos, K.M. *et al.* (2000) Genetic control of domestication traits in pearl millet (*Pennisetum glaucum* L., Poaceae). *Theor. Appl. Genet.*, **100**, 147–159.

Poncet, V., Martel, E., Allouis, S. *et al.* (2002) Comparative analysis of QTL affecting domestication traits, between two domesticated × wild pearl millet (*Pennisetum glaucum* L., Poaceae) crosses. *Theor. Appl. Genet.*, **104**, 965–975.

Prabha, D., Negi, Y.K. and Khanna, V.K. (2012) Assessment of genetic diversity of barnyard millet accessions using molecular markers. *Indian J. Plant Genet. Resour.*, **25** (2), 174–179.

Prabhu, R. and Meenakshi Ganesan, N. (2013) Genetic diversity studies in Ragi [*Eleusine coracana* (L.) Gaertn.] with SSR and ISSR markers. *Mol. Plant Breed.*, **4** (17), 141–145.

Preston, J.C. and Kellogg, E.A. (2006) Reconstructing the evolutionary history of paralogous *APETALA1/FRUITFULL*-like genes in grasses (Poaceae). *Genetics*, **174**, 421–437.

Puranik, S., Bahadur, R.P., Srivastava, P.S. and Prasad, M. (2011) Molecular cloning and characterization of a membrane associated NAC family gene, *SiNAC from foxtail millet* [*Setaria italica* (L.) P. Beauv.]. *Mol. Biotechnol.,* **49** (2), 138–150.

Qi, X., Lindup, S., Pittaway, T.S. *et al.* (2001) Development of simple sequence repeat markers from bacterial artificial chromosomes without subcloning. *BioTechniques*, **31**, 355–361.

Qi, X., Pittaway, T.S., Lindup, S. *et al.* (2004) An integrated genetic map and a new set of simple sequence repeat markers for pearl millet, *Pennisetum glaucum*. *Theor. Appl. Genet.*, **109**, 1485–1493.

Qingshan, L. and Dahlberg, J.A. (2001) Chinese sorghum genetic resources. *Econ. Bot.*, **55**, 401–425.

Quinby, J.R. (1967) The maturity genes of sorghum. *Adv. Agron.*, **19**, 267–305.

Quinby, J.R. (1973) The genetic control of flowering and growth in sorghum. *Adv. Agron.*, **25**, 125–162.

Ragab, R., Dronavalli, S., Maroof, M.S. and Yu, Y. (1994) Construction of a sorghum RFLP linkage map using sorghum and maize DNA probes. *Genome*, **37**, 590–594.

Rajaram, V., Nepolean, T., Senthilvel, S. *et al.* (2013) Pearl millet [*Pennisetum glaucum* (L.) R. Br.] consensus linkage map constructed using four RIL mapping populations and newly developed EST-SSRs. *BMC Genomics*, **14**, 159.

Rajput, S.G., Plyler-Harveson, T. and Santra, D.K. (2014) Development and characterization of SSR markers in proso millet based on switchgrass genomics. *Am. J. Plant Sci.*, **5**, 175–186.

Rakshit, S., Gomashe, S.S., Ganapathy, K.N. *et al.* (2012) Morphological and molecular diversity reveal wide variability among sorghum Maldandi landraces from south India. *J. Plant. Biochem. Biotechnol.*, **21**, 145–156.

Rami, J.F., Dufour, P., Trouche, G. *et al.* (1998) Quantitative trait loci for grain quality, productivity, morphological and agronomical traits in sorghum (*Sorghum bicolor* L. Moench). *Theor. Appl. Genet.*, **97**, 605–616.

Ramu, P., Kassahun, B., Senthilvel, S. *et al.* (2009) Exploiting rice-sorghum synteny for targeted development of EST-SSRs to enrich the sorghum genetic linkage map. *Theor. Appl. Genet.*, **119**, 1193–1204.

Ramu, P., Billot, C., Rami, J.F. *et al.* (2013) Assessment of genetic diversity in the sorghum reference set using EST-SSR markers. *Theor. Appl. Genet.*, **126**, 2051–2064.

Rana, B.S., Tripathi, D.P. and Rao, N.G.P. (1976) Genetic analysis of some exotic × Indian crosses in sorghum. XV. Inheritance of resistance to sorghum rust. *Indian J. Genet.*, **36**, 244–249.

Rana, B.S., Rao, M., Indira, S. *et al.* (1999) Technology for Increasing Sorghum Production and Value Addition, Director and Project Coordinator (AICSIP) National Research Centre for Sorghum, Hyderabad, India.

Rao, G.M.R., Patil, S.J. and Anahosur, K.H. (1993) Genetics of charcoal rot resistance in rabi sorghum. *Karnataka J. Agric. Sci.*, **6**, 113–116.

Reddy, V.G., Upadhyaya, H.D. and Gowda, C.L.L. (2006) Characterization of world's foxtail millet germplasm collections for morphological traits. *J. SAT Agric. Res.*, **2**, 1–3.

Reddy, P.S., Fakrudin, B., Rajkumar, Punnuri, S.M. *et al.* (2008) Molecular mapping of genomic regions harboring QTL for stalk rot resistance in sorghum. *Euphytica*, **159**, 191–198.

RESMISA (2012) *Supporting Millets in India: Policy Review and Suggestions for Action. 2012*, Revalorising Small Millets in Rainfed Regions of South Asia (RESMISA). Prepared by DHAN foundation, Krishnagiri, Tamil Nadu, India, p. 46.

Ritter, K.B., Jordan, D.R., Chapman, S.C. *et al.* (2008) Identification of QTL for sugar-related traits in a sweet × grain sorghum (*Sorghum bicolor* L. Moench) recombinant inbred population. *Mol. Breed.*, **22**, 367–384.

Rodriguez-Herrera, R., Rooney, W.L., Rosenow, D.T. and Frederiksen, R.A. (2000) Inheritance of grain mold resistance in grain sorghum without a pigmented testa. *Crop Sci.*, **40**, 1573–1578.

Rooney, L.W. and Serna-Saldivar, S.O. (1991) Sorghum, in Handbook of Cereal Science and Technology (eds K. Lorenz and K. Kulp), Markel Dekker, New York, pp. 233–270.

Rooney, W.L. and Aydin, S. (1999) Genetic control of a photoperiod-sensitive response in *Sorghum bicolor* (L.) Moench. *Crop Sci.*, **39**, 397–400.

Sabadin, P.K., Malosetti, M., Boer, M.P. *et al.* (2012) Studying the genetic basis of drought tolerance in sorghum by managed stress trials and adjustments for phenological and plant height differences. *Theor. Appl. Genet.*, **124**, 1389–1402.

Saidou, A.A., Mariac, C., Luong, V. *et al.* (2009) Association studies identify natural variation at *PHYC* linked to flowering time and morphological variation in pearl millet. *Genetics*, **182**, 899–910.

Salimath, S.S., de Oliveira, A.C., Bennetzen, J.L. and Godwin, I.D. (1995) Assessment of genome origins and genetic diversity in the genus Eleusine with DNA markers. *Genome*, **38** (4), 757–763.

Satish, K., Srinivas, G., Madhusudhana, R. *et al.* (2009) Identification of quantitative trait loci for resistance to shoot fly in sorghum [*Sorghum bicolor* (L.) Moench]. *Theor. Appl. Genet.*, **119**, 1425–1439.

Satish, K., Gutema, Z., Grenier, C. *et al.* (2012) Molecular tagging and validation of microsatellite markers linked to the low germination stimulant gene (*lgs*) for *Striga* resistance in sorghum [*Sorghum bicolor* (L.) Moench]. *Theor. Appl. Genet.*, **124**, 989–1003.

Schloss, S.J., Mitchell, S.E., White, G.M. *et al.* (2002) Characterization of RFLP probe sequences for gene discovery and SSR development in *Sorghum bicolor* (L.) Moench. *Theor. Appl. Genet.*, **105**, 912–920.

Schontz, D. and Rether, B. (1999) Genetic variability in foxtail millet [*Setaria italica* (L.) P. Beauv.]: Identification and classification of lines with RAPD markers. *Plant Breed.*, **118**, 190–192.

Seetharama, N., Bidinger, F.R., Rao, K.N. *et al.* (1987) Effect of pattern and severity of moisture deficit stress on stalk rot incidence in Sorghum I. Use of line source irrigation technique, and the effect of time of inoculation. *Field Crops Res.*, **15**, 289–308.

Sehgal, D., Rajaram, V., Armstead, I.P. *et al.* (2012) Integration of gene-based markers in a pearl millet genetic map for identification of candidate genes underlying drought tolerance quantitative trait loci. *BMC Plant Biol.*, **12**, 9.

Senthilvel, S., Jayashree, B., Mahalakshmi, V. *et al.* (2008) Development and mapping of simple sequence repeat markers for pearl millet from data mining of expressed sequence tags. *BMC Plant Biol.*, **8**, 119.

Serraj, R., Hash, C.T., Rizvi, S.M.H. *et al.* (2005) Recent advances in marker-assisted selection for drought tolerance in pearl millet. *Plant Prod. Sci.*, **8** (3), 334–337.

Sharma, H. (1985) Screening for sorghum midge [*Contarinia sorghicola*] resistance and resistance mechanisms, in *Proceedings of International Sorghum Entomology Workshop, College Station, Texas (USA), July 15–21, 1984*, ICRISAT, Patancheru, India, pp. 275–292.

Shehzad, T., Okuizumi, H., Kawase, M. and Okuno, K. (2009) Development of SSR-based sorghum (*Sorghum bicolor* L. Moench) diversity research set of germplasm and its evaluation by morphological traits. *Genet. Resour. Crop Evol.*, **56**, 809–827.

Shiringani, A.L., Frisch, M. and Friedt, W. (2010) Genetic mapping of QTL for sugar-related traits in a RIL population of *Sorghum bicolor* L. Moench. *Theor. Appl. Genet.*, **121**, 323–336.

Shiringani, A.L. and Friedt, W. (2011) QTL for fibre-related traits in grain × sweet sorghum as a tool for the enhancement of sorghum as a biomass crop. *Theor. Appl. Genet.*, **123**, 999–1011.

Singh, S. (1977) Breeding grain sorghum for cold tolerance. International Sorghum Workshop held at ICRISAT during, pp 6–12.

Singh, F., Singh, R.M., Singh, R.B. and Singh, R.K. (1980) Genetic studies of downy mildew resistance in pearl millet, in Trends in Genetical Research on Pennisetums (eds V.P. Gupta and J.L. Minocha), Wesley Press, Ludhiana, India, pp. 171–172.

Singh, S.D. and Talukdar, B.S. (1998) Inheritance of complete resistance to pearl millet downy mildew. *Plant Dis.*, **82**, 791–793.

Singh, A.K., Rana, M.K., Singh, S. *et al.* (2013) Assessment of genetic diversity among pearl millet [*Pennisetum glaucum* (L.) R. Br.] cultivars using SSR markers. *Range Manag. Agrofor.*, **34** (1), 77–81.

Singhal, D., Gupta, P., Sharma, P. *et al.* (2011) *In-silico* single nucleotide polymorphisms (SNP) mining of *Sorghum bicolor* genome. *Afr. J. Biotechnol.*, **10**, 580–583.

Soto, P.E. (1974) Ovipositional preference and antibiosis in relation to resistance to a sorghum shoot fly. *J. Econ. Entomol.*, **67**, 265–267.

Sreenivasulu, N., Miranda, M., Prakash, H.S. *et al.* (2004) Transcriptome changes in foxtail millet genotypes at high salinity: identification and characterization of a *PHGPX* gene specifically upregulated by NaCl in a salt-tolerant line. *J. Plant Physiol.*, **161**, 467–477.

Srinivas, G., Satish, K., Murali Mohan, S. *et al.* (2008) Development of genic-microsatellite markers for sorghum staygreen QTL using a comparative genomic approach with rice. *Theor. Appl. Genet.*, **117**, 283–296.

Srinivas, G., Satish, K., Madhusudhana, R. *et al.* (2009a) Identification of quantitative trait loci for agronomically important traits and their association with genic-microsatellite markers in sorghum. *Theor. Appl. Genet.*, **118**, 1439–1454.

Srinivas, G., Satish, K., Madhusudhana, R. and Seetharama, N. (2009b) Exploration and mapping of microsatellite markers from subtracted drought stress ESTs in *Sorghum bicolor* (L.) Moench. *Theor. Appl. Genet.*, **118**, 703–717.

Srinivasachary, Dida, M.M., Gale, M.D. and Devos, K.M. (2007) Comparative analyses reveal high levels of conserved colinearity between the finger millet and rice genomes. *Theor. Appl. Genet.*, **115** (4), 489–499.

Stenhouse, J.W., Bandyopadhyay, R., Singh, S.D. and Subramanian, V. (1998) Breeding for grain mold resistance in sorghum, in *Genetic Improvement of Sorghum and Pearl Millet, Proceedings of the International Conference, September 22–27 1996, Holiday Inn Plaza, Lubbock, Texas, USA*, University of Nebraska, Lincoln, USA, pp. 326–354.

Subudhi, P.K. and Nguyen, H.T. (2000) Linkage group alignment of sorghum RFLP maps using a RIL mapping population. *Genome*, **43**, 240–249.

Subudhi, P.K., Rosenow, D.T. and Nguyen, H.T. (2000) Quantitative trait loci for the stay green trait in sorghum (*Sorghum bicolor* L. Moench): consistency across genetic backgrounds and environments. *Theor. Appl. Genet.*, **101**, 733–741.

Sumanth, M., Sumathi, P., Vinodhana, N.K. and Sathya, M. (2013) Assessment of genetic distance among the inbred lines of pearl millet [*Pennisetum glaucum* (L.) R. Br.] using SSR markers. *Int. J. Biotech. & Allied Fields*, **1** (3), 153–162.

Supriya, A., Senthilvel, S., Nepolean, T. *et al.* (2011) Development of a molecular linkage map of pearl millet integrating DArT and SSR markers. *Theor. Appl. Genet.*, **123**, 239–250.

Takai, T., Yonemaru, J.I., Kaidai, H. and Kasuga, S. (2012) Quantitative trait locus analysis for days-to-heading and morphological traits in an RIL population derived from an extremely late flowering F_1 hybrid of sorghum. *Euphytica*, **187**, 411–420.

Tao, Y., Manners, J.M., Ludlo, M.M. and Henzell, R.G. (1993) DNA polymorphism in grain sorghum [*Sorghum bicolor* (L.) Moench]. *Theor. Appl. Genet.*, **86**, 679–688.

Tao, Y.Z., Jordan, D.R., Henzell, R.G. and McIntyre, C.L. (1998) Identification of genomic regions for rust resistance in sorghum. *Euphytica*, **103**, 287–292.

Tao, Y.Z., Henzell, R.G., Jordan, D.R. *et al.* (2000) Identification of genomic regions associated with stay green in sorghum by testing RILs in multiple environments. *Theor. Appl. Genet.*, **100**, 1225–1232.

Tao, Y.Z., Hardy, A., Drenth, J. *et al.* (2003) Identifications of two different mechanisms for sorghum midge resistance through QTL mapping. *Theor. Appl. Genet.*, **107**, 116–122.

Taramino, G., Tarchini, R., Ferrario, S. *et al.* (1997) Characterization and mapping of simple sequence repeats (SSRs) in *Sorghum bicolor*. *Theor. Appl. Genet.*, **95**, 66–72.

Thakur, R.P., Rai, K.N., Khairwal, I.S. and Mahala, R.S. (2008) Strategy for downy mildew resistance breeding in pearl millet in India. *J. SAT Agric. Res.*, **2**, 11.

Thudi, M., Senthilvel, S., Bottley, A. *et al.* (2010) A comparative assessment of the utility of PCR-based marker systems in pearl millet. *Euphytica*, **174**, 253–260.

Tuinstra, M.R., Grote, E.M., Goldsbroug, P.B. and Ejeta, G. (1996) Identification of quantitative trait loci associated with pre-flowering drought tolerance in sorghum. *Crop Sci.*, **36**, 1337–1344.

Tuinstra, M.R., Grote, E.M., Goldsbrough, P.B. and Ejeta, G. (1997) Genetic analysis of post-flowering drought tolerance and components of grain development in *Sorghum bicolor* (L.) Moench. *Mol. Breed.*, **3**, 439–448.

Tuinstra, M.R., Ejeta, G. and Goldsbrough, P. (1998) Evaluation of near-isogenic sorghum lines contrasting for QTL markers associated with drought tolerance. *Crop Sci.*, **38**, 835–842.

Upadhyaya, H.D., Gowda, C.L.L., Pundir, R.P.S. *et al.* (2006) Development of core subset of finger millet germplasm using geographical origin and data on 14 quantitative traits. *Genet. Resour. Crop Evol.*, **53**, 679–685.

Upadhyaya, H.D., Gopal Reddy, V., Gowda, C.L.L. and Singh, S. (2007) A minicore collection of sorghum [*Sorghum bicolor* (L.) Moench] for enhancing utilization of germplasm in crop improvement, in *The ASA-CSSA-SSSA International Annual Meetings, November 4–8, 2007*, New Orleans, Louisiana.

Upadhyaya, H.D., Pundir, R.P.S., Gowda, C.L.L. *et al.* (2008) Establishing a core collection of foxtail millet to enhance the utilization of the germplasm of an underutilized crop. *Plant Genet. Resour.*, **7**, 177–184.

Upadhyaya, H.D., Gowda, C.L.L., Reddy, K.N. and Singh, S. (2009) Augmenting the pearl millet core collection for enhancing germplasm utilization in crop improvement. *Crop Sci.*, **49**, 573–580.

Upadhyaya, H.D., Sarma, N.D.R.K., Ravishankar, C.R. *et al.* (2010) Developing a mini core collection in finger millet using multilocation data. *Crop Sci.*, **50**, 1924–1931.

Upadhyaya, H.D., Yadav, D., Reddy, K.N. *et al.* (2011) Development of pearl millet mini core collection for enhanced utilization of germplasm. *Crop Sci.*, **51**, 223–227.

Upadhyaya, H.D., Ravishankar, C.R., Narasimhudu, Y. *et al.* (2011) Identification of trait-specific germplasm and developing a mini core collection for efficient use of foxtail millet genetic resources in crop improvement. *Field Crops Res.*, **124**, 459–467.

Upadhyaya, H.D., Sharma, S., Gowda, C.L.L. *et al.* (2011) Developing proso millet (*Panicum miliaceum* L.) core collection using geographic and morpho-agronomic data. *Crop Pasture Sci.*, **62**, 383–389.

Upadhyaya, H.D., Wang, Y.H., Sharma, R. and Sharma, S. (2013a) SNP markers linked to leaf rust and grain mold resistance in sorghum. *Mol. Breed.*, **32**, 451–462.

Upadhyaya, H.D., Wang, Y.H., Sharma, R. and Sharma, S. (2013b) Identification of genetic markers linked to anthracnose resistance in sorghum using association analysis. *Theor. Appl. Genet.*, **126**, 1649–1657.

Upadhyaya, H.D., Dwivedi, S.L., Singh, S.K. *et al.* (2014) Forming core collections in barnyard, kodo, and little millets using morphoagronomic descriptors. *Crop Sci.*, **54**, 2673–2682.

Upadhyaya, H.D. (2015) Establishing core collections for enhanced use of germplasm in crop improvement. *Ekin J. Crop Breed. and Gen.*, **1-1**, 1–12.

Uptmoor, R., Wenzel, W., Friedt, W. *et al.* (2003) Comparative analysis on the genetic relatedness of *Sorghum bicolor* accessions from Southern Africa by RAPDs, AFLPs and SSRs. *Theor. Appl. Genet.*, **106**, 1316–1325.

Vadez, V., Deshpande, S.P., Kholova, J. *et al.* (2011) Stay-green quantitative trait loci's effects on water extraction, transpiration efficiency and seed yield depend on recipient parent background. *Funct. Plant Biol.*, **38**, 553–566.

Varshney, R.K. (2014) Towards developing a reference genome sequence of pearl millet (*Pennisetum glaucum* L.), in *Abstracts, Plant and Animal Genome XXII Conference, January 11–15, 2014*, San Diego, CA.

Veeranagamallaiah, G., Chandraobulreddy, P., Jyothsnakumari, G. and Sudhakar, C. (2007) Glutamine synthetase expression and pyrroline-5-carboxylate reductase activity influence proline accumulation in two cultivars of foxtail millet (*Setaria italica* L.) with differential salt sensitivity. *Environ. Expt. Bot.*, **60**, 239–244.

Veeranagamallaiah, G., Ranganayakulu, G.S., Thippeswamy, M. *et al.* (2009) Aldose reductase expression contributes in sorbitol accumulation and 4-hydroxynon-2-enal detoxification in two foxtail millet (*Setaria italica* L.) cultivars with different salt stress tolerance. *Plant Growth Regul.*, **59**, 137–143.

Vetriventhan, M., Upadhyaya, H.D., Anandakumar, C.R. *et al.* (2012) Assessing genetic diversity, allelic richness and genetic relationship among races in ICRISAT foxtail millet core collection. *Plant Genet. Resour.*, **10** (3), 214–223.

Wallace, J.G., Upadhyaya, H.D., Vetriventhan, M. *et al.* (2015) The genetic makeup of a global barnyard millet germplasm collection. *The Plant Genome* **8** (1), 7 p.

Wanous, M.K. (1990) Origin, taxonomy and ploidy of the millets and minor cereals. *Plant Var. Seeds*, **3**, 99–112.

Wang, Z.M., Devos, K.M., Liu, C.J. *et al.* (1998) Construction of RFLP-based maps of foxtail millet, *Setaria italica* (L.) P. Beauv. *Theor. Appl. Genet.*, **96**, 31–36.

Wang, Y.W., Samuels, T.D. and Wu, Y.Q. (2011) Development of 1,030 genomic SSR markers in switchgrass. *Theor. Appl. Genet.*, **122** (4), 677–686.

Wang, C., Jia, G., Zhi, H. *et al.* (2012) Genetic diversity and population structure of Chinese foxtail millet [*Setaria italica* (L.) Beauv.] landraces. G3 (Bethesda), **2**, 769–777.

Wang, J., Wang, Z.L., Yang, H.Q. *et al.* (2013) Genetic analysis and preliminary mapping of a highly male-sterile gene in foxtail millet (*Setaria italica* L. Beauv.) using SSR markers. *J. Integr. Agric.*, **12** (12), 2143–2148.

Wang, Z.L., Wang, J., Yuan, F. *et al.* (2014) Construction of genetic map of foxtail millet [*Setaria italica* (L.) P. Beauv.] using PCR-based molecular markers. *Sci. Agric. Sinica*, **47** (17), 3492–3500.

Williams, R.J. and Rao, K.N. (1981) A review of sorghum grain moulds. *Tropical Pest Management*, **27**, 200–211.

Wu, Y.Q., Huang, Y., Porter, D.R. *et al.* (2007) Identification of a major quantitative trait locus conditioning resistance to greenbug biotype E in sorghum PI 550610 using simple sequence repeat markers. *J. Econ. Entomol.*, **100**, 1672–1678.

Wu, Y. and Huang, Y. (2008) Molecular mapping of QTL for resistance to the greenbug *Schizaphis graminum* (Rondani) in *Sorghum bicolor* (Moench). *Theor. Appl. Genet.*, **117**, 117–124.

Xu, G.W., Magill, C., Schertz, K. and Hart, G. (1994) A RFLP linkage map of *Sorghum bicolor* (L.) Moench. *Theor. Appl. Genet.*, **89**, 139–145.

Xu, W., Subudhi, P.K., Crasta, O.R. *et al.* (2000) Molecular mapping of QTL conferring stay-green in grain sorghum (*Sorghum bicolor* L. Moench). *Genome*, **43**, 461–469.

Xu, J., Li, Y., Ma, X. *et al.* (2013) Whole transcriptome analysis using next-generation sequencing of model species *Setaria viridis* to support C_4 photosynthesis research. *Plant Mol. Biol.*, **83**, 77–87.

Yabuno, T. (1987) Japanese barnyard millet (*Echinochloa utilis*, Poaceae) in Japan. *Econ. Bot.*, **41**, 484–493.

Yadav, R.S., Hash, C.T., Bidinger, F.R. *et al.* (2002) Quantitative trait loci associated with traits determining grain and stover yield in pearl millet under terminal drought-stress conditions. *Theor. Appl. Genet.*, **104**, 67–83.

Yadav, R.S., Bidinger, F.R., Hash, C.T. *et al.* (2003) Mapping and characterization of QTL × E interactions for traits determining grain and stover yield in pearl millet. *Theor. Appl. Genet.*, **106**, 512–520.

Yadav, R.S., Hash, C.T., Bidinger, F.R. *et al.* (2004) Genomic regions associated with grain yield and aspects of post-flowering drought tolerance in pearl millet across stress environments and tester background. *Euphytica*, **136**, 265–277.

Yadav, S., Jain, S., Jain, V. and Jain, R.K. (2007) Genetic analysis of CMS, restorer, hybrid and open-pollinated genotypes of Indian pearl millet [*Pennisetum glaucum* (L.) R. Br.] using ISSR markers. *Ind. J. Biotech.*, **6**, 340–348.

Yadav, C.B., Muthamilarasan, M., Pandey, G. *et al.* (2014) Development of novel microRNA-based genetic markers in foxtail millet for genotyping applications in related grass species. *Mol. Breed.*, **34**, 2219–2224.

Yadav, C.B., Bonthala, V.S., Muthamilarasan, M. *et al.* (2014) Genome-wide development of transposable elements-based markers in foxtail millet and construction of an integrated database. *DNA Res.*, **2014**, 1–12.

Yamaguchi, H., Utano, A.Y.A., Yasuda, K. *et al.* (2005) A molecular phylogeny of wild and cultivated *Echinochloa* in East Asia inferred from non-coding region sequences of trnT-L-F. *Weed Biol. Manag.*, **5**, 210–218.

Yang, L., Jin, G., Zhao, X. *et al.* (2007) PIP: a database of potential intron polymorphism markers. *Bioinformatics*, **23**, 2174–2177.

Yohannes, T., Tesfamichael, A., Kiambi, D. *et al.* (2015) Marker-assisted introgression improves *Striga* resistance in an Eritrean farmer-preferred sorghum variety. *Field Crops Res.*, **173**, 22–29.

Yonemaru, J.I., Ando, T., Mizzubayashi, T. *et al.* (2009) Development of genome-wide simple sequence repeat markers using whole-genome shotgun sequences of sorghum [*Sorghum bicolor* (L.) Moench]. *DNA Res*, **16**, 187–193.

Zhang, J., Liu, T., Fu, J. *et al.* (2007) Construction and application of EST library from *Setaria italica* in response to dehydration stress. *Genomics*, **90**, 121–131.

Zhang, G., Liu, X., Quan, Z. *et al.* (2012) Genome sequence of foxtail millet (*Setaria italica*) provides insights into grass evolution and biofuel potential. *Nat. Biotechnol.*, **30**, 549–554.

Zhang, S., Tang, C.J., Zhao, Q. *et al.* (2014) Development of highly polymorphic simple sequence repeat markers using genome-wide microsatellite variant analysis in foxtail millet [*Setaria italica* (L.) P. Beauv.]. *BMC Genomics*, **15**, 78.

Zhao, L., Zhao, Q., Ao, G. and Yu, J. (2009) The foxtail millet *Si69* gene is a Wali7 (wheat aluminium-induced protein 7) homologue and may function in aluminium tolerance. *Chinese Sci. Bullet.*, **54**, 1697–1706.

Zhao, L.Q., Pan, W.J., Ma, J.F. *et al.* (2010) Identification of AFLP markers linked to a novel rust resistance gene in foxtail millet. *Sci. Agric. Sinica*, **43** (21), 4349–4355.

Zhao, W.G., Lee, G.A., Kwon, S.W. *et al.* (2012) Development and use of novel SSR markers for molecular genetic diversity in Italian millet (*Setaria italica* L.). *Genes Genom.*, **34** (1), 51–57.

Zheng, L.Y., Guo, X.S., He, B. *et al.* (2011) Genome-wide patterns of genetic variation in sweet and grain sorghum (*Sorghum bicolor*). *Genom. Biol.*, **12**, R114.

Zou, G., Zhai, G., Feng, Q. *et al.* (2012) Identification of QTL for eight agronomically important traits using an ultra-high-density map based on SNPs generated from high-throughput sequencing in sorghum under contrasting photoperiods. *J. Exp. Bot.*, **63**, 5451–5462.

14

Strategies to Build Sustainable Millet Seed Systems

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14.1 Introduction

It has been estimated that over 90% of the crops in developing countries are still planted with farmers' varieties and farm-saved seed (Almekinders *et al.,* 1994; Almekinders and Louwaars, 1999; Maredia *et al.,* 1999; World Bank, 1998). The formal seed sector focuses on high-value and hybrid crops and most favourable agro-ecosystems as trading in these crops and areas is most profitable. Thus open-pollinated varieties and self-pollinating crops are left to the mercy of small-scale unorganised seed companies and public-sector seed companies and the informal seed systems. As the access to quality seed becomes acute, the smallholder farmers depend for their seed security by saving their own seeds required for the next season, thus reducing opportunities for seed replacement with new varieties (Fig. 14.1). With privatisation or commercialisation of public-sector seed activities, the formal public-sector seed activities have tended to focus on a narrow range of crops grown by larger farmers (Fig. 14.2), thereby reducing supplies of seeds of new varieties of subsistence crops to smallholder farmers even further (Bengtsson, 2007). Nevertheless, there are a number of examples throughout the world where seeds of cultivars are supplied by successful small- to medium-scale seed enterprises or farmer-led organisations. Some of them may have succeeded in creating a vibrant seed business and be able to respond to the demand for quality seeds. Identifying these and determining the key factors leading to their success will contribute to efforts to replicate the innovations in similar agro-ecological conditions for millets.

Existing literature on millet seed systems (Pray and Ramaswami, 2001; Pray *et al.,* 2001; Bantilan and Deb, 2002; Evenson and Gollin, 2003) has focussed mainly on the two major millet crops, sorghum and pearl millet. Analysis has typically been restricted to describing the role of the formal seed sector in millet-crop improvement and use of improved seed, although there are several exceptions.

In the millet seed systems, formal channels for seed transactions encompass traders in the district market yards, seed exchanges through private dealers and distributors and seeds marketed by private companies where hybrids are in vogue. Millet seeds exchanged through agents in formal channels is often branded, the transactions are monetised, and those engaged in the business are usually full-time traders. In contrast, traders operating in shandies or village markets are part-time. Seeds traded in shandies are not

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branded, since they originate from farmers from the surrounding villages or communities. To some extent, the seeds are identified by their village name or, in some cases, by the farmer's name (if the farmer is reputed in the locality for the quality of seeds). The seed exchanges are monetised but the prices are not based on 'the existing market prices', nor are they 'fixed' – they vary according to the demand and quality (physical purity) of the seeds. Seed dealers/distributors in the formal seed-supply chain are vital links between the formal seed-producing firms and farming communities. The changing composition of cereal seed markets in dry land ecosystems refers to a point in two time periods, mostly for certified seeds. Saved seed is a dominant but declining source of seeds for all the crops.

The existing millet seed systems involve the formal seed sector, which is an official or private control of seed monitored through the entire process of breeding, multiplication, processing and storage, leading to the final product. The informal seed sector is simply the farmers themselves that provide each other and themselves with seed for sowing. This seed may be cleaned manually, but is otherwise untreated and thus a potential carrier of various diseases. Therefore, strengthening of the seed system at community level should involve all possible aspects of modern seed activities. In industrialised countries, the formal seed sector provides the vast majority of seed to farmers, while both seed systems are present in developing countries. Despite large investments in formal seed systems in developing countries over the past 30 years, the seed demands of about 90–95% of smallholder farmers are still met by informal sources at the farm and community levels.

Although the informal seed sector provides a dynamic and flexible system of seed supply, usage, handling, trade and exchange, continuous use of untested seed inevitably leads to degeneration of seed quality. Farmers depend on their own seed for sowing, not only because of inadequate access to seed from the formal seed sector, but also because the formal seed sector more often provides seeds of a limited range of cultivars and varieties of food and fodder crops, which do not always fulfil the needs of farmers. On-farm growing and maintenance of locally adapted landraces, cultivars and wild species help the farmer decrease the impact of a series of production constraints like drought, flooding, heat, cold, pests and diseases. In many developing countries, problems created by seed-borne diseases are ignored and control measures

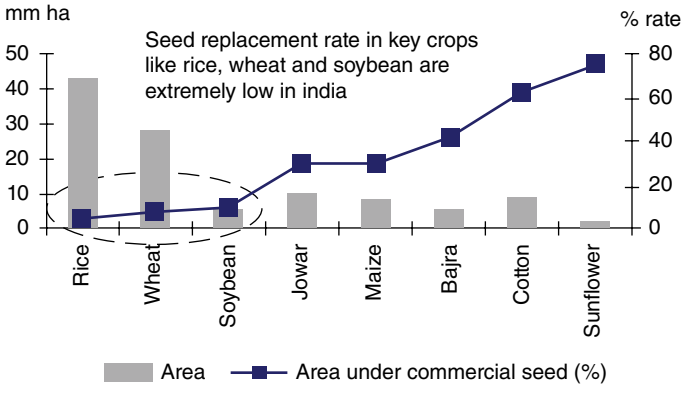

Figure 14.1 Seed replacement in key foodgrain crops. Source: Tonapi *et al.* (2012). (*See color plate section for the color representation of this figure.*)

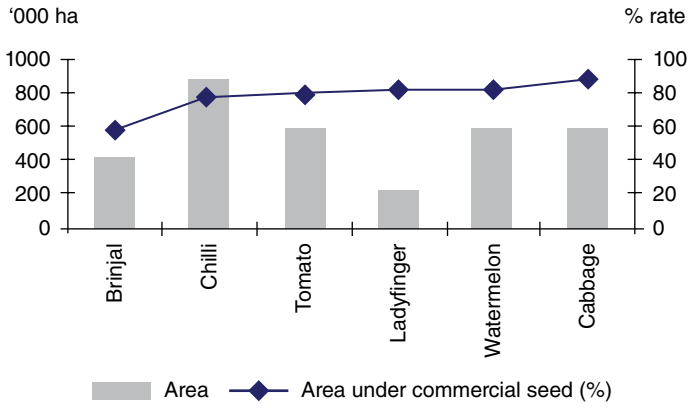

Figure 14.2 Seed replacement rate in cash crops. Source: Tonapi *et al.* (2012). (*See color plate section for the color representation of this figure.*)

unknown or inadequate. The consequence is often poor seed quality, dissemination and build-up of seed-borne diseases and yields far below potential. The quality of the seed must be known before it is sown. A farmer using healthy seed will be able to increase yield of his harvest dramatically. However, the health and quality of seed are not always apparent to the naked eye. Seed supply from both formal and informal systems suffers from a series of problems due to the lack of economic resources for education, research and quality control.

14.2 Factors Leading to Sustainable Seed Security

14.2.1 Overview of Seed Systems

Seed systems can be grouped into two types: (i) formal seed systems, and (ii) informal seed systems. Informal systems are also referred to as local, traditional or farmer seed systems. Both systems have their own limitations.

14.2.1.1 Formal Seed Systems

Formal seed systems are easier to characterise as they are deliberately constructed, involving a chain of activities leading to clear products – certified seed of verified varieties (Louwaars, 1994). The chain usually starts with plant breeding and selection, resulting in different varieties, hybrid parents including hybrids and materials leading to formal cultivar release and maintenance (Fig. 14.3). In practice, these systems may be constrained in their capacity to meet the diverse needs of farmers in developing countries. The framework for a performance analysis of a formal seed sector has been discussed by several authors (Pray and Ramaswami, 1991; Cromwell *et al.*, 1992; Friis-Hansen, 1992). The guiding principles in the formal system are maintenance of varietal identity and genetic purity and production of seed with optimal physical, physiological and sanitary quality. The central premise of the formal system is that there is a clear distinction between seed and grain. This distinction is less clear in informal seed systems.

14.2.1.1.1 Limitations of Formal Seed Systems

- The varieties developed are often not adopted by small farmers due to complex environment stresses and low input conditions.
- The formal seed sector has difficulty in addressing the varied needs of small farmers in marginal areas.
- They offer only a limited range of varieties
- The formal seed sector is reluctant to produce and market varieties of the major millets because they may not be commercially feasible. Even if it does produce such varieties, they may not reach small farmers in remote rural areas.
- The interest of the private sector may cease to be served once the varieties are sold to farmers because the latter tend to save their own seed for the next season and hence will not buy again.
- Prohibitive seed prices are a limitation for resource-poor farmers.
- Poor logistics in seed diffusion and high seed demand constrain formal seed programmes.
- Formal seed systems are sensitive to natural disasters and political or other turmoil.

14.2.1.2 Informal Seed Systems

Village seed systems or farmers' seed systems or local seed systems are different names for the informal seed system, in which farmers procure seed by different methods and practices depending on the situation and location. In an informal seed system, farmers themselves produce, disseminate and access seed directly from their own harvest, through exchange and barter among friends, neighbours and relatives; and through local grain markets. Encompassing a wide range of variations, local systems are characterised by their flexibility. The varieties disseminated may be landraces or mixed races and may be heterogeneous. In addition, the seed is of variable quality in terms of purity and physical and physiological parameters. While some farmers treat seed specially, there is not always a distinction between seed and grain.

14.2.1.2.1 Limitations of Informal Seed Systems

- The seed quality is often suboptimal due to biotic stresses and storage problems.
- Seed exchange is limited to a geographical area and governed by cultural barriers.
- Crop failures or low yields have a tremendous affect on the availability of seed and local prices.
- When a local seed system collapses, it is not easy to restore it in a short time. In such a situation, local varieties (land races) are easily lost and replaced by relief-supplied seeds.

14.2.2 Seed Sources for Informal and Formal Seed Systems

In fact, millet seed systems in dry land ecosystems are basically influenced by their pace of seed replacement, seed-to-grain price ratios, distance to seed sources and the quantity of seed traded by formal and informal means. The richness of materials grown at the household and community levels is in general positively affected by the quantities of seed sold by dealers and in local weekly open-air markets, as well as the rate of seed replacement. Distances to different seed sources also influence the diversity of crops and varieties in these communities. In the marginal environments, crop and variety use

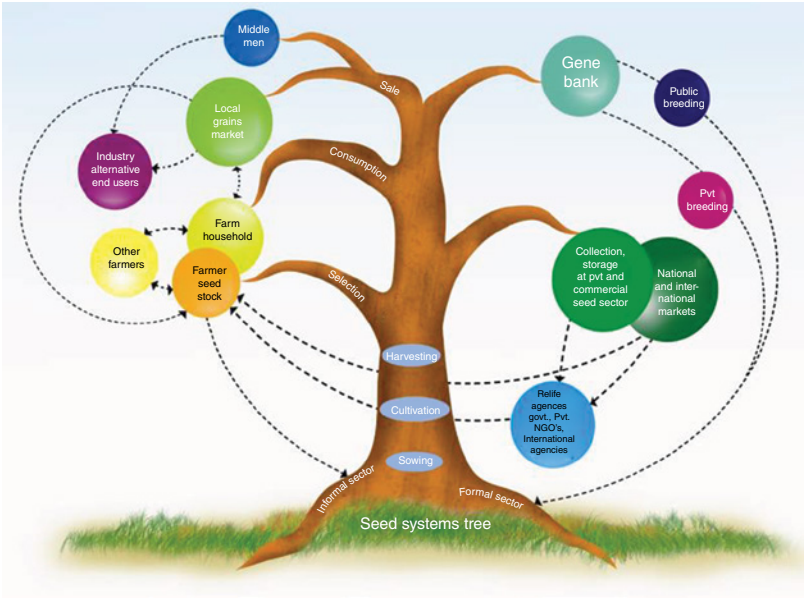

Figure 14.3 Seed systems tree. Source: Ravinder Reddy *et al.* (2007). (*See color plate section for the color representation of this figure*.)

decisions, and the crop biodiversity levels that result, and take place within the context of local seed markets and the national seed industry.

14.2.3 Challenges for Seed Sector in Marginal Environments

The major challenges the millet seed sector faces in the marginal environments of are:

1) The extent and persistence of farm-saved seeds
2) Variation in R&D investment across seasons dryland crops
3) Seed sector regulations, in particular the enactment of recent plant-variety protection and farmers' rights legislation in India

The extent and continued use of farm-saved seeds in dryland crops, which constitute mainly the varieties, on the one hand discourages the entry of commercial sector in developing new research products and also from the perspective of public sector to add any kind of incentives for their already existing research. Though farm-saved seeds promote the use of local or traditional varieties to some extent, thus conserving the land races, over time it does not provide adequate choices to the farmers to diversify their portfolio and thus improve productivity. One of the most pressing concerns related to seed supply of modern varieties is how to establish sustainable seed provision systems for commodities that cannot be economically supplied through a centralised, formal seed industry. The seed supply bottleneck primarily affects self-pollinating crops seeds saved and sown year after year in local systems.

14.2.4 Indian Scenario

A robust seed system guarantees the sustainability of its agriculture to ensure that the products of modern plant breeding and local farmer ingenuity are widely available.

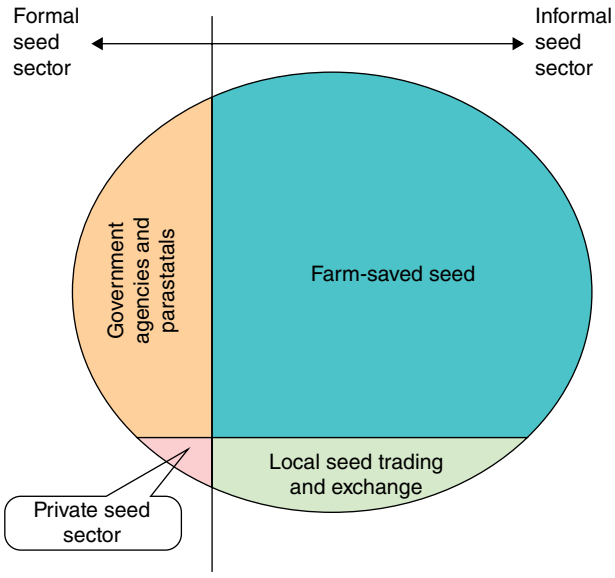

Figure 14.4 Seed supply scenario in formal and informal seed sector in India. *Source:* Ravinder Reddy *et al*. (2007). (*See color plate section for the color representation of this figure*.)

National seed systems usually include several elements. A commercial seed sector is necessary to ensure efficient seed supply. Both public and private seed systems are relatively well developed in India; hence the possibilities of delivering plant-breeding innovations to farmers are better. An unanswered question however is: how do resource-poor farmers react to a complex commercial seed provision system? Recent innovations in adaptive and participatory research go a long way in addressing the first concern, but much remains to be done regarding seed system diagnosis.

Even in a relatively mature seed system such as the Indian one, the movement of information between farmers and seed providers leaves much room for improvement (Fig. 14.4). Seed-secure farmers tend to maintain their own varieties with limited influx of new varieties. In addition, awareness about variety selection is not always well developed in traditional farming communities. It may also reflect the fact that, in traditional self-contained seed systems, the same genetic material may be easily available from neighbours, thus reducing the risk of seed procurement and accesses. The farmers source seed off-farm from other farmers, and farmer communities often identify certain individual farmers as reliable sources of good-quality seed. The proportion of the farming community involved as seed-producers-cum-distributors is very small. Furthermore, it is often difficult to establish whether these local seed suppliers are making a conscious effort to produce high-quality seed, or if they are simply well-endowed farmers, they always have surplus grain to sell as 'seed' during the next planting season. Seed sources have been related to wealth status, with rich farmers maintaining their own seed stocks but poor farmers having to to buy or borrow seed every year. Fodder is less susceptible to drought than grain production as some fodder can be harvested even in years when grain production fails. This undoubtedly influences the choice of crops and varieties and is well illustrated by the farmers in the project areas where our interventions took place.

Table 14.1 Quality seed requirement and gap in demand in India.

Crop	Seed requirement (million tonnes)	Seed distributed (million tonnes)	Gap (SRR: 25%) (million tonnes)	Gap (SRR: 33%) (million tonnes)	Gap (SRR:100%) (million tonnes)
Cereals	**7.35**	**1.47**	**0.36**	**0.98**	**5.88**
Paddy	3.23	0.58	0.23	0.50	2.66
Wheat	3.68	0.75	0.17	0.48	2.93
Maize	0.19	0.08	−0.03	−0.02	0.11
Pearl millet	0.05	0.02	−0.009	−0.006	0.027
Pulses	**0.83**	**0.13**	**0.08**	**0.15**	**0.70**
Oil seeds	**1.42**	**0.39**	**−0.04**	**0.08**	**1.03**
Sunflower	0.011	0.008	−0.005	−0.004	0.003
Rapeseed / mustard	0.038	0.016	−0.007	−0.004	0.022
Groundnut	0.64	0.16	0.001	0.054	0.481
Soybean	0.71	0.21	−0.030	0.029	0.500
Fibres	**0.608**	**0.026**	**0.127**	**0.177**	**0.583**
Cotton	0.037	0.023	−0.013	−0.011	0.014
Jute	0.572	0.003	0.140	0.188	0.569

Source: Singh and Chand, 2011.

14.2.5 Barriers to Seed Dissemination and Socio-Economic Constraints

Poor distribution of inputs and produce in a region results from poor infrastructure. Farmers have little access to seeds of improved varieties, as is evident from Quality seed requirement and gap in demand in India (Table 14.1). The key to overcoming this problem is to make available a range of modern varieties to farmers and train them on how to efficiently produce seeds of selected varieties, using modern technologies. In fact, seed and product markets should target national and regional markets. More than 60% of farmers purchase seed from the market through cash and credit. Thus, there is a need to link farmers to credit institutions. Information on seed supply and demand across has to be disseminated across countries. The approach is to maintain an inventory of variety traits, growing varieties with preferred traits for evaluation and selection by farmers and producing breeder and foundation seed of newly released varieties and those in advanced stages of testing. These are some of the ways of establishing sustainable seed systems. Besides, organising field days and variety demonstrations at the community level, monitoring the adoption of improved varieties, identifying constraints to broaden adoption, and developing a community-based seed production system form an integral part of the strategy. Despite the penetration of markets in the local economy, traditional coping strategies based on local processes of seed exchange are still important. Any successful developmental intervention aimed at increasing the resilience of seed systems should take into account these traditional exchange practices. For example, a better strategy for improving local institutions and seed-exchange networks could be aimed

at increasing production and multiplication of seeds at the local level and facilitate movement of people between the two areas, rather than distributing seeds from outside to farmers. Development projects should be innovative and poverty-focussed. It is crucial to reduce the poor man's vulnerability by increasing farmers' access to credit and other valuable production assets, which in turn are important for establishing and maintaining social relations that will help to evolve seed and food security in the long run.

14.2.5.1 Sound Informal Seed Systems: Most Suitable for Dry Land Ecosystems

Scientifically developed informal seed systems are the best, where the formal sector finds seed distribution difficult and farmers cannot reach seed markets easily. They may also be appropriate in smaller, limited agro-ecological zones, where the formal seed market is disinterested or unable to cater because of limited market for specific varieties or because widely marketed varieties may not suit that region or another important reason is an economic consideration, as profit margins are lower. They are also suitable in cases where the crops involved have a high seed rate and are bulky in nature, which translates into higher transportation costs and low profits.

14.2.5.2 Sustaining Viability of Informal Systems with Innovative Seed Delivery Models

The main purpose of alternative seed delivery system is to address the seed availability problems of smallholder farmers. Hence, ways of strengthening seed systems that could potentially address the needs and counter the vulnerabilities of smallholder farmers in these areas using specific seed delivery models need to be explored.

Most of the community-based informal seed production models/schemes are initiated because farmers are concerned about the non-availability of quality seeds at planting time. Many farmers do not have access to improved varieties; and would not be able to afford them even if they were. So introduction of alternative seed systems models must impact farmers' access to seeds of improved varieties at affordable costs. The quality of seed produced by community-based system or farmer seed systems is guaranteed only by its seller or village seed committee, because they are not processed and are uncertified. The seed so produced is low priced, available at farmers' doorsteps at the right time, and provides access to all farmer groups in the village. The regulatory and legal framework of national seed rules and regulations in many countries hampers the development of informal seed systems. National seed regulations are mostly based on international standards, which are often incompatible or irrelevant to the realities of farmers' seed systems. The restrictions imposed by national seed authorities on free exchange and marketing of seed, especially compulsory variety registration and seed certification, as practiced by many developed and developing countries are constraints on the efficient functioning of the formal seed sector and on the development of alternative seed systems. On the other hand, regulatory frameworks are crucial for the development of a national seed system (Tripp, 2003).

The major source of seed for small-scale farmers comes from their own on-farm savings, seed exchange, borrowings and local traders. Nevertheless, farmer's community systems of seed supply are under pressure due to recurring natural calamities such as drought, crop failure, storage problems and poverty. In drought situations, farmers depend on subsidised seed supply by government agencies, which meets only 30–40% seed requirement of smallholder farmers (Ravinder Reddy, 2005). In order to strengthen the seed delivery system, interventions are required to strengthen informal seed supply

systems, such as establishing village-based seed banks as alternative seed systems for seed security. The alternate village-based seed delivery models that may enable sustainability of community seed systems in the dry land ecosystems need to have following objectives:

1) To improve seed availability and access to improved varieties of seed to small and resource-poor farmers
2) Build capacity of stakeholders at the community level to enhance sustainable supply of good-quality seed, and timely supply at affordable prices

14.2.5.3 Alternate Village-Based Seed Delivery Models

14.2.5.3.1 Model 1: Individual Farmer as Seed Bank

This model (Figure 14.5) can be developed as a local seed system for different crops. Most effectively, this seed system will benefit farmers for crops that require high seed rate, which are bulky in nature, or crops that involve high transport and package costs. This model involves training a couple of farmers in each village in seed production technology and supporting them by supplying breeder seed and technology backstopping.

14.2.5.3.1.1 The Pros and Cons of the Model

- This model can be tried even in remote areas where NGOs are unwilling to take up operations.
- External finance is not required as all the costs are usually met by the farmer/seed producer.
- Effective and provides wider scope for dissemination and adoption of improved varieties through informal seed channels.
- Technical institutional services are not justifiable for individual farmers.
- Farmers are still unwilling to save seed because of storage pests and other financial debts.
- Procurement of breeder seed is difficult at the farmer level once the project is completed.
- There is no control on the selling price of seed.

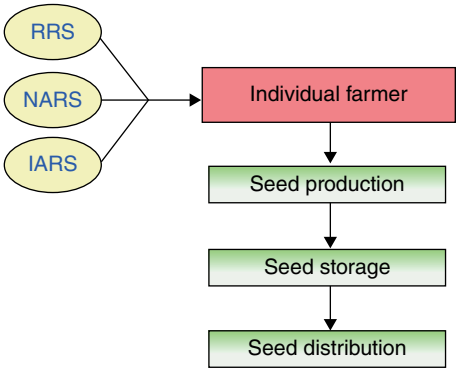

Figure 14.5 Model 1: Individual farmer as seed bank. (*See color plate section for the color representation of this figure.*)

- There is no control on seed distribution to different communities in the village.
- Seed distribution is limited to select groups.

14.2.5.3.2 Model 2: Village-Based Seed Banks

The concept of 'seed bank' (Figure 14.6), which advocates village self-sufficiency in production and distribution of quality seeds, is fast gaining ground. Seed villages or village seed banks operate with utmost transparency, mutual trust and social responsibility. Though this is not an entirely new concept, it is being promoted to reduce farmers' dependence on external inputs.

14.2.5.3.2.1 Advantages of Village-Based Seed Banks

- Availability of improved varieties in sufficient quantity within the village
- Assured and timely supply of seed
- Decentralised seed production
- Availability of improved variety seed at a low price
- Improved seed delivery system to resource-poor farmers
- Reduced dependence on external seed sources and hence an effective measure to curb spurious-seed trade
- Encourages village level trade and improves village economy
- Social responsibility of the seed production and delivery system
- A step ahead towards sustainable crop production
- Avoidance of diseases carried through seed (seed-borne pathogens) that have been produced and imported from different agro-ecoregions
- Scope for farmers' participatory varietal selection
- Availability of true-to-type varieties and healthy seed

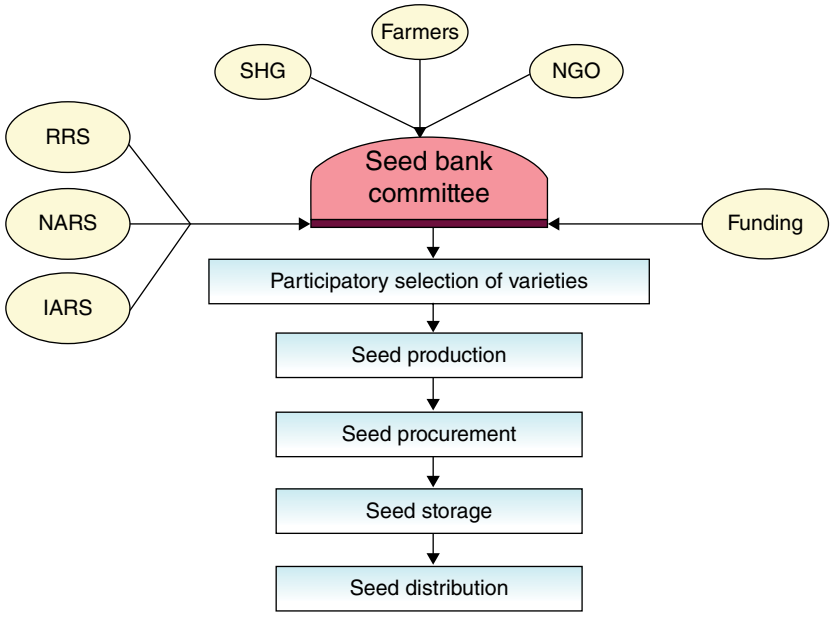

Figure 14.6 Model 2: Village based seed banks. (*See color plate section for the color representation of this figure.*)

14.2.5.3.2.2 Constraints

- Reluctance of farmers when it comes to adopting quality seed production practices
- Additional investment for inputs in seed production
- Lack of buy-back assurance to farmers from SHGs/NGOs
- Proper seed storage facilities and management in villages
- Lack of funds with SHGs/NGOs for seed procurement, packaging, storage and transportation
- Fixing of a minimum support price for seed procurement
- Technical support for seed production and its monitoring
- Responsibility of quality control aspects and monitoring of seed production
- Regular availability, accesses and procurement of breeder seed for seed production
- Willingness of farmers to participate in seed bank activities

14.2.5.4 Small-Scale Seed Enterprises Models

14.2.5.4.1 Model 3: SHG-Mediated System

In this model, Self Help Group (SHG) is empowered to take up the task of seed production (Figure 14.7). Members, however, need to develop skills in planning and seed-production techniques as well as support in terms of storage. Alternatively arrangements may be worked out with nearest market yard or state warehouses to have the seed-storage facility. The most critical aspect in this model is technical support and supply of breeder seed. Given the proper support, this model could provide significant benefits to farmers as it ensures the opportunity for all members and groups to share the profits of seed production. This model performs two tasks: meeting seed requirements of farmers as well as conserving a wide range of crop genetic diversity.

In most developing countries, the formal sector is far smaller than the informal seed sector. The latter is the major source of planting material for smallholder farmers, contributing 80–90% of the seed requirement of smallholder farmers (Monyo *et al.* 2003; Ravinder Reddy, 2004). Strategies to improve quality of seed, accesses and availability of

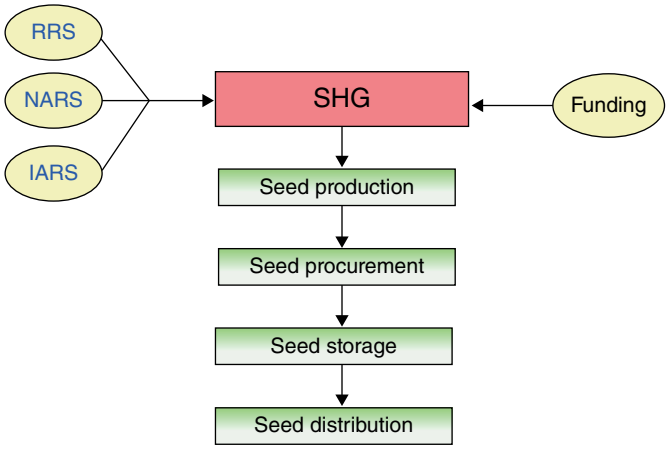

Figure 14.7 Model 3: SHG-mediated system. (*See color plate section for the color representation of this figure.*)

improved varieties, multiplication and dissemination and availability of seed on time at affordable prices to resource-poor smallholder farmers can bring about changes in the food security in developing countries. Support from state/national governments, and international organisations or any other funding agencies should be targeted at improving the efficiency of these investments by strengthening technical capabilities of SHGs, NGOs, farmer cooperatives, Krishi Vigyan Kendras (KVKs) and schemes to improve or develop village-based seed programmes through seed multiplication, quality control and marketing activities.

14.2.5.4.1.1 Pros and Cons

- Improved availability and access to improved varieties by all groups of farmers.
- Minimum overheads.
- Seed is stored in the village.
- Seed available at reasonable price and at the right time.
- Control on fixing procurement and selling price of seed.
- Priority for farmers' preferred varieties.
- Need for institutional support for technical backstopping and supply of breeder seed.
- Fund for procurement of seed.

14.2.5.4.2 Model 4: Non-Governmental Organisation (NGO)–Mediated System

In this model (Figure 14.8), an NGO may be given the responsibility for a cluster of villages. These organisations select and engage farmers in seed production on a contract basis, and preference is given to crops and varieties that are in demand in particular area. Basically, NGOs are involved in mobilising farmers/seed producers, planning seed multiplication, training, procuring, processing and marketing seed. Similar to other models, NGOs has to depend on other institutions for procuring foundation/basic seed stocks for multiplication.

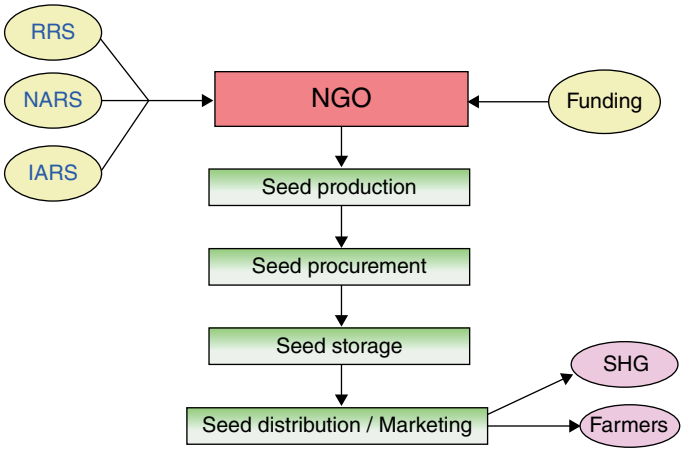

Figure 14.8 Model 4: NGO-mediated system. (*See color plate section for the color representation of this figure.*)

14.2.5.4.2.1 Pros and Cons

- Operates in a couple of villages.
- Storage of seed within the village.
- Seed distribution within the operational areas.
- Selling price can be fixed by discussions with farmers.
- Improved seed availability and access for all groups of farmers.
- Minimum overhead costs.
- Need institutional support for technical backstopping and supply of breeder seed.
- Fund required for seed procurement.

14.2.5.4.3 Model 5: KVK-Mediated System

In this model (Figure 14.9), Krishi Vigyan Kendras (KVKs – Farm Science Centres) are given the responsibility to implement the model.

14.2.5.4.3.1 Pros and cons

- Targets large operational area (many villages).
- Centralised production; needs large storage place (such as warehouses).
- Comparatively greater overhead costs.
- Involves more than one crop and variety in production.
- Less scope for farmers' participation and their choice of varieties.
- More inclined towards commercial seed trade.
- No scope for involving farmers in fixing procurement and selling prices.
- Model needs infrastructure.
- KVKs usually have fairly good technical capabilities.
- Institutional funds are generally available to some extent.

Each of the five models tested can thus be a harbinger of seed-system sustainability upon implementation based on the environments and regions they operate. The comparative statement comparing all the five models across each component working towards seed-system sustainability is given in Table 14.2.

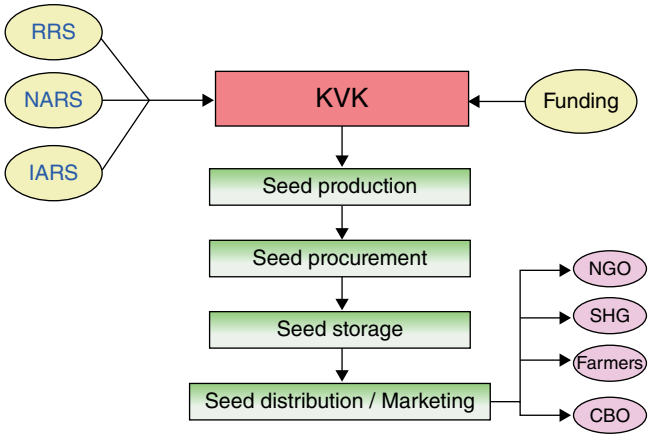

Figure 14.9 Model 5: KVK-mediated system. (*See color plate section for the color representation of this figure.*)

Table 14.2 Comparative chart of different seed systems models.

	Models				
Components	**Model 1**	**Model 2**	**Model 3**	**Model 4**	**Model 5**
Organisation/ community involved	Individual farmer	VIllage Seed Bank (VBSB)	SHG	NGO	KVK
Breeder seed source	Research institute or project scientist	Research institute or project scientist	Research institute or project scientist	Research institute or project scientist	Self or research institutions
Responsibility for transport of source seed	Research institute or project scientist	Research institute or project scientist	Research institute or project scientist	Research institute or project scientist	Self
Sourcing of other inputs	Farmer	Seed bank committee/ farmers	Farmers	Farmers/NGO	Farmers/ KVK
Choice of crop/ variety	Farmers	Farmers	Farmers	NGO/farmer	KVK
Training in seed production	Project scientist (PS)	Farmers	Farmers	NGO	KVK
Seed production monitoring	Project scientist	PS, NGO, village seed bank committee (VSBC) members	PS, SHG	PS, NGO	PS, KVK
Seed quality assurance	Farmer	VSBC	SHG	NGO	KVK
Cleaning, packing, and transportation	Farmer	Farmers	Farmers	NGO	KVK
Marketing	Farmer	VSBC	SHG	NGO	KVK
Fixing procurement and selling price	Farmer	VSBC	SHG	NGO	KVK
Funding for seed production	Farmer	Farmers	Farmers	Farmers/NGO	Farmers/ KVK
Funding for seed procurement	Farmer	Village organisations (VO)/VSBC	VO, self	VO, self, other organisations	Self, other organisations

Table 14.2 (Continued)

	Models				
Components	**Model 1**	**Model 2**	**Model 3**	**Model 4**	**Model 5**
Sustainability issues	Technical support, supply of breeder seed	Technical support, supply of breeder seed, funding, takes over of role once project completed, incentives for farmers for maintaining quality	Incentives for farmers for maintaining quality, technical support, breeder seed supply, funding for seed procurement	Farmer produce fetch low price because there is no external quality control, certification, supply of breeder seed, funding	Marketing, cost of seed, selection of varieties, incentives for farmers for maintaining seed quality, certification

14.3 Developing a Community-Based Millet Seed System

For centuries, farmers all over the world have selected and saved seeds to grow in the next season. But the lack of basic knowledge on scientific seed production, quality control, and innovative interventions has resulted in inferior seed quality and resultant low yields. What needs to be imparted to community seed systems is to have quality control, produce, process, treat, test, store, trade and barter; and re-sow the seeds for food, feed, and fodder and livelihood security. In fact, farmer-saved seed quality is always constrained by poor harvests, inadequate on-farm storage facilities (Meena Kumari, 2006), insufficient means to multiply quality seed, and poor seed-distribution systems. There is thus a need to strengthen local capacity to produce, store and distribute seed of many crop varieties, including some traditional varieties that are useful for diverse and evolving farming systems.

14.3.1 Steps for Strengthening Community Seed Production, Seed Saving and Storage

a) Appropriate policies for seed production and seed distribution to help focus efforts of government-supported initiatives on the varietal needs of resource-poor farmers in particular, with attention, where necessary, on the needs of women farmers, and minor crops that are inadequately covered by the private sector.
b) Provide and promote small-scale seed enterprises and strengthen linkages between gene banks, plant-breeding organisations, seed producers, and small-scale seed production and distribution enterprises.
c) Strengthen seed quality-control schemes for small-scale enterprises and provide appropriate incentives, credit schemes, and so on, to facilitate the emergence of seed enterprises, paying attention to the needs of the small farming sector, of women and of vulnerable or marginalised groups.
d) Provide support to and strengthen farmers' organisations so that they can more effectively express demand for their seed requirements, paying particular attention to the needs of women and of vulnerable or marginalised groups.
e) Provide training and infrastructural support to farmers in seed technology, in order to improve the physical and genetic quality of farmer-saved seed.

f) Develop approaches to support small-scale, farmer-level seed distribution, learning from the experiences of community and small-scale seed enterprises already underway in some countries.
g) Seed quality of farm-processed seed can be as good as and often better than certified seed if farmers take the first step by selecting the right variety, controlling purity with good rotation and follow standard agronomic practices to achieve disease and weed control. They can choose a mobile seed processor that can offer the equipment, management and expertise to achieve the standard.

14.3.2 Seed Production

- The plants grown from the seeds will have similar characteristics to the parent plants, unless the parent plants come from F1 hybrid seeds. Seeds should be selected from strong and healthy plants to harvest and save.
- It is very important to remove unhealthy or diseased plants from the field as soon as they are noticed. Also try to remove plants with undesirable characteristics from the field before they flower and pollinate other plants, but make sure that there is a diversity of characteristics in the field.
- If a farmer wants to develop or introduce specific characteristics in a plant, they can do this by controlling the pollination of plants for seed production. To combine desirable characteristics in plants, the farmer can transfer the pollen from a chosen individual plant to fertilise another chosen plant. For plants such as maize, which are usually wind-pollinated, the farmer can shake the male flower over the female flower to transfer the pollen.
- If plants are being cross-pollinated for particular characteristics, the farmer must stop the flowers being pollinated by pollen from plants with other characteristics. This can be done by isolating the plants.
- Provide isolation for crops as prescribed.
- Seeds must be dried to the prescribed levels before storing them to improve their storage life. This is because moisture in the seed may encourage mould, bacteria or other pests and diseases affect seed viability.
- Seeds should not be dried too much or too rapidly as they may crack or lose their ability to germinate. They can be dried outside in the morning sun or partial-shade, but should not be left in strong sunlight.
- To dry seeds, spread them out thinly on paper, cloth, flat basket or plate in a warm place off the ground. They should not be dried on metal as this may become too hot. Turn them over several times a day to ensure that they dry evenly. When the seeds do not feel damp or stick together they are likely to be ready for storage.
- Any seeds that are immature, broken, diseased or infested with pests should be taken out. Stones, dirt and seeds from other plants should also be removed.
- Winnowing can remove smaller light contaminants such as dust, weed seeds and dry leaves. To winnow the seeds, place them in a large flat container and toss them into the air when there is a gentle wind, then catch them in the container. The light contaminants will be blown away by the wind.

14.3.3 Seed Certification

- To encourage decentralised seed production, the 'truthfully labeled' designation could be used as an alternative to the existing system of centralised public certification.

In this case, no field inspection is made, producers are wholly responsible for seed quality and are required to describe certain quality aspects on the label (Tripp and Van der Burg, 1997). However, under such a system, there is a need to develop enforcement mechanisms that might operate by involving individuals (possibly extension agents) who have been trained by the public certification agency in field inspections for artisan-quality seed, or by shifting the responsibility for quality control to an autonomous or local-level public institution, including seed-certification agencies. In both cases, producers should pay for field-inspection services.

14.3.4 Seed Storage

- Seeds must be stored in a way that prevents them from being attacked by pests or diseases, and that maintains their quality. Some seeds can be stored for a long time without losing their germination rate, and others can only be stored for a few months. This depends on the type of seed, the moisture content of the seed and the storage conditions. Good storage conditions for seeds are: low moisture, low temperature, low light, protection against rodents and protection against insect pests and diseases.
- High temperatures can encourage biological activity in the seeds and shorten their storage life, particularly if there is any moisture in the seeds. Bright light can also be damaging to stored seeds. Seed containers should be kept in a cool area and out of direct sunlight.
- To keep rodents such as rats and mice away from seeds, they should be stored in a clean, hygienic area. The floor should be swept so there are no scraps of food that may attract rodents. Seed containers should be well sealed and, if possible, kept off the ground so that rodents cannot get in. Sometimes seeds are stored in specially built huts that are raised off the ground.
- Storage weevils, fungi and bacteria can infest seeds when in storage and damage them. Only seeds that are free of pests should be stored. Weevils, fungi and bacteria start to multiply in warm and moist conditions. To prevent this from happening, the seeds should be kept dry and cool. Appropriate pesticides/substances may be mixed with the seeds to help prevent pests and diseases. Mixing the seeds with clean, dry sand and filling the container will prevent weevils moving around.
- The quality of the seeds affects how well they will store and their ability to germinate and grow well in the field. Testing the seed before storage ensures that only good-quality seeds are stored. A germination test gives an idea of the proportion of plants that are likely to grow from a certain quantity of seed, and will show how many seeds must be sown in order to obtain the desired number of plants. Use between 10 and 100 seeds, depending on how many seeds there are.
- To test the germination rate, place the seeds some distance apart on a clean damp cloth or paper towel. For large seeds it is better to use sterilised soil. Soil can be sterilised by pouring boiling water over the soil to kill germs. The seeds should be placed somewhere warm, but out of direct sunlight. Keep the seeds damp, but not too wet, by sprinkling with water or covering with a clean damp cloth or paper towel.
- If none of the seeds have germinated, it may be necessary to leave them for more time, keeping them warm and damp. If most of the seeds have germinated and have healthy-looking roots and shoots, the rest of the seeds from that harvest should be viable and suitable for storage and planting. If less than half of the seeds have germinated, or if many of them are unhealthy, the rest of the seeds from that harvest are probably also

unhealthy with low germination rate. The farmer may decide not to store these seeds. If seed is in short supply, these seeds may still be stored and planted, but a note should be made that they are not good-quality seeds. It may be useful to test the quality of seeds before storage, and to test home saved seeds and seeds that have been bought or exchanged, before planting them.

14.3.5 Developing a Community Seed Programme

- The level of response from farmers to development initiatives varies from one place to another. While farmers do become self-reliant within a few seasons, some of the factors motivating them as seed growers include a good harvest and increased incomes from sale of seed. A poor harvest in the first season though can discourage farmers and lead to them giving up.
- A minimum of 5 years is required to develop a sustainable community seed programme. The first 3 years should focus on capacity building; such as technical training in seed production, business skills, group dynamics, leadership and getting farmers to understand the seed production process.
- The last 2 years should concentrate on exit strategies or final handing over of the management of seed production to the community. Some of the important activities during this last stage include taking farmers on an orientation visit to places such as research stations and gene-banks (for seed sources) and the State Seed Certification Agencies (SSCA). This acquaints farmers with certification procedures and expenses. In addition, seed producers should visit seed companies and other service providers (e.g. NGOs) as potential market outlets. A study visit to other more experienced seed growers associations would be of benefit to new seed growers.

14.3.6 Steps in Developing a Community Seed-System Module

A basic model for developing a community seed programme detailed in the following text is the principal model and has universality in developing community seed systems in semi-arid tropics. Even otherwise, a model developed for a specific area/village/region may not yield the same result (Dixit *et al.,* 2005), because of variation in the willingness of stakeholders, crops and varieties grown, climatic conditions, socio-economic effects and possible biotic factors.

14.3.6.1 Reconnaissance Survey

After identifying areas of operation, the NGO or project implementing agency (PIA) should carry out a reconnaissance survey on seed needs assessment (SNA) (Ravinder Reddy *et al.,* 2006). This is done as a series of participatory dialogues to engage communities in the problem diagnosis on all matters relating to seed and to achieve the community's commitment to act and develop its own solutions. The SNA will also identify knowledge gaps that can be corrected during training. Still more, the SNA should assist communities in developing an action plan on what needs to be done, while remembering that the role of the NGO is only to facilitate this process.

14.3.6.2 Participatory Selection of Crops/Varieties

It is the role of the communities themselves to decide on the crops and varieties to be multiplied. There is a tendency for farmers to select only improved varieties at the expense of other important local varieties. Facilitators should check that this pattern

does not persist. Farmers should be encouraged to select a good mix of crop types (crop diversity). Locally adapted varieties would be ideal in the first year. These tend to increase chances of success since farmers already have adequate experience growing them. The NGO should be proactive in promoting farmers participatory selection of varieties/crops for a particular area/ region/village with desirable characters (Dixit *et al.*, 2005).

14.3.6.3 Selection of Seed Growers

Once the crops for multiplication have been identified through farmers' participatory selection and agreed upon, then communities can select individuals who they feel should become their seed growers. Since food legumes are known to be conserved and multiplied mostly by women, it is only appropriate and advantageous that seed production of such crops be done by them. To help farmers carefully select their local seed growers, the NGOs can help facilitate a process developing criteria for selecting seed growers. Some suggested criteria are:

- Should be resident of the village
- Should be a farmer with land holding
- Must be trustworthy
- Willing to attend training programmes without fail
- Should be friendly in nature and approachable by others
- Inclination to put sincere efforts
- Must be willing to work in a team
- Experienced in growing one or more crops intended for multiplication
- Must be honest and willing to repay seed loans

Having a set of criteria helps farmers choose seed growers correctly without bias. Experience has shown that where an NGO decides to interpose and select farmer seed growers, other farmers have had to secure seed for them instead.

14.3.6.4 Capacity Building

After seed growers have been identified, technical training should follow. The seed growers are trained in basic seed-production techniques including rules and regulations including seed certification methods, seed health management and seed storage management. Training is enhanced when followed by an educational tour to areas where similar programmes exist. This is farmer-to-farmer learning. Farmers must be trained in business skills and some basic group dynamics and leadership.

As with all farmer-training, the trainer should be conversant with the principles of adult learning and facilitation skills. Training can be conducted by competent extension officers so long as they fully understand the basic seed production standards and provisions in the Seeds Act of 1966, for seed quality control.

14.3.6.5 Procurement of the Basic Seed and Distribution

The NGO or farmers need to secure the basic seed (foundation seed) for their seed production activities (Ravinder Reddy *et al.,* 2006). Basic seed can be difficult to secure. Therefore, start searching for a proper seed source much before the start of season. However, where poor weather has affected the growing season, it would be advisable to provide seed for the following season. It is advisable to subcontract breeders recognised by government authorities or research organisations to produce the basic seed in

specified quantities as a means of ensuring seed supply for farmers. Contact arrangements may be worked out.

In the absence of the basic seed, a seed grower can plant certified seed but only for one season. Thereafter, farmers must secure the basic seed for quality seed and long-term benefits.

14.3.6.6 Formation of Seed Growers' Association

Some seed growers certainly prefer to work as individuals but, in seed growing, the formation of an association has the following advantages:

- Registration is cheaper for a group than for individuals, or self-help groups can take this activity right away without any registration.
- It is cost-effective to work as a team when procuring the basic seed and selling seed – there is the benefit of bulk buying and selling.
- Group contributions can be used for paying for activities such as crop inspections, seed sampling and testing.
- During the early years of seed growing, the team is important for providing mutual support, encouragement and a collective voice.
- However, for farmers to work effectively as a group, a needs assessment can determine whether they need to be trained in group dynamics, leadership, record keeping, conflict management and business skills.
- The seed-grower association would be required, in the longer term, to mobilise funds to sustain their seed-growing activities.

14.3.6.7 Seed Marketing

- The success of a community seed project lies in the ability of the seed growers to sell their seed. Some farmers have used field days, weekly village markets, village local market days, as a way of advertising the available seed to fellow farmers. Others have used public meetings and ceremonies in their villages to sell the seed. Seed growers should be innovative in adopting ideas that are workable within their rural setup. Seed growers, however, should be careful not to price their seed beyond other local farmers' willingness to pay.
- Wherever possible, help establish a credit scheme such as a revolving fund. This will enable community-based organisations to buy up seed from seed growers that will then generate new loans for resource-poor farmers. Some farmers do loan seed to other farmers, to be repaid later in the form of grain, labour or livestock.
- After selling off their produce, farmers should be encouraged to save some of the income for purchasing new seed, and covering other overheads with the next growing season.
- Many development projects have used community-level seed production as the starting point for commercial seed development. Results have been disappointing, with little commercial sustainability. Reasons for lack of success are twofold – inattentiveness to transaction costs (for making contracts for source seed, ensuring quality control and obtaining information) and a lack of experience and resources for marketing. Community-level seed projects need more appropriate goals to be successful, such as testing and disseminating new varieties, developing farmers' experimentation capacities and forming better links between farmers and researchers.

Success Story in Post-Rainy-Season Sorghum

To enhance the on-farm productivity and to develop a sustainable integrated post-rains sorghum seed value chain, the consortium of ICRISAT, ICAR, state governments, private, public and people institutions – the Directorate of Sorghum Research, Hyderabad, Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani and Mahatma Phule Krishi Vidyapeeth (MPKV), Rahuri, Krishi Vignana Kendras (KVKs), State Seed Development Corporation (Mahabeej), National Seeds Corporation (NSC), private seed companies, and farmers' associations (FAs) – aimed for convergence of individual resources and knowledge to increase crop productivity and farmers' incomes by reducing the gap between on-station sorghum yields (2.5 – 3.0 t ha^{-1}) and farmers' yields (0.75–0.58 t ha^{-1}) by adding value to grain and stover and by providing market linkages. From the HOPE project that commenced in 2009, more than 300000 farmers were benefitted directly and indirectly through project interventions. The seed consortium developed a work plan to produce 29000 tonnes of improved varieties of seed to meet the requirement of 2.9 m ha in Maharashtra in 4 years. In the first 5 years of project implementation, the project directly covered 33000 farmers, and the impact of the interventions reached more than 300000 farmers in Maharashtra. The implementation of technologies led to significant increase in grain productivity (by 39%) and stover productivity (by 29%) in project villages. The early adoption study results indicated that the HOPE interventions enhanced technology adoption rates, reduced the yield gaps (by 30%), increased the productivity and gave higher returns to farmers (36–41%). They also indicated that, for every single farmer covered by HOPE project directly, five to six non-HOPE farmers benefited.

14.4 The Alternative Integrated Seed-System Model

The alternative seed-system model envisages integration of formal and informal seed systems to achieve the objective of providing quality seed of self-pollinated crop (improved varieties) at the right time and at reasonable prices to small-scale farmers. The model can be implemented in two steps.

14.4.1 Step 1

This involves farmer-participatory selection of improved varieties (Figure 14.10). Interested and resourceful farmers should be identified in the project villages to take up demonstration of improved varieties under the guidance of scientific staff enabled by consortium institutions. The assumptions for Step 1 are: (i) resourceful farmers are capable of imbibing technology faster – along with the capacity to absorb shocks, if any – than small-scale farmers; (ii) external finance is not required, and resourceful farmers can absorb expenses pertaining to seed production; (iii) resourceful farmers can afford to take a risk in conducting the trials; (iv) the general tendency of small farmers is to follow examples set by big farmers and village leaders; and (v) the word of resourceful farmers on improved varieties and yields spreads easily in the village, and hence dissemination of results is faster and more effective.

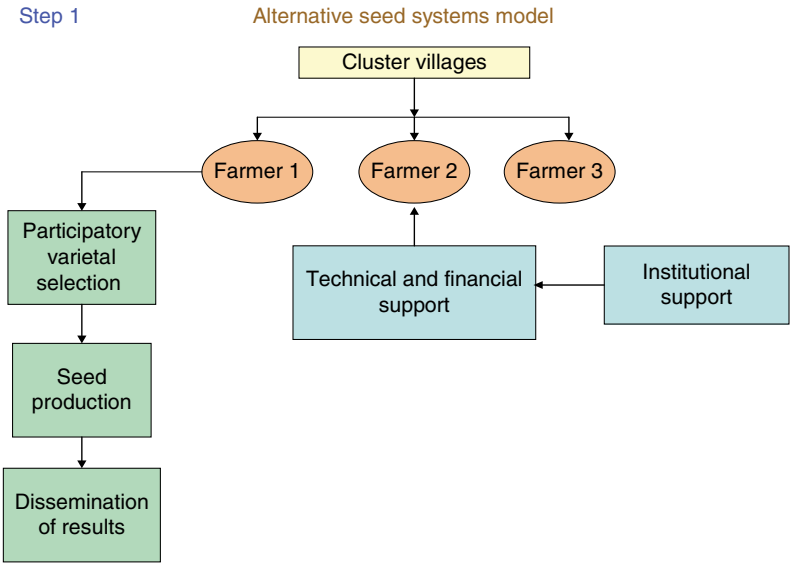

Figure 14.10 Step 1 for the alternative seed system model. *Source:* Ravinder Reddy *et al.* (2007). (*See color plate section for the color representation of this figure.*)

14.4.2 Step 2

The experience gained in Step 1 relating to the performance of improved varieties then is discussed in village assemblies (*grama sabhas*). The activities to be carried out in Step 2 should be discussed in focus group meetings in all the nucleus villages. Seed produced in the previous season (Step 1) should then be distributed to other interested farmers to grow in the next season on the principles of the village seed-bank concept, (Step 2; Figure 14.11). Village seed bank committees (VSBCs) should select seed growers (farmers) for the next season in the nucleus villages.

After the focus group meetings, stakeholders in the village belonging to VSBCs will be invited to invest in the VSBs as a micro seed enterprise for procuring seed produced in the village and storing it in the village seed bank for sale in next season. This will help to derive two-pronged benefits to the communities in the form of dividend for the SHGs and good-quality seed supply to farmers.

14.4.3 Sensitising Stakeholders

The concept of village seed banks is to have discussion elaborately in grama sabhas to sensitise the stakeholders. Farmers need to be convinced about self-funding for the procurement of seed and storage of seed as it needs investment.

14.4.4 Formation of Village Seed Bank Committees

The main function of these committees is to help reduce costs on seed production and delivery of seed and, at the same time, help farmers reduce their individual cost of production, processing and marketing. Once they become self-reliant, the associations serve as useful mechanisms to broaden the outreach of development programmes at little or no additional cost. They help build rural social capital by establishing self-help

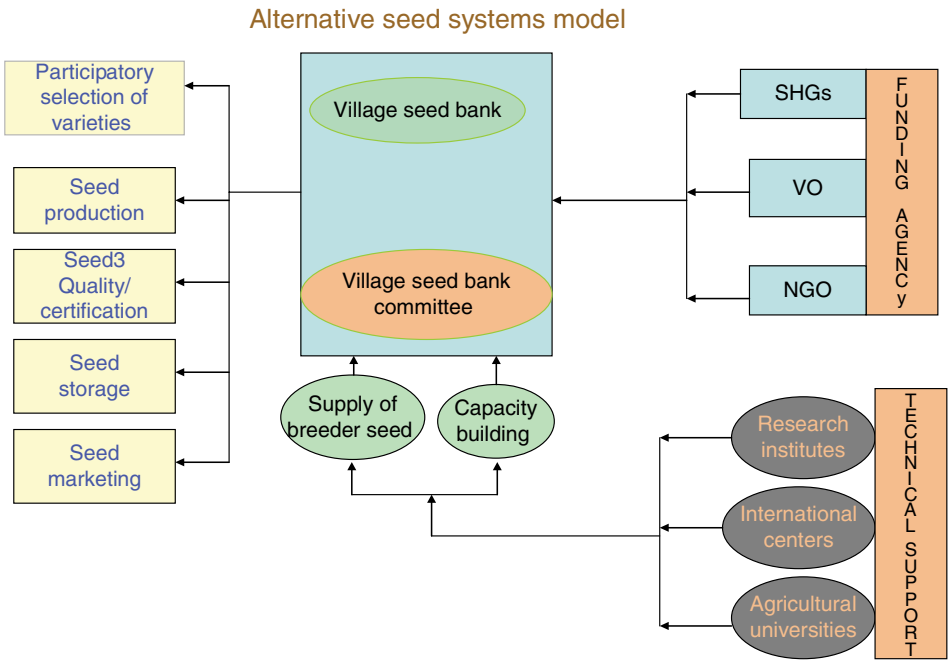

Figure 14.11 Flow diagram showing the organisation of a village seed bank. *Source:* Tonapi *et al.* (2012). (*See color plate section for the color representation of this figure.*)

linkages and encouraging broad-based collective action on village-level seed enterprises. The following guidelines may be used for developing and strengthening seed bank committees:

- Make farmers understand the advantages of associations.
- Allow all sections of the farm community to join the project.
- Understand small farmers' strengths, potentials and weaknesses in procuring seed.
- Empower women farmers (SHGs) to join the association to increase their potential in organising and investing in developing micro seed enterprises.
- Link farmers' associations to research institutions/organisations for procuring foundation seed for seed production.
- Build capacities of farmers in crop production, production of quality seed and scientific storage methods.

The concept of village seed banks (VSBs) when taken by enthusiasm by the self-help groups (SHGs), village organisations (VOs) and farmer groups, the proposal for constituting a village committee to manage the seed bank can be taken forward by the village *sarpanch* (village head) by conducting a grama sabha for electing the seed bank office bearers and members. Presidents of SHGs become members of VSBCs with 30% representation and participate in the selection of the other members and office-bearers. The committee members then need to be trained in various activities of cooperative societies (such as rules and regulations, book-keeping, accounts, audit, electing the executive body and tenure of the committee, etc.). The roles and responsibilities of the VSBCs need to be charted out during the gram sabhas, as follows: (i) selecting

seed producers; (ii) procurement of seed from seed producers; (iii) selecting proper storage space in the village; (iv) fixing the procurement and selling prices of seed; and (v) mobilising funds by promoting memberships and investment in the VSBs. The VSBC can then pass a resolution to ensure the quality of seed and redistribution of procured seed to the village-member farmers. Their responsibilities also include decisions regarding allocation of seed quantities to each farmer in the nucleus village and satellite villages in the cluster.

14.4.5 Farmer-Participatory Selection of Varieties

To promote uptake of improved varieties having farmer-preferred characters and market traits, foundation seed of selected varieties could be procured from various research institutions (consortium partner institutions) and seed is provided at subsidised rates to selected farmers to take up on-farm trials in comparison with their local varieties with the assistance of the village representatives. These varieties need to be evaluated along with the local variety in farmers' fields in the nucleus villages. Seed thus produced shall be shared with other interested farmers for sowing in the forthcoming season.

At the end of the season, VSBCs, VOs and the farmers need to be involved in the evaluation of the varieties based on yield, fodder value, tolerance to moisture stress and other varietal characters such as tolerance to pests and diseases. These trials provide an opportunity for the selected farmers to evaluate the varieties under their management conditions and to make a selection using criteria determined on the basis of their preference for specific traits. Regular monitoring visits have to be undertaken to the trial sites during the cropping season and off-type plants have to be removed before harvest. Farmers will then observe different varietal characteristics (genetic and morphological) expressed by the varieties grown in their fields. On-field meetings need to be conducted at the end of the cropping season to document the traits preferred by the farmers.

Demonstrations, field visits and field days shall be used to provide extension advice and training in pre-harvest crop management to the collaborating farmers and the CBOs. Farmer-participatory selection of varieties shall then be conducted during farmers' field days where men and women farmers will be grouped separately and their preferences documented. The criteria used by the farmers for the selection of varieties based on a combination of the attributes should also be documented.

14.4.6 Capacity Building

Imparting training to stakeholders is a part of each activity to strengthen farmers' capabilities to tackle the situation technically and manage through appropriate decisions. A number of training programmes need to be conducted on improved production techniques such as method of sowing, sowing by seed-cum-fertiliser drill, inter-cultural operations, optimum plant population, spacing, seed storage technology, integrated pest management (IPM), etc., in the project villages to enhance production. On-farm training programmes also need to be organised for focus groups in the cluster villages during field visits. A lot of emphasis shall be given to educate farmers and develop awareness on improved method of cultivation. Young educated farmers should be given printed technical information (bulletins, flyers and posters) on improved cultivation practices, seed production and certification, integrated pest and disease management (IPDM), grain storage methods and management.

14.4.7 Institutional Linkages

The pre-project studies (baseline survey) need to be conducted to have the overall dimension of productivity constraints related to:

- Farmers' institutions
- Improved production technologies
- Access to improved-cultivar seeds
- Access to institutions

The interactions with farmers and the project team's previous experiences, will help us decide whether farmers' associations are viable platforms to bring farmers together, build their capacities and enable them to gain access to resources, inputs (seed) and markets. This would directly help them in reducing uncertainty and transaction costs, and empower them to make choices relating to the feasibility, productivity and profitability of village-level seed enterprises. It would also help to pinpoint asymmetric access rules, and allow farmers to raise their voice and be heard.

Evidently, improvement of farmers' livelihoods depends on the strength of their coming together. Access to resources is influenced by the extent to which farmers are organised and the institutional arrangements available, and finally the contextual social and political structure that prevails. Farmers' organisations, therefore, would have a vital role to play in rural change. Thus, we shall have enabled systems to help increase farmers' access to improved varieties and availability of seed and improved production technology that can improve farm productivity. This role was in the past held by agricultural extension services and research institutions. Now public spending on extension and research is shrinking, and institutional changes, such as privatisation of farm services, have thrown it open to many new actors.

Rural communities are often heterogeneous in their technical demands – apart from the fact that many local decision-making systems are not well-organised, or are dominated by elites of the local area. Farmers' associations appear as an attractive approach for articulating such demands. Few areas that need to be identified for immediate collaboration are based on developing a common understanding of the issues of seed availability and technology development for enhancing productivity as they relate to the needs of the rural poor – for instance, sharing of experiences between scientists and farmers, higher levels of coordination with various research institutes, NGOs and KVKs, for ongoing field operations and support for initiative-linked activity, focusing on the involvement of various institutions to interact with farmers' associations and linking them to development of farmers' learning platforms. Village seed bank committee members are thus trained and linked with various institutions like Regional Agricultural Research Stations (RARS) and local NGOs for the supply of breeder seed and technical backstopping. For procedural and legal advice on farmers' associations, they can be linked with cooperative societies to ensure administrative sustainability.

14.4.8 Funding

To sustain the VSBs, regular inflow of finance is essential for the procurement of seed from seed producers and storage in warehouses till the next crop season and to meet interest on the capital raised. VSBCs need to be strengthened in managing seed banks as a micro seed enterprise through investments from seed bank members, committee office-bearers, and SHGs. A micro seed enterprise business model can be developed

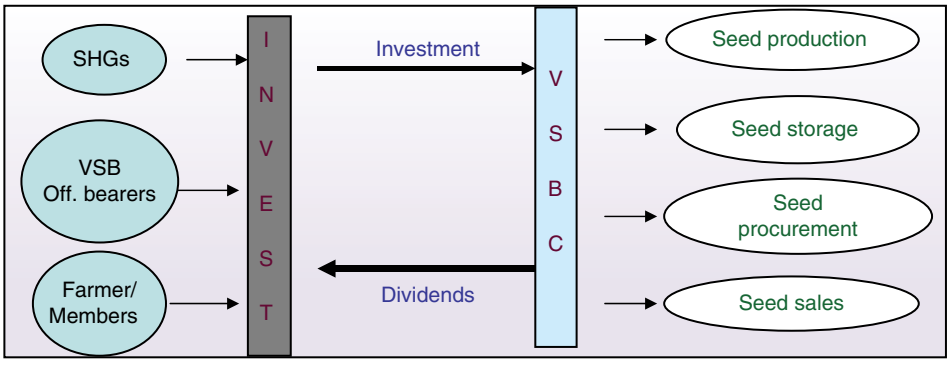

Figure 14.12 Fund flow diagram. *Source:* Tonapi *et al.* (2012). (*See color plate section for the color representation of this figure.*)

(Figure 14.12) to attract investors in the village, especially SHGs. These SHGs can get loans from scheduled banks at a low interest rate (0.25%), and they can invest in VSBs as a profitable venture. Apart from this, SHG members who are also the members and office-bearers of seed bank committees are responsible for managing VSB activities by involving themselves from the beginning of the venture. This addresses the sustainability of VSBs by involving farmers in production, procurement, storage and distribution of seed. Variation in the procurement price and selling price of seed in the market has a wide gap because production, grading, transportation and storage take a major chunk of the selling price owing to the bulkiness of the seed that farmers produce. No private seed company may show interest in trading bulky seed, as profit margins are very low. Taking advantage of this factor, seed production, grading and storing of seed within the village by farmers have a major sliding advantage in this model. Hence, it may be profitable as a micro rural seed enterprise.

14.4.9 Advantages of Village Seed Banks

- Availability of seed of improved varieties in sufficient quantities within the village.
- Assured and timely supply of seed material to farmers.
- Decentralised seed production.
- Availability of improved-variety seed at lower prices.
- Improved seed delivery to resource-poor farmers.
- Reduced dependence on external seed sources and effective curbs on spurious seed trade.
- Good opportunity for SHGs to invest and develop a village seed enterprise.
- Encourages village-level trade and improves village economy.
- Social responsibility of seed production and delivery system.
- A step toward sustainable crop production.
- Avoid introduction of diseases carried through seed (seed-borne pathogens) that is produced and imported from other agro-ecoregions.
- Scope for farmer-participatory varietal selection and feedback to the scientific community on the performance of cultivars.
- Availability of true-to-type varieties and healthy seed within the reach of farmers at affordable prices.

- The probability of sustainability is high because involving farmers from the beginning of VSB establishment, seed production, storage and marketing through their own investment and sharing the benefits.

14.4.10 Constraints of Village Seed Banks

- Willingness of farmers to adopt quality seed-production practices.
- Additional investment for inputs in seed production.
- Buy-back assurance to farmers from FA/SHGs/NGOs.
- Proper seed-storage facilities and management at village level.
- Availability of funds with FA/SHGs/NGOs for seed procurement, packing, storage and transportation.
- Fixing minimum support price for seed procurement.
- Technical support for seed production and its monitoring.
- Responsibility of quality-control aspects and monitoring of seed production.
- Availability, access and procurement of breeder seed from research institutes for seed production at regular intervals.

14.5 Need for a Policy Framework to Build a Viable Local Seed System

Dryland agriculture in India encompasses a wide diversity of crops, from cereals to millets, minor millets, pulses, fibre and many under-utilised crops which are cultivated for subsistence farming basically for self-consumption. As the farm-saved seed constitute the bulk of the seed requirements in these areas, the cultivar and seed replacement rates (CRR and SRR) are extremely poor, and old obsolete varieties and land races still rule the roost among farmers. Thus, new varieties evolved by public and private institutions have not reached these areas. The formal sector either produce very little or none of the seeds and varieties preferred by the farmers in the dry regions. Private seed industry's domain is hybrids and high-value crops that provide higher profits to them, since seeds of these preferred crop varieties are seldom produced by them, as the poor purchasing power of the growers does not attract them either. Hence, the choicest of local varieties preferred by farmers are seldom available. The main reasons that limit the supply of quality seeds in dryland ecosystems (Anonymous, 2011) are:

- Smaller holdings, subsistence nature, low external input use and poor investments are the key issues restricting the seed production programme.
- Area restrictions imposed by the seed certification agencies and the seed production organisations do not permit the small holders to get into the seed production programme.
- Seed quality assurance other than official certification standards are not in vogue; truthfully labelled seeds are not encouraged.
- These areas frequently suffer drought or some other natural vagaries that de-motivate growers; seed-production agencies are averse to entering such high-risk areas, and normally prefer to work on the peripheries where they find better production conditions.
- Contingencies in traditional farming systems and cropping systems were not just to maintain the extra buffer stock, but also the contingent crops, varieties besides the contingent extra buffer stock.

- Therefore, there is a need for a good contingency plan to ensure the availability of seed of various crops for different sowing situations, and the availability of the same for the next year should be ensured.
- Subsidies are only allowed on the larger formal recommendation domain, new and notified varieties, released by the government – either state or central – and hence most of the farmer-preferred varieties remain out of the realm of the subsidies.

Traditional/community system of addressing a contingency situation is fast disappearing. Community participation in the government system of contingency planning and its implementation is missing. According to the proceedings and recommendations of the workshop on 'Evolving an Alternative Paradigm for Seeds Systems for Rainfed Agriculture: Revitalising Rainfed Agriculture (RRA) network' (Anonymous, 2011), the issues that need to be addressed by the policymakers are:

- How do the rainfed farmers presently handle contingency situations?
- What kind of losses are the farmers facing in the absence of an appropriate system of handling contingency situations?
- What improvement is required in existing systems?
- What should be the scale of contingency plan – community-level or state-level? Or upto what scale of activity can be handled by the community, and from when will the state have an active role in a contingency?
- Who will help the community to evolve and implement the appropriate contingency plan and required preparations?
- How can the community itself ensure the availability of seed material for a contingency situation?
- Who will produce the seed? Who will store it? What about the viability of seed?
- What roles can the organised private and public sector systems play? The general situation today is that seeds are being produced from various sources, including farmers/ICAR/SAUs/KVKs/state government/private industry, and to a certain extent by NGOs, SHGs or CBOs or institutions set up by them. One of the most critical gaps that is being felt is about how we are going to address the needs of a large variety of varied ecosystems that are not being addressed now – especially those of the harsh or less fertile areas?

14.5.1 The Role NARS Has to Play in Strengthening the Community Seed Systems

1) There should be a survey of each agro-ecosystem to develop a detailed report and an atlas of available seeds on one hand; on the other hand, assessments of the seed and varietal requirements from each area need to be compiled.
2) The ICAR/SAU system produces satisfactory source material in the form of breeder seeds, but the outreach and extension programmes are non-existent or very weak. There is no real participation of farmers in the selection of varieties that are taken up for production and correction is needed at this level.
3) The current system of seed production is heavily weighted in favour of hybrid seeds. There needs to be a definite shift of emphasis so that traditional varieties are produced without mismatches.
4) The informal seed system, which still caters to a large section of local needs, needs to be recognised by the policymakers with active intervention and support to provide

access and availability of local and traditional varieties through multiplication distribution to have better seed replacement rate.
5) Research must also actively consider and include the extant local varieties, the role that can be played by them and how they can be improved.
6) Specifically in the case of cotton, it was mentioned that there is an alarming decline in the indigenous varieties that are cultivated, and even those that have to be cultivated as a legal requirement accompanying GM crops is not being met. There is a need to specifically nurture and encourage indigenous varieties.
7) It is to be noted that there is nothing in the policy framework that is actually stopping anyone from taking up work on community seed systems. However, it is also a fact that these are not considered and recognised as fashionable/hot favourite areas to work on, and as a result this kind of work does not lead to publications and recognition by way of promotions.

14.5.2 The Role of the State and the Central Agencies

The ICAR–Agricultural Universities–KVK system has the responsibility to select the seeds and produce them at the level of nuclear and breeder seeds. After this, the responsibility of large-scale multiplication, production and distribution at a farmer's level rests with the state government. The systemic flaws at the level of the basic seeds at ICAR–SAU–KVK needs to be improved with the involvement of farmers to meet the varietal requirement.

14.5.3 The Role of Public/Private Partnership in Local Seed Availability

There is a greater need to usher in public/private partnership to strengthen the community seed systems through popularisation of farmer-bred varieties through seed-savers' groups. There is a need for having community varietal testing pilots, multiplication and promotion through seed banks in collaboration with research and development institutions. In fact, establishment of networks of community seed banks, documentation on seeds, participatory plant breeding, varietal production and marketing through seed co-operatives convergence with research and development organisations, establishment of cluster-level seed banks by federation of SHGs will go a long way in making available the choicest of the varieties to the communities in dry areas. Linking them with credit organisations for financial needs in the initial stage and with certification agencies and NARS for quality control will help in ensuring access to quality seeds.

14.5.4 Identification of the Components for Village-Based or Community Seed Production Systems

- Some major factors to be taken into consideration when developing village-based seed bank systems for use by smallholders include issues such as need assessment, policy issues, market issues, appropriate technology required, seed system studies, inputs, capacity building and funding.
- Plant breeding stands at the head of a long series of steps in seed provision. In order for the products of plant breeding to be delivered to farmers, there must be: (i) adequate, direct interaction between plant breeders and farmers, and (ii) careful attention to the co-ordination of all of the intermediate steps of seed provision.
- The nature of seed demanded by farmers differs. Large- and medium-scale farmers use markets to purchase uniform genetic materials that are highly responsive to

chemical inputs and embody specific characteristics (e.g. colour and uniformity of grain size) rewarded by the market. By contrast, more subsistence-oriented smallholders may value characteristics such as drought tolerance, early maturity or good storage characteristics more than fertiliser responsiveness. Because of the small size of their landholdings, mixed cropping practices, and the strategy of minimising production risks by diversifying the variety base, smallholders also demand relatively small quantities of seed, but for a number of varieties of the same crop, and recycle seed over more seasons than larger commercial farmers.

- Strategies to improve seed quality must begin with strengthening the public agricultural R&D sector on a long-term, sustainable basis. It will be especially important to build the capacity to move from homogeneous seed recommendations to the development and dissemination of varieties targeted to specific agro-ecological zones and the needs of different groups of farmers. To facilitate this process, target groups of farmers should be defined more precisely, zoning of breeding plots and field trials can be improved, and management incentive systems should be developed to reward researchers and extension agents when new technology is adopted by target groups.
- Strengthening public and private extension programmes to increase farmer knowledge about the benefits of using new seed and transmitting information about farmer preferences to researchers will also help increase the demand for new seed. Initiatives that improve post-harvest product utilisation (that expand output markets) and lower production risks are also important: seed users will be willing to pay more for new seed if their expected returns from planting the seed are increased by either lowering risks or increasing their revenues. Thus, measures to strengthen the downstream sectors of the economy are as important as strengthening the seed system itself.
- Farmers need to be better integrated in every aspect of the seed system:
  - As active participants in seed research and release processes
  - As vital links in seed production and distribution through farmer-to-farmer seed exchange networks
  - As independent seed entrepreneurs producing seed for the local market
  - As contract seed producers and informed agents/seed traders linked with other private and public seed companies
- The government now has a critical but different role to play in:
  - Providing public goods that promote efficient seed-sector performance
  - Developing and enforcing regulations for a heterogeneous seed sector
  - In the short- and medium-term, facilitating linkages between formal and informal sector seed suppliers as the seed system matures
  - Direct distribution of seed or seed vouchers following disasters
- Public research and extension agencies also need to consider how farmers who may be unable to purchase seed through the market but could benefit significantly from access to varieties with improved drought and disease resistance. For crops/regions where there is currently no commercial seed market, disseminating seed directly to farmers so that they are absorbed into the traditional system of seed supply may be a more effective strategy than trying to supply it through the higher-cost market channels, if potential users are unlikely to be able to afford them.
- More recently, NGOs have also played a role in strengthening the informal seed system, providing a technical liaison with national and international research systems, educating farmers on better seed selection, storage and processing, and providing technical and financial assistance to rural seed enterprises. This support has increased

farmer access to improved varieties following the contraction of government-sponsored research and seed supply services. Two cautions are necessary, however. First, since NGO programmes are temporary, instead of relying on them to link smallholders and research organisations, creating incentives and funding for research and extension systems to link with smallholder organisations directly would be better. Second, a more careful analysis of the economics and sustainability of the smallholder seed firms being promoted by NGOs are needed.

- Farmers irrespective of landholding have draught and milch animals. Awareness about breeds and fodder is quite satisfactory due to presence of milk co-operative societies. Small- and medium-scale farmers prefer local varieties for food and feed. Also, there is a need for creating awareness and capacity building with regard to improved varieties of food-feed crops such as sorghum, pigeon pea and other forage crops (stylo, para grass and napier grass). Large- and medium-scale farmers are aware of maize hybrids and their cultivation practices. Farmers are tending towards cultivation of maize hybrids, because of high returns per unit area. Sorghum and pigeon pea crops are sown with own-saved seed by a majority of farmers across all groups. Some farmers are using F_2 generation (own-saved seed) maize hybrids with 20–30% less yield.
- The commercial demand and cultivation of fodder/forage crops in many watershed villages is weak because of a poorly developed livestock sector in which animals are kept mainly on subsistence. The demand for fodder/forage seed will depend on the development of the livestock sector in that particular village and value-added industry to livestock products. However, if the livestock sector develops, particularly in terms of value-added industries, it is expected that demand for intensive fodder cultivation will increase. This will translate into a 'derived demand' for seed, in order to meet the fodder crop requirements. The concept of 'derived demand' is useful, as it helps to explain (i) the inter-relationships between livestock development, fodder promotion and seed production; and (ii) how these factors could be used as integral components of policies supporting livestock.

14.5.5 Strengthening Stakeholders of Community Seed Systems

Specifically rural community seed programmes should be provided with technical backstopping by international, national and or state research institutes to strengthen the stakeholders, and render them self-sufficient. Measures could include:

- Farmers' participatory evaluation of genotypes suitable for a particular agro-eco-region.
- Maintenance of farmer-preferred varieties (landraces) currently being grown, as well as modern selected genotypes.
- Capacity building of stakeholders in seed-production technologies, seed health and storage management and, in general, integrated pest and disease management strategies.
- Creating awareness of improved agricultural practices and information on improved seed material suitable for their agro-ecological region is important to bring about greater food security.
- Training farmers in better selection, treatment and storage practices of seed produced from their own farms, as 80% of seed used by smallholder farmers comes from their own saved seed or local seed systems in developing countries. Training would

help increase production through better use of own genetic resources, indirectly conserving the crop biodiversity in the region.

- Training farmers in seed-health management and seed-storage methods is important to preserve the viability of seed until the next season. Seed-borne microorganisms and storage insects can make seed unproductive during storage – a major problem that smallholder farmers face. This is even more pronounced in leguminous seed, and control is particularly difficult.
- Training in selection and timely harvesting of a crop as well as post-harvest precautions are essential for good harvests.
- Making varieties developed by national, international and state research centres available to smallholder farmers. These modern varieties must be multiplied and disseminated through formal and informal seed delivery channels at affordable prices. Several strategies were implemented by ICRISAT and partners in Tanzania (Rohrbach *et al.,* 2000) and Zimbabwe (Monyo *et al.,* 2003).
- Ensuring that village seed committee members undertake the responsibility of producing quality seed. Low costs of seed can be maintained only if locally produced seed stays unprocessed and uncertified. The statutory standards of commercial seed are too expensive for the informal sector. Evolving a policy to certify village/community-based seed production without taxing smallholder farmers would offer greater scope for production of quality seed to improve the informal system.

14.5.6 Interventions Required for Developing Informal Seed Systems

In order to ensure that quality seeds of preferred varieties are accessible to poor resource farmers, a systematic pathway combining a set of activities starting from the identification of preferred genotypes to variety demand stimulation and seed accessibility must be established from the beginning. It is very clear that the crop breeding pattern and seed system arrangement have influence on the availability and seed accessibility to farmers, mostly the poor and marginalised. Therefore, imposing generic formal or private-sector-led seed systems may not be the best solution (Zerbe, 2001). In order to accelerate the use of improved varieties, some major steps are important and required:

- Farmer-to-farmer seed exchange and local seed markets function throughout the dry regions but are not adequately linked to systems for improved seed. Locally operating institutions such as NGOs, extension services, KVKs, social organisations, farmers' associations, could play an important role in improving farmers' access to quality seed. If given an appropriate enabling legal framework, such organisations could help link farmers to other seed producers, research institutions and importantly small commercial seed companies working in similar agro-ecosystems locally and regionally.
- Traditional seed systems do not fully cater to current farmer needs. Even traditional crops and varieties benefit from maintenance of source quality seed (with varietal purity and seed health). For improved or national varieties, links between farmer seed producers and sources of foundation seed are important. Even more critical are linkages that allow seed producers access to new varieties, which are not available in the informal sector.
- Farmer seed producers can be efficient and at least some have the potential to expand as specialised, small- or medium-sized local seed enterprises. Farmer associations, SHGs, NGOs, KVKs and social organisations have a potential role in promoting improvements in production, marketing and distribution systems for traditional

farmer seed producers. This may involve linkages between research organisations for technical backstopping and the formal seed sector for improved varieties. For these interventions to be sustainable, they must be based on training and market development and not on direct government subsidies.

- Sustainable, competitive seed systems require substantial re-orientation of government policies and programmes involving seed distribution. Rather than attempting to directly supply seed to farmers, government programmes will need to provide support services that allow development of formal and informal seed enterprises to respond to the market demand for seed. This essentially seeks to offer farmers a great range of choice in terms of varieties and sources of seed. Indirect subsidies may still be important for competitiveness among enterprises.
- Government programmes may focus on the development of informal seed sector linking NGOs, KVKs and farmer seed producers to sources of improved foundation seed and in helping to expand marketing systems for farmer-produced seed. Programmes will need to be vigilant in eliminating subsidised seed distribution that restricts development of sustainable local seed sector. Key to success in strengthening informal seed systems will be improving farmer and seed producer access to information on product and seed prices and market options.
- Development of alternative seed systems is eminent. The formal seed sector has shown little or no interest in seed multiplication for crops with high seeding rate and low multiplication rates. Transportation, processing, bagging and certification costs make the seed expensive for the farmers to buy. Community-based or village-based seed production and distribution schemes may have impact on smallholder livelihoods. Including local crops in the PDS may have a positive chain reaction.
- Develop separate and more localised and diversified seed standards, and alternate seed certification such as Growers Group Certification (GGC) with Internal Control System, and Participatory Guarantee System (similar to the organic certification).
- Create local professionals and pool of local human resources, create better infrastructure and logistical support, special attention to micro–stock–hypothecation, to remunerate for seed-stock retention period.
- Economy of scale and proliferation of activities as farmer collectives create and nurture the viable institutions.
- Pushing National Food Security Mission (NFSM), Rashtriya Krishi Vigyan Yojana (RKVY), Agriculture Technology Management Agency (ATMA), National Rainfed Area Authority (NRAA), etc., to include rainfed seed systems development in their programmatic intervention, and repackage 'Seed Village Concept' of NSC and GOI.
- Set research and development priorities with farmers and other stakeholders, and engage farmers and traders in the varietal testing system and their conditions.
- Avail foundation seeds preferred by both formal and local seed productions regularly;
- Engage farmers, farmers' organisations, extension services and development organisation in the intervention so that early information and awareness about promising genotypes is raised and demand is stimulated for effective scaling up.
- The farmers' seed producer-organisations need to be incorporated in the rain-fed areas, and the poor and small marginal farmers may become shareholders. These organisations should be encouraged to produce the seeds of farmer-preferred crops and varieties.
- Benchmarking the SRR for farmer-preferred crops should be undertaken.

- Develop partnership with other service providers, including traders and development partners, so that various seed-related activities are shared among partners.
- Encourage complementarity among formal and informal seed sector and, more importantly, sharing of seeds horizontally (farmer-to-farmer).
- In order to improve the quantity produced to meet the demand and increase local stock of the varieties, other yield-enhancing technologies are also required; therefore, the interventions should go beyond the seed aspects to other non-seed technologies (agronomic practices).
- In local decentralised seed systems, the grain/seed merchants are the key stakeholders in the seed dissemination and outlets for seed producers; thus, their engagement and linkages to seed producers will pay a great dividend. Facilitating linkages between farmers and a range of other actors providing seed-systems-related services is another tool to improving seed-system effectiveness.

14.6 Conclusion

An effective means of improved seed distribution is farmer-to-farmer seed exchange. This may be primed to a limited extent by supplies of improved seed from public agencies, agricultural research stations and NGOs to farmers in easily accessible villages. However, such a system is very slow. To speed up the flow of adapted improved varieties to farmers, there is a need to form a network, formal and informal or integrated seed systems between community-based organisations and research institutes, public and private seed multiplication agencies, involved in various aspects of seed production. This network will identify bottlenecks in the seed-production chain, and catalyse or instigate applied and adaptive research and policy changes that may be required to ensure rapid movement of new cultivars into local seed delivery systems, benefiting smallholder farmers and small and resource-poor farmers who need them. This approach will require continued interaction between the various institutions, policymakers and stakeholders.

An effective means of improved seed distribution is farmer-to-farmer seed exchange. This may be primed to a limited extent by the supplies of improved seed from public agencies, agricultural research stations and nongovernmental organisations to farmers in easily accessible villages. However, such a system is very slow. To speed up the flow of seeds of adapted, acceptable, improved varieties to farmers, there is a need to form a network between research institutes, agencies involved in quality control, various NGOs and community-based organisations (SHGs, farmer schools, farmer youth clubs, farmer associations) interested in various aspects of seed production and utilisation. For high-value or low-value crops, the basic farmer demand is for quality seed of improved varieties. The most economical way would be to produce seed at the village level through community-based seed systems and sell it to local communities without incurring the extra costs of processing and certification. Village-based seed banks provide an alternative solution to this problem and help farmers become self-reliant. This initiative needs organised communities, institutional technical backstopping and continued interaction between various institutions, policymakers and stakeholders to strengthen local seed systems to enhance seed productivity in the dry lands. Therefore, VSB is an efficient and sustainable model that can be scaled to suit other crops and other areas.

References

Almekinders, C.J.M., Louwaars, N.P. and de Bruijn, G.H. (1994) Local seed systems and their importance for an improved seed supply in developing countries. *Euphytica*, **78**, 207–216.

Almekinders, C.J.M. and Louwaars, N.P. (1999) *Farmers' Seed Production: New Approaches and Practices*, Intermediate Technology Publications, London.

Anonymous (2011) Evolving an Alternative Paradigm for Seeds Systems for Rainfed Agriculture: Revitalizing Rainfed Agriculture (RRA) network, in *Proceedings and Recommendations of the Workshop, January 27–28, 2011*, ICECD Campus, Bopal, Ahmedabad, organized by Satvik: Promoting Ecological Farming, Bhuj, Kutch (Gujarat).

Bantilan, M.C.S. and Deb, U.K. (2002) Grey to green revolution in India: Role of public-private – international partnership in research and development. Paper presented at the BAEAIAAE conference on 'Public-private sector partnership for promoting rural development' held at Dhaka, October 2–4, 2002.

Bengtsson, F. (2007) Review of Information Available on Seed Security and Seed Aid Interventions in Ethiopia, Eritrea, Mali and Sudan. DCG Report No. 51. Drylands Coordination Group, Oslo, Norway. Available from: http://www.drylands-group.org/Articles/1323.html (accessed 24 November 2009).

Cormwell, E., Friis-Hansen, E. and Turner, M. (1992) *The Seed Sector in Developing Countries: A Framework for Performance Analysis*, ODI, London.

Dayakar Rao, B., Tonapi, V.A., Hyma Jyothi, S. and Seetharama, N. (2004) Supply and distribution of quality seed: Need for sustained approach. Paper presented at XVII Annual Conference on Agricultural Marketing, Organised by the Indian Society of Agricultural Marketing (ISAM), Acharya NG Ranga Agricultural University, Hyderabad, Andhra Pradesh, 5–7 February 2004. *Abstract in Indian Journal of Agricultural Marketing (Conference special),* **17**, 260.

Dixit, S., Wani, S.P., Ravinder Reddy, C. *et al.* (2005) Participatory varietal selection and village seed banks for self-reliance: Lessons learnt, in *Global Theme on Agroecosystems, (Report No 17).* International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Andhra Pradesh, India, p. 20.

Evenson, R.E. and Gollin, D. (2003) Review: Assessing the impact of the green revolution, 1960 to 2000. *Science*, **300** (2), 758–762.

Friis-Hansen, E. (1992) *The Performance of the Seed Sector in Zimbabwe: An Analysis of the Influence of Organisational Structure*, ODI, London.

Louwaars, N. (1994) *Seed Supply Systems in the Tropics: International Course on Seed Production and Seed Technology*, International Agricultural Center, Wageningen, The Netherlands.

Maredia, M., Howard, J., Boughton, D. *et al.* (1999) Increasing Seed System Efficiency in Africa: Concepts, strategies and issues, in *Michigan State University International Development Working Paper*, Department of Agricultural Economics—MSU East Lansing Michigan, pp. 12–13.

Meena Kumari, K.V.S., Ankaiah, R., Tonapi, V.A. and Ravinder Reddy, Ch. (2006) Seed health status of certified and farmer seed samples of groundnut varieties in Andhra Pradesh. Paper presented at XII National Seed Seminar on "Prosperity through quality seed", *Indian Society of seed technology, New Delhi* and ANGRAU, Hyderabad, February 24–26, 2006, Abstracts (PS II-88): (Compendium of Abstracts), p. 93.

Monyo, E.S., Mgonja, M.A. and Rohrbach, D.D. (2003) An analysis of seed systems development, with special reference to smallholder farmers in southern Africa: Issues and challenges. *Paper presented at the Workshop on Successful Community Based Seed Production Strategies*, co-organised by CIMMYT and ICRISAT, August 3–6, 2003, Harare, Zimbabwe.

Pray, C.E. and Ramaswami, B. (1991) *A Framework for Seed Policy Analysis*, IFPRI, Washington, DC, USA.

Pray, C.E. and Ramaswami, B. (2001) Liberalization's impact on the Indian seed industry: Competition, research, and impact on farmers. *International Food and Agribusiness Management Review*, **2** (3), 407–420.

Pray, C.E., Ramaswami, B. and Kelley, T. (2001) The impact of economic reforms on R&D by the Indian seed industry. *Food Policy*, **26** (6), 587–598.

Ravinder Reddy, Ch. (2004) Seed systems in the semi-arid tropics of Andhra Pradesh, in *Enhanced Livelihoods of Poor Livestock Keepers through Increasing Use of Fodder,* September 2–3, 2004, ICRISAT, Patancheru, India.

Ravinder Reddy, C. (2005) Alternative informal seed systems models for seed security, in *National Partners Workshop of Fodder Innovation Project, February 25, 2005*, ILRI, ICRISAT Centre, Patancheru, India.

Ravinder Reddy, C., Gurava Reddy, K., Thirupathi Reddy, G. and Wani, S.P. (2006) Increased Adoption of seed treatment for groundnut disease management through farmers participatory evaluation': A Micro study in Kurnool District of Andhra Pradesh, India. *Manage Extension Research Review*, **7** (1), 101–109.

Ravinder Reddy, Ch., Vilas A. Tonapi, Bezkorowajny, P.G. and Seetharama, N. (2007) *Seed System Innovations in Semi-Arid Tropics of Andhra Pradesh. Fodder Innovation Project, International Livestock Research Institute (ILRI)*, International Crops Research Institute for semi-Arid Tropics, Patancheru, India, pp. 224, ISBN 978-92-9066-502-1.

Rohrbach, D.D., Mtenga, K., Kiriwaggulu, J.A.B. *et al.* (2000) *Comparative Study of Three Community Seed Supply Strategies in Tanzania. International Crops Research Institute for the Semi-Arid Tropics*, Bulawayo, Zimbabwe.

Singh, H. and Chand, R. (2011) The Seeds Bill, 2011: Some Reflections. *Economic and Political Weekly*, **46** (51), 22–25.

Tonapi, V.A., Ravinder Reddy, C., Tomar, B.S. *et al.* (2012) *Strategies to Build Viable Community Seed Systems in Dry Land Ecosystems for Sustainable Seed and Food Security in India*, Directorate of Seed Research, Kushmaur, Kaithauli, UP, India, p. 44.

Tripp, R. and Van der Burg, W. (1997) The conduct and reform of seed quality control, in *New seed and old laws: regulatory reform and the diversification of national seed systems* (ed. R. Tripp), Intermediate Technology Publications, London.

Tripp, R. (2003) *How to cultivate a commercial seed sector. Paper presented for symposium Sustainable Agriculture in the Sahel*, December 1–5, 2003, Bamako, Mali. Available at: http://www.syngentafoundation.org/db/1/447.pdf

World Bank (1998) Regional Technical Meeting on Seed Policy and Programmes for Sub-Saharan Africa (1998: Abidjan, Côte d'Ivoire) & World Health Organization & Food and Agriculture Organization of the United Nations (1999). *Seed policy and programmes for sub-Saharan Africa: proceedings of the Regional Technical Meeting on Seed Policy and Programmes for Sub-Saharan Africa : Abidjan, Côte d'Ivoire, 23–27 November 1998*. Food and Agriculture Organization of the United Nations, Rome

Zerbe, N. (2001) Seed of hope, seeds of despair: towards a political economy of the seed industry in southern African. *Third World Quarterly*, **22** (4), 657–673.

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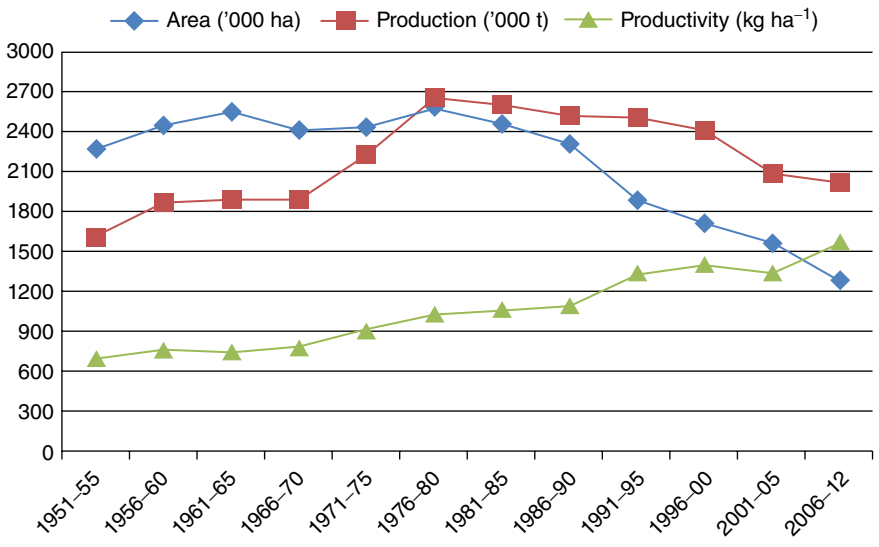

Figure 3.1 Quinquennial area, production and productivity of finger millet in India.
Source: Krishnegowda *et al.*, 2015.

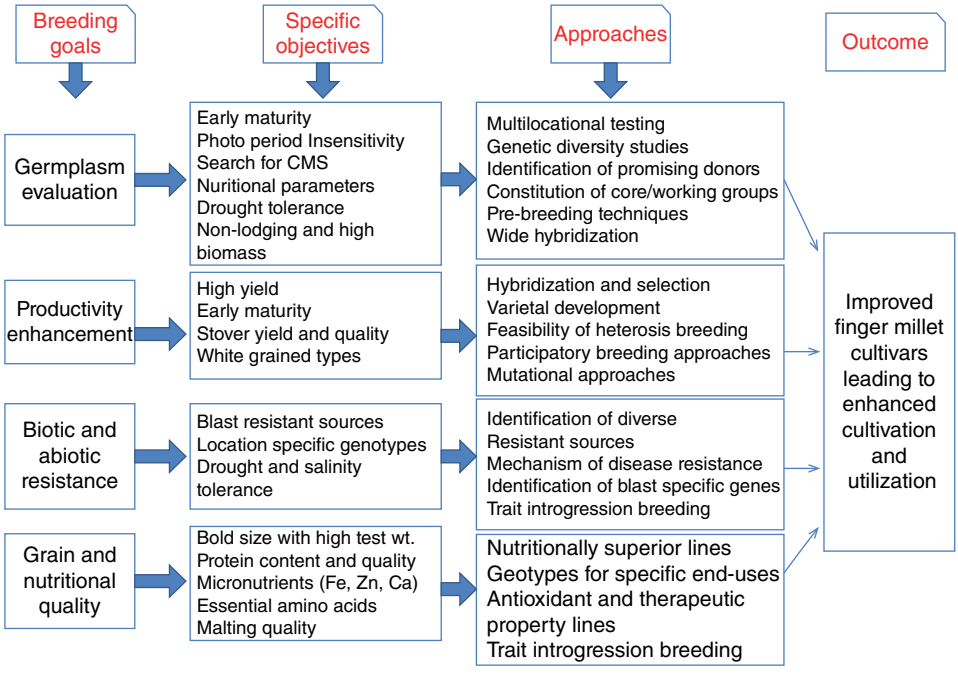

Figure 3.3 Priorities and approaches for genetic improvement in finger millet.

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Plate 4.1 Foxtail millet – field view.

Plate 4.2 Foxtail millet – a single panicle.

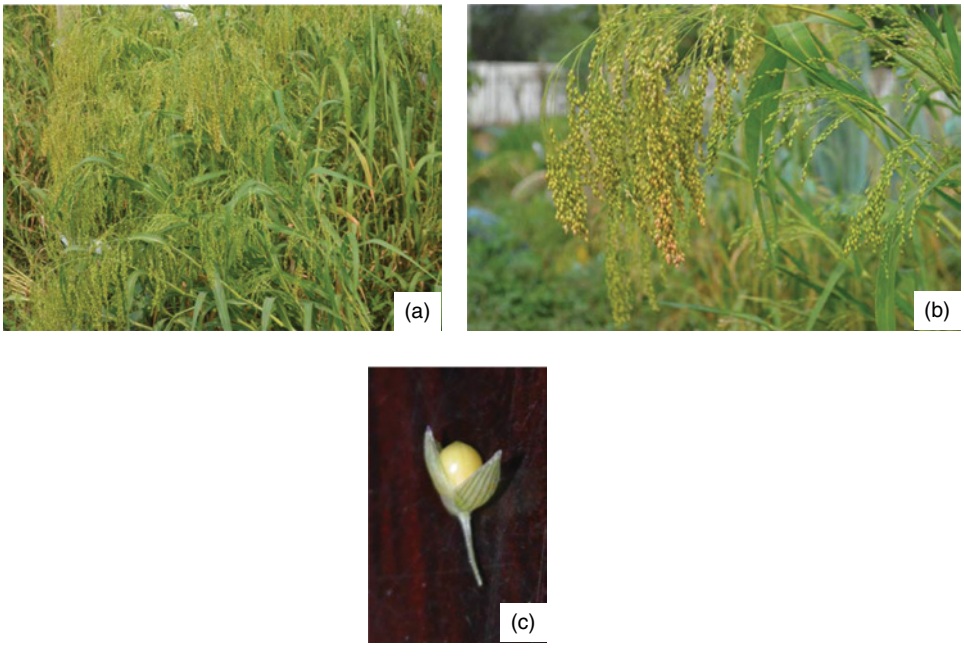

Figure 5.1 (a) Proso millet crop; (b) panicles; (c) seed enclosed in glumes and clasping lemma and palea.

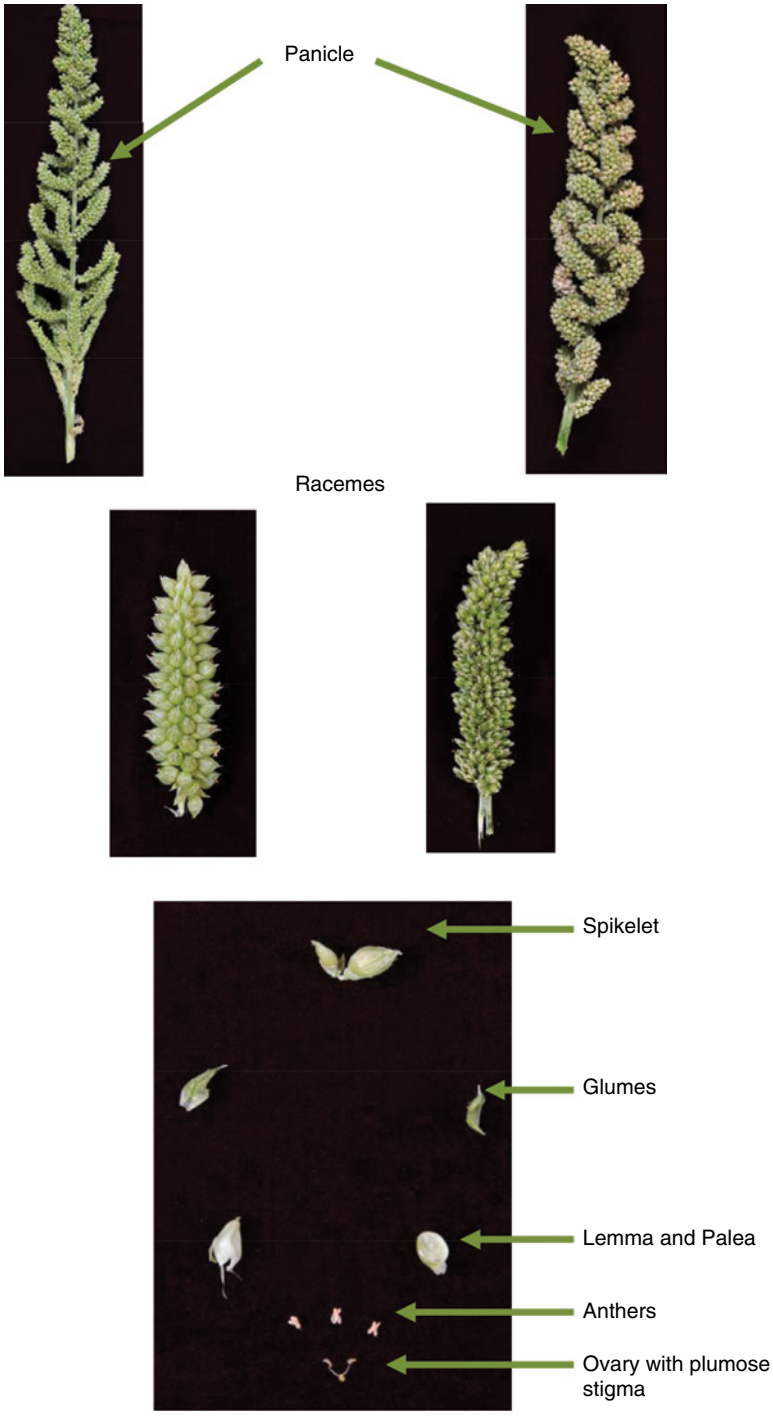

Plate 7.1 Barnyard millet inflorescence and floral parts. (Photo credit: H.S. Gawali).

Plate 8.1 Kodo millet – field view.

Plate 8.2 Kodo millet – racemes.

Figure 10.1 Sorghum shoot fly damage.

Figure 10.2 Sorghum stemborer damage.

Figure 10.3 Sorghum shoot bug damage.

Figure 10.4 Sorghum aphid damage.

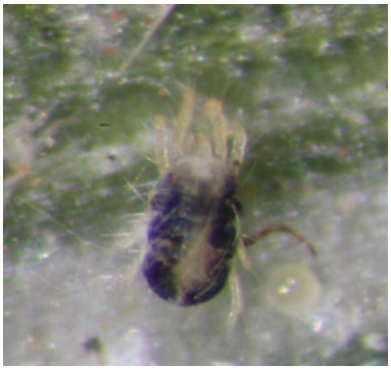

Figure 10.5 Spider mite on sorghum.

Figure 10.6 Cutworm damage in sorghum.

Figure 10.7 Sorghum leaf feeding by red pumpkin beetle.

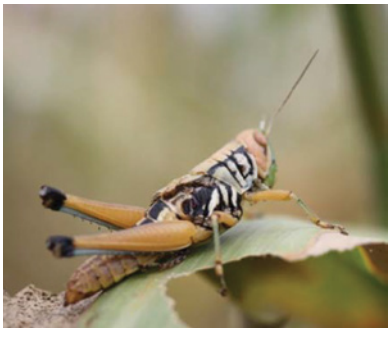

Figure 10.8 Grasshopper in sorghum.

Figure 10.9 Spodoptera on sorghum earhead.

Figure 10.10 Termite damage in sorghum.

Figure 10.11 Shoot fly damage in pearl millet.

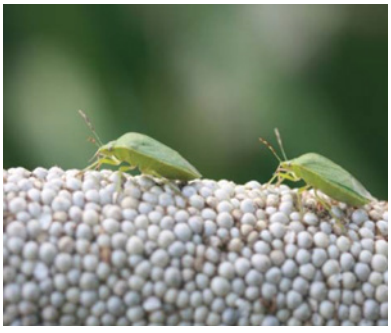

Figure 10.12 Green bug on pearl millet.

Figure 10.13 Green bug on kodo millet.

Figure 10.14 Hairy caterpillar on proso millet.

Figure 10.15 Green bug on barnyard millet.

Figure 10.16 Air-entrainment chamber.

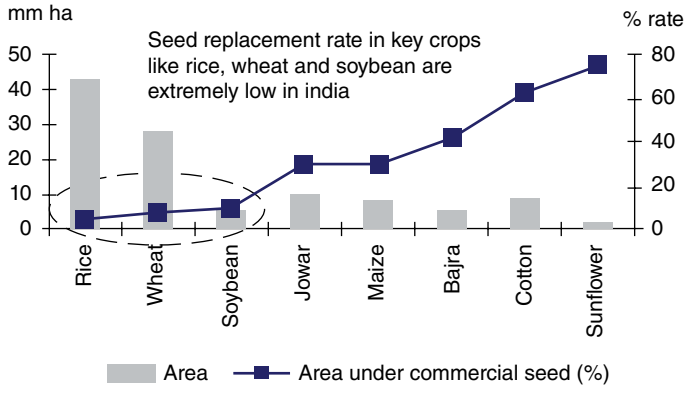

Figure 14.1 Seed replacement in key foodgrain crops. *Source:* Tonapi *et al.* (2012).

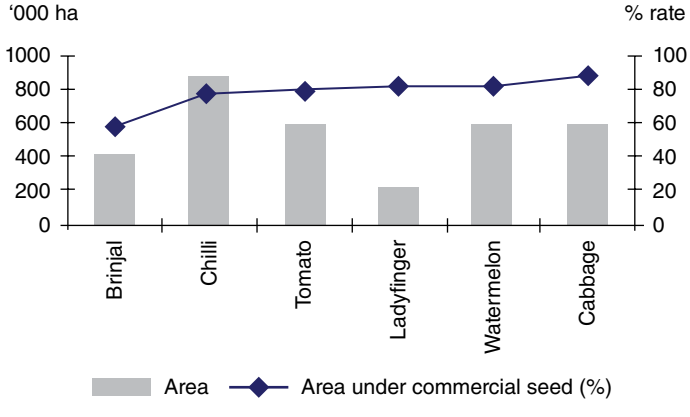

Figure 14.2 Seed replacement rate in cash crops. *Source:* Tonapi *et al.* (2012).

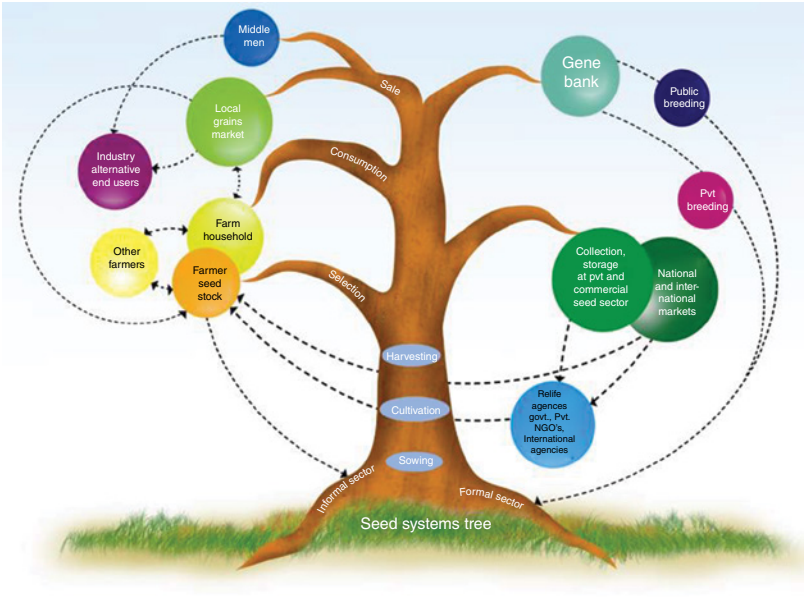

Figure 14.3 Seed systems tree. *Source:* Ravinder Reddy *et al*. (2007).

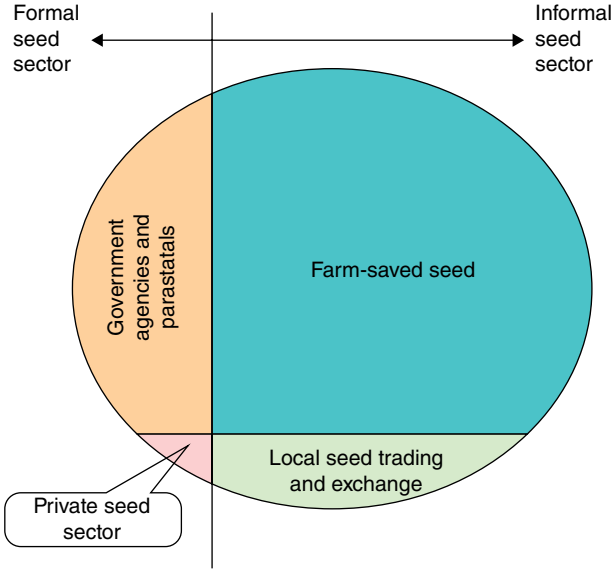

Figure 14.4 Seed supply scenario in formal and informal seed sector in India. *Source:* Ravinder Reddy *et al*. (2007).

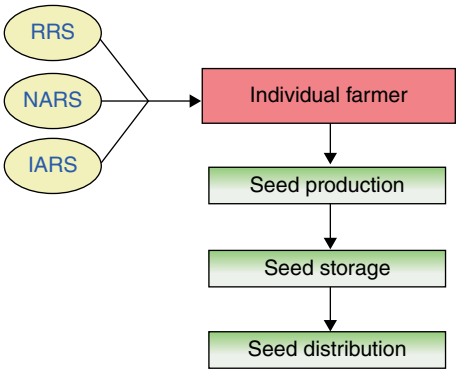

Figure 14.5 Model 1: Individual farmer as seed bank.

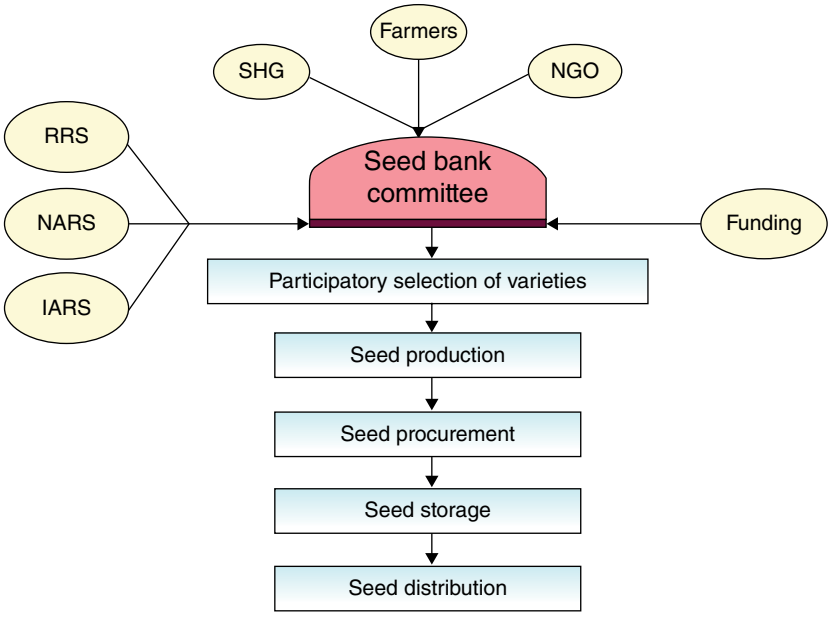

Figure 14.6 Model 2: Village based seed banks.

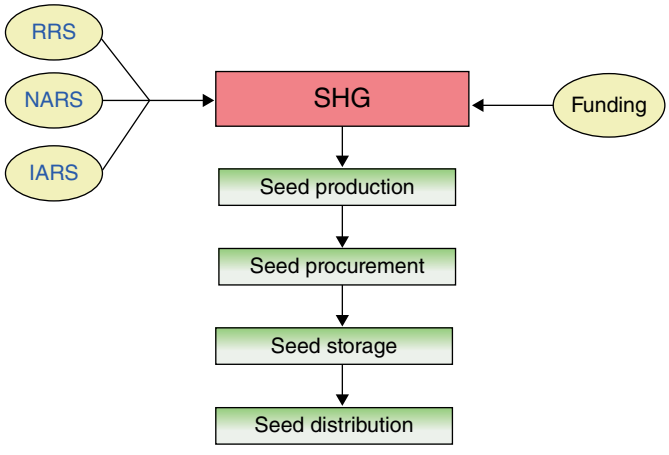

Figure 14.7 Model 3: SHG-mediated system.

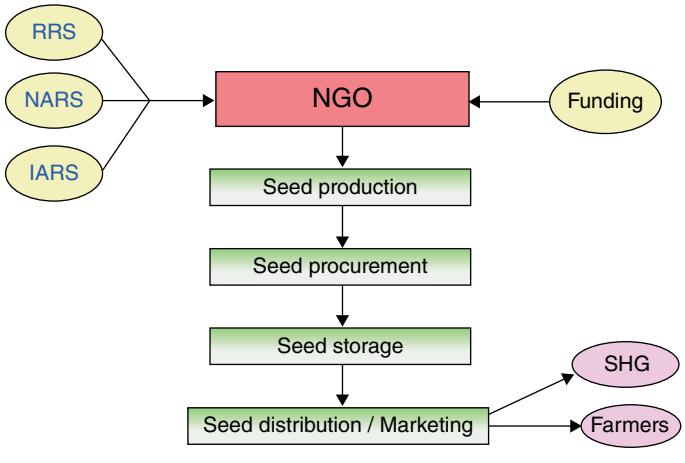

Figure 14.8 Model 4: NGO-mediated system.

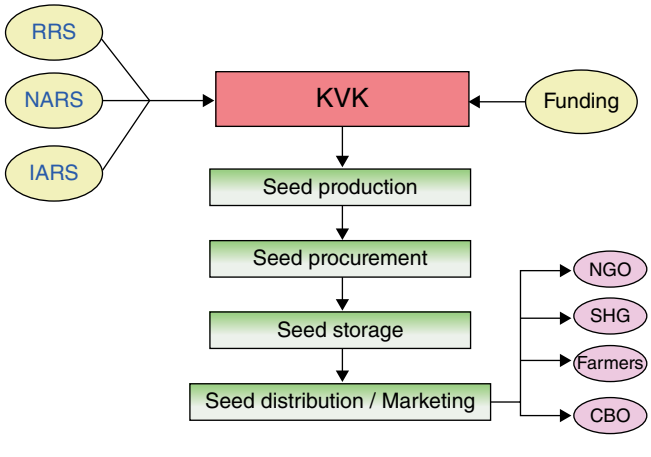

Figure 14.9 Model 5: KVK-mediated system.

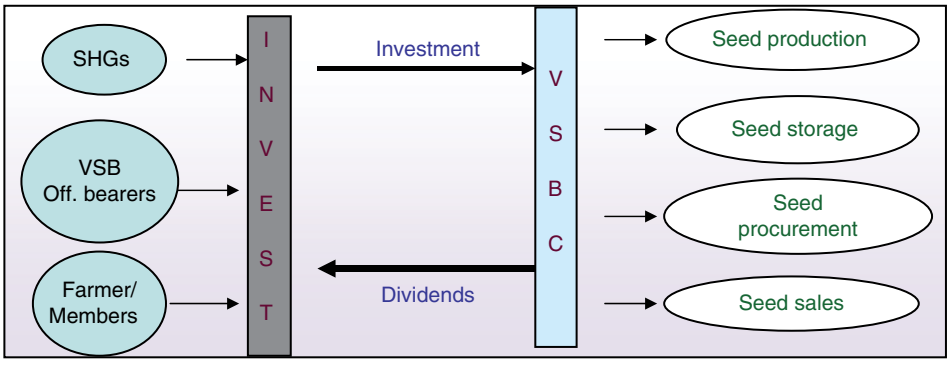

Figure 14.12 Fund flow diagram. *Source:* Tonapi *et al.* (2012).

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